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(71) Applicants (*for all designated States except US*): **UNIVERSITE CATHOLIQUE DE LOUVAIN** [BE/BE]; Place de l'Université 1, B-1348 Louvain-la-Neuve (BE). **LA DEFENSE NATIONALE** [BE/BE]; rue de Lambertmont 8, B-1000 Bruxelles (BE).

(72) Inventors; and

(75) Inventors/Applicants (*for US only*): **GALA, Jean-Luc** [BE/BE]; Countrylaan 24, B-1932 Sint-Stevens-Woluwe (BE). **IRENGE, Léonid** [BE/BE]; rue du Campanile 6/b.101, B-1200 Woluwe-St-Lambert (BE).

(74) Agents: **DE CLERCQ, Ann** et al.; De Clercq, Brants & Partners, E. Gevaertdreef 10a, B-9830 Sint-Martens-Latem (BE).

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(54) Title: ASSAY FOR DETECTING AND IDENTIFYING MICRO-ORGANISMS

(57) Abstract: The present invention also relates to an assay for detecting and identifying micro-organisms, and in particular bacteria. The present invention also relates to an assay for detecting micro-organisms, and in particular bacteria, in a sample, and for the discrimination thereof. More in particular the present invention relates to an assay for the molecular identification of bacteria according to Gram-, genus- species- and strain-specificity based on multigenotypic testing of bacterial DNA from human, animal or environmental samples.



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Assay for detecting and identifying micro-organisms

Field of the invention

The present invention relates to an assay and a method for diagnosing and identifying micro-organisms, and in particular bacteria. The present invention also relates to an assay and a method for detecting micro-organisms, and in particular bacteria, in a sample, and for the discrimination thereof.

More in particular the present invention relates to an assay and a method for the molecular identification of bacteria according to Gram-, genus- species- and strain-specificity based on multigenotypic testing of bacterial DNA from human, animal or environmental samples.

Background

In the medical and veterinary clinical setting, detection and species identification of harmful bacteria infecting biological fluids or tissues is a pre-requisite for appropriate and timely relevant antibiotherapy. Such identification is classically performed by conventional microbiological methods (culture on solid medium or in liquid phase). These conventional methods have however their own limitations.

Culture is always followed by phenotypic identification, which is based on the biochemical features of the bacteria. Usually, the whole process requires 48 to 72 hours to be completed. This period is unfortunately too long, considering the speed of bacterial growth in infected tissues and, for some bacteria, the pathological effects related the toxins that they produce. This time is also too long when bacteria are spread in the environment (aerosol, food or water contamination), where germs are able to infect humans or animals and spread rapidly on a epidemic way from an infected to a healthy body on a very short time. There is therefore a need for the rapid detection and identification of pathogenic bacterial agent(s) involved in human or animal infections or present in the environment.

A stream of studies carried out recently has confirmed that molecular identification is more efficient than phenotypic identification (Bosshard *et al*, 2003; Bosshard *et al*, 2004; Lecouvet *et al*, 2004) and genotypic definition of bacteria species has now become the gold standard (Clarridge, 2004). There is therefore an increasing need for identifying bacterial species with more reliable methods. While obvious in the hospital setting, it is also of interest of the post September 2001 era, where accuracy and speed in identification of deadly bacteria are priorities.

Aside of the time required for routine microbiologic detection, another limiting factor is sometimes the lack of bacterial growth, generating a false-negative microbiologic result. False-negative bacterial cultures are not unusual in the clinical practice, even when clinical and biological signs clearly suggest a florid and active infection (Lecouvet *et al*, 2004). This false-negativity may be due to a low organism burden, non-culturable or slowly growing micro-organisms or, most often, to prior antibiotic therapy (Trampuz *et al*, 2003; Tzanakaki *et al*, 2003). In this case, a false-negative result hampers correct etiological diagnosis regarding the bacterial origin of the infectious disease, and precludes the use of early targeted antibiotherapy. As delayed antibiotherapy may increase the risk of worse clinical outcome (Gutierrez *et al*, 1998; Yu *et al*, 2003, Lecouvet *et al*, 2004), this situation often prompts the use of empiric, broad spectrum and sometimes long-term therapy, and certainly when there is no microbiologic result.

The higher sensitivity, speed and accuracy of DNA amplification by PCR for identification of bacteria is expected to reduce the time to diagnosis, to improve the diagnostic rate, and to allow an early choice of specific antibiotic treatment. Over the last decade, this expectation has fuelled the development of numerous promising DNA assays for detecting and identifying bacteria at the species- or genera-level in human and environmental samples (Jonas *et al*, 2003 ; Palomares *et al*, 2003 ; Poyart *et al*, 2001 ; Xu *et al*, 2002).

These assays remain however restricted to single species and/or genera (Brakstad *et al*, 1992 ; Poyart *et al*, 2001 ; Vannuffel *et al*, 1998). Such restriction has various disadvantages. For instance, in the absence of any indication on the presence of bacterial agents in an environmental sample or in a biological tissue/fluid sample from human or animal origin suspected to be infected but showing no bacterial background due to the presence of a normal bacterial flora, molecular screening methods have to be applied which target the greatest as possible number of potentially pathogenic bacteria including the most feared bacteria (*Staphylococci*, *Streptococci*, *Bacillus anthracis*, *Enterobacteriaceae*, *Neisseria*, *etc...*) that could be used by bioterrorists. In this case, the use of specific markers or well-defined genera requires multiple and/or repeated testing to confirm or exclude a bacterial diagnosis. Considering the cost of this strategy as well as the limited amount DNA usually available for one sample, this is practically impossible to be performed.

In another example, in samples from tissues showing a bacterial background due the presence of a normal flora, the identification of a well defined panel of pathogenic bacteria recognized as "prior key targets" in the clinical setting considered (e.g. community-acquired pneumonia) remains very difficult.

In view of the above, there is therefore a need for the rapid detection and identification of pathogenic bacterial agent(s) involved in human or animal infections or present in the environment.

There is also a need for identification and diagnostic tools, which allow screening for the presence of pathogenic bacterial agent(s), and to detect and identify these pathogenic bacteria within a bacterial background.

In particular, it is clear that there is a great need in the art for molecular screening/detection and identification assays and methods having a range of specificity that is as wide as possible in order to quickly detect the presence of bacteria (bacterial detection step), while allowing in parallel or subsequently, to identify the present bacterial species, genera and, optionally the strain (bacterial identification step).

In a first aspect, the present invention therefore aims to provide an improved assay for detecting micro-organisms, and in particular bacteria. It is further an aim of the invention to provide an improved assay for diagnosing bacterial infection of a sample and/or tissue.

In another aspect, the present invention also aims to provide an improved assay and method for the identification of micro-organisms. More in particular, the invention aims to identify and provide a series of specific, molecular markers for the detection and/or identification of micro-organisms, and preferably bacteria, in a Gram-, genus- species- and/or strain-specific way.

Summary

The present invention relates to an assay for detecting and identifying one or more micro-organisms in a sample, characterized in that said assay comprises the use of at least two conserved molecular markers. Preferably said micro-organisms are bacteria. In a preferred embodiment, the assay of the present invention is characterized in that it comprises the use of at least one molecular marker that is conserved in Gram-positive bacteria and at least one molecular marker that is conserved in Gram-negative bacteria.

In the prior art, in order to detect the presence of bacteria in samples or tissues, extremely conserved molecular markers are generally used. The most commonly used sequences for detecting bacteria are the sequence of the gene coding for ribosomal DNA (16S rDNA gene) (Klaschik *et al*, 2002) and the 16S-23S intergenic region (Gurtler & Stanisich, 1996). However, ribosomal gene 16S rDNA does not always allow the distinction between species, as illustrated for the *Bacillus* species (La Scola *et al*, 2003). This is a major drawback in the 16S rDNA gene sequence identification method, because in some species, a sequence can be ambiguous since it does not distinguish between two closely related

clinical species but disclosing however a distinct virulence phenotype (for instances, *Escherichia coli* K12 versus *Escherichia coli* O157:H7). This remark applies to the intergenic spacer 16S-23S rDNA as well (Gianinno *et al*, 2003). There is therefore a need to develop a molecular identification system which better discriminate bacteria than the 16S rDNA and the intergenic spacer 16S-23S rDNA.

In accordance with the present invention two series of conserved molecular markers were identified and characterized which are extremely suitable for permitting the detection and genotyping of micro-organisms, and in particular of bacteria, in a Gram-specific way. More in particular these molecular markers comprise on one hand markers preferentially conserved in Gram-positive bacteria and the other hand markers that are preferentially conserved in Gram-negative bacteria. The present invention now allows, by a combined use of these two types of conserved molecular marker sequences, to detect bacteria in a sample and to genotype these bacteria in a gram-specific way as well as in a genera-, species-, and even sometimes, strain-specific manner.

So far, in conventional microbiology, one distinguishes the bacteria according to the structure of their wall (the wall is present in all bacteria except mycoplasmas). This structure conditions the color of bacteria after Gram staining (Gram is made of several successive steps including treatment with purple gentian, Lugol's solution, alcohol and fuchsin). The bacteria whose wall is permeable to alcohol lose their purple staining (violet gentian) and coloured in red (fuchsin), defining so what is considered as a Gram-negative bacteria. In Gram-positive bacteria, the wall is primarily made by peptidoglycane. In Gram-negative bacteria, the peptidoglycane layer is thin and the wall has a more complex structure. In the clinical practice, the choice of antibiotherapy relies primarily on Gram stain. Indeed, antibiotics targeting the bacterial wall are much more on Gram-positive bacteria. As already stated above, several clinical studies show that any delay with the initiation of antibiotherapy results in increased mortality and hospital morbidity. Practically, the microbiologic identification (culture) comes too late.

Such approach provides many advantageous compared to conventionally applied detection strategies, wherein no such gram-specificity is involved. The present invention now permits by the use two series of conserved molecular markers to rapidly determine the gram-phenotype of bacteria in a sample and as a consequence to rapidly determine the most suitable antibiotherapy to be applied. This can be substituted to the conventional Gram staining procedure which is far less sensitive.

In a preferred embodiment, the assay of the present invention is further characterized in that the molecular marker that is conserved in Gram-positive bacteria comprises PurA or

PstI. In a more preferred embodiment the molecular maker that is conserved in Gram-positive bacteria is selected from the group comprising the Spy0160 (marker I), Spy1372 (marker II), SpyM3_0902 & SpyM3_0903 (marker III) and Spy1527 (marker IV) marker sequences. In yet another more preferred embodiment, the molecular maker that is conserved in Gram-positive bacteria is selected from the group comprising the sequences with SEQ ID NOs 1-62, 64-107, 109-111, 117-129, 137, 145-148, 150-193, 233-237, 240-241, 255, 326-395, 397-399, 404-425.

Another preferred embodiment of the invention relates to an assay that is characterized in that the molecular maker that is conserved in Gram-negative bacteria is selected from the group comprising the Ecs0036 (marker V), HI1576 (marker VI), EG10839 and EG11396 (marker VII), and HI0019 (marker VIII) sequences.

In yet another preferred embodiment the molecular maker that is conserved in Gram-negative bacteria is selected from the group comprising the sequences with SEQ ID NOs 63, 108, 112-116, 130-136, 138-144, 194-232, 238-239, 242-254, 256-325, 396, 400-403, 426-461.

Table 1 summarizes sequences used in accordance with the present invention for the detection and identification of Gram-positive and Gram-negative bacteria.

Table 1

Gram-positive bacteria					
Sequence	Gene	Marker	Sequences found in Gram-positive bacteria (SEQ ID NOs:)	Overlapping sequences found in Gram-negative bacteria (SEQ ID NOs:)	Sequences found in other organisms (SEQ ID NO:)
Spy0160	PurA	I	1-62 ; 326-359	63	
Spy1372	PstI	II	64-107 ; 109-111 ; 117-129 ; 137 ; 145-148 ; 360-395 ; 397-399	108 ; 112-116 ; 130-136 ; 138-144 ; 396 ; 400-403	149 (<i>Cryptococcus neoformans</i>)
SpyM3_0902 & SpyM3_0903	Hypothetical protein	III	150-180; 404-412		
Spy1527	Hypothetical protein	IV	181-193; 413-425		

Gram-negative bacteria					
Sequence	Gene	Marker	Sequences found in Gram-negative bacteria	Overlapping sequences found in Gram-positive bacteria	Sequences found in other organisms

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Ecs0036	carB	V	194-232 ; 238-239 ; 242-254 ; 431-442	233-237 ; 240-241 ; 255	
HI1576	pgi	VI	256-277; 426-430		
EG10839 & EG11396	sfrB & yigC	VII	278-303; 443-451		
HI0019	yleA	VIII	304-325; 452-461		

The present invention also relates to the use of an assay as defined herein for diagnosing bacterial infection of a sample.

The foregoing and other objects, features and advantages of the invention will become more readily apparent from the following detailed description of preferred embodiments.

Description of the figures

Figure 1 represents the amplification of a molecular marker I (Spy0160 or *pur A*) in Gram-positive bacteria.

Figure 2 represents the amplification of a molecular marker II (Spy1372 or *ptsI*) in Gram-positive bacteria.

Figure 3 represents the amplification of a molecular marker III (SpyM3_0902 & SpyM3_0903) in Gram-positive bacteria.

Figure 4 represents marker I (*purA*) sequences amplified from different Gram-positive bacteria (SEQ ID NOs 1-62), and from a Gram-negative bacterium (SEQ ID NO: 63)

Figure 5 represents marker II (*ptsI*) sequences amplified from Gram-positive bacteria (SEQ ID NOs: 64-107; SEQ ID NOs: 109-111, SEQ ID NOs: 117-129, SEQ ID NO: 137, SEQ ID NOs 145-148), from some Gram-negative bacteria (SEQ ID NOs 108, 112-116, 130-136, 138-144) and from the fungi *Cryptococcus neoformans* (SEQ ID NO: 149).

Figure 6 represents marker III (SpyM_0902 & SpyM_0903) sequences amplified from Gram-positive bacteria (SEQ ID NOs 150-180).

Figure 7 represents marker IV (putative GTP-binding factor plus 160 nt downstream this ORF) sequences amplified from Gram-positive bacteria (SEQ ID NOs 181-193)

Figure 8 represents the amplification of a molecular marker V (Ecs0036 or *carB*) in Gram-negative bacteria.

Figure 9 represents sequences amplified with molecular marker V (*carB*) from various Gram-negative bacteria (SEQ ID NOs 194-232, 238-239, 242-254) and from various Gram-positive bacteria (SEQ ID NOs 233-237, 240-241, 255)

Figure 10 represents the amplification of a molecular marker VI (HI1576 or *pgi*) in Gram-negative bacteria.

Figure 11 represents sequences amplified with molecular marker VI (HI1576 or *pgi*) from various Gram-negative bacteria (SEQ ID NOs 256-277).

5 **Figure 12** represents sequences amplified with molecular marker VII (EG10839 & EG11396 or *sfrB* & *yigC*) in Gram-negative (SEQ ID NOs 278-303).

Figure 13 represents sequences amplified with molecular marker VIII (HI0019 or hypothetical *yleA* protein) in Gram-negative bacteria (SEQ ID NOs 304-325).

10 **Figure 14** represents marker I (Spy0160 or *purA*) sequences amplified from different Gram-positive bacteria (SEQ ID NOs 326-359).

Figure 15 represents marker II (Spy1372 or *pstI*) sequences amplified from Gram-positive bacteria (SEQ ID NOs: 360-395; SEQ ID NOs: 397-399), and some Gram-negative bacteria (SEQ ID NOs 396, 400-403).

15 **Figure 16** represents marker III (SpyM_0902 & SpyM_0903) sequences amplified from Gram-positive bacteria (SEQ ID NOs 404-412).

Figure 17 represents marker IV (Spy1527, a putative GTP-binding factor plus 160 nt downstream) sequences amplified from Gram-positive bacteria (SEQ ID NOs 413-425).

Figure 18 represents sequences amplified with molecular marker VI (HI1576 or *pgi*) from various Gram-negative bacteria (SEQ ID NOs 426-430).

20 **Figure 19** represents sequences amplified with molecular marker V (Ecs0036 or *carB*) from various Gram-negative bacteria (SEQ ID NOs 431-442).

Figure 20 represents sequences amplified with molecular marker VII (EG10839 & EG11396 or *sfrB* & *yigC*) in Gram-negative (SEQ ID NOs 443-451).

25 **Figure 21** represents sequences amplified with molecular marker VIII (HI0019, hypothetical *yleA* protein) in Gram-negative bacteria (SEQ ID NOs 452-461).

Detailed description of the invention

The following definitions serve to illustrate the terms and expressions used in the different embodiments of the present invention as set out below.

30 An "isolated" nucleic acid molecule is one which is separated from other nucleic acid molecules which are present in the natural source of the nucleic acid. For example, with regards to genomic DNA, the term "isolated" includes nucleic acid molecules which are separated from the chromosome with which the genomic DNA is naturally associated.

The term "probe" or "nucleic acid probe" refers to single stranded sequence-specific oligonucleotides which have a base sequence which is sufficiently complementary to hybridize to the target base sequence to be detected.

5 The term "primer" refers to a single stranded DNA oligonucleotide sequence capable of acting as a point of initiation for synthesis of a primer, extension product which is complementary to the nucleic acid strand to be copied. The length and the sequence of the primer must be such that they allow to prime the synthesis of the extension products. Preferably the primer is about 5-50 nucleotides long. Specific length and sequence will depend on the complexity of the required DNA or RNA targets, as well as on the conditions
10 of primer use such as temperature and ionic strength.

The term "target" refers to nucleic acid molecules originating from a biological sample which have a base sequence complementary to the nucleic acid probe of the invention. The target nucleic acid can be single-or double-stranded DNA (if appropriate, obtained following amplification) and contains a sequence which has at least partial complementarity with at
15 least one probe oligonucleotide.

The phrase "a (biological) sample" refers to a specimen such as a clinical sample (pus, sputum, blood, urine, etc.) of human or animal, an environmental sample, bacterial colonies, contaminated or pure cultures, purified nucleic acid, etc. in which the target sequence of interest is sought.

20 The term "polynucleic acid" corresponds to either double- stranded or single-stranded cDNA or genomic DNA, containing at least 10, 20, 30, 40 or 50 contiguous nucleotides.

A polynucleic acid which is smaller than 100 nucleotides in length is often also referred to as an oligonucleotide. Single stranded polynucleic acid sequences are always represented in the present invention from the 5' end to the 3' end. By "oligonucleotide" is
25 meant a nucleotide polymer generally about 10 to about 100 nucleotides in length, but which may be greater than 100 or shorter than 10 nucleotides in length.

The term "homologous" is synonymous for identical and means that polynucleic acids which are said to be e. g. 90% homologous show 90% identical base pairs in the same position upon alignment of the sequences.

30 "Hybridization" involves the annealing of a complementary sequence to the target nucleic acid (the sequence to be detected). The ability of two polymers of nucleic acid containing complementary sequences to find each other and anneal through base pairing interaction is a well-recognized phenomenon.

The term "stringency" indicates one used to describe the temperature and solvent
35 composition existing during hybridization and the subsequent processing steps. Under high

stringency conditions only highly complementary nucleic acid hybrids will form; hybrids without a sufficient degree of complementarity will not form. Accordingly, the stringency of the assay conditions determines the amount of complementarity needed between two nucleic acid strands forming a hybrid. Stringency is chosen to maximize the difference in stability between the hybrid formed with the target and the non-target nucleic acid.

By "complementary" is meant a property conferred by the base sequence of a single strand of DNA which may form a hybrid or double stranded DNA: DNA, through hydrogen bonding between Watson-Crick base pairs on the respective strands. Adenine (A) usually complements thymine (T), while guanine (G) usually complements cytosine (C).

By "hybrid" is meant the complex formed between two single stranded nucleic acid sequences by Watson-Crick base pairings or non-canonical base pairings between the complementary bases.

Molecular Marker sequences

In a first aspect, the present invention provides conserved molecular markers for the detection and/or identification of one or more micro-organisms, and preferably bacteria. More in particular, the present invention provides two series of conserved molecular markers which are extremely suitable for permitting the detection and genotyping of micro-organisms, and in particular of bacteria, in a Gram-specific way.

The term "*molecular marker*" and "*molecular marker sequence*" are used herein as synonyms. These terms refer to isolated and purified nucleic acid (DNA) molecules. The term "*conserved molecular marker*" as used herein refers to a coding or non coding DNA sequence, which can be found in the genome of various bacterial species, showing a sequence identity with an original sequence which is superior to or equal to 50%, and preferably superior to or equal to 65%, and more preferably superior to or equal to 80%.

According to the present invention, two series of conserved genetic markers were characterized: one preferentially conserved in Gram-positive bacteria and the other preferentially conserved in Gram-negative bacteria.

In a preferred embodiment, the molecular markers that are conserved in Gram-positive bacteria comprise Spy0160 (PurA) or Spy1372 (PstI). More preferably the markers that are conserved in Gram-positive bacteria are selected from the group comprising Spy0160 Spy1372, SpyM3_0902 & SpyM3_0903, and Spy1527 marker sequences

In another preferred embodiment, the molecular markers that are conserved in Gram-positive bacteria are any of the sequences with SEQ ID NOs 1-62, 64-107, 109-111, 117-129, 137, 145-148, 150-193, 233-237, 240-241, 255, 326-395, 397-399, 404-425.

In yet another preferred embodiment, the molecular markers that are conserved in Gram-negative bacteria are selected from the group comprising Ecs0036, HI1576, EG10839 & EG11396, and HI0019.

In another preferred embodiment, the molecular markers that are conserved in Gram-negative bacteria are any of the sequences with SEQ ID NOs 63, 108, 112-116, 130-136, 138-144, 194-232, 238-239, 242-254, 256-325, 396, 400-403, 426-461. However, it should be clear from the present invention that the present invention is not limited to the molecular marker sequences conserved in Gram-positive and in Gram-positive bacteria as described herein. Other conserved molecular marker sequences that can be characterized and identified for various other Gram-positive bacteria and other Gram-negative bacteria including according to the invention are considered to be included in the present application as well.

In another embodiment, the invention relates to the use of at least two conserved molecular markers for detecting bacteria in a sample.

In a preferred embodiment, the invention relates to the use of at least two conserved molecular markers for detecting and genotyping a bacterium on the basis of the Gram phenotype in a sample. Preferably, the invention relates to the use of at least one molecular marker that is conserved in Gram-positive bacteria and at least one molecular marker that is conserved in Gram-negative bacteria for detecting and genotyping a bacterium. In particularly preferred embodiment, the invention relates to the use of at least one molecular marker that is conserved in Gram-positive bacteria selected from the group comprising Spy0160, Spy1372, SpyM3_0902 & SpyM3_0903, Spy1527, or any of the sequences with SEQ ID NOs 1-62, 64-107, 109-111, 117-129, 137, 145-148, 150-193, 233-237, 240-241, 255, 326-395, 397-399, 404-425, and at least one molecular marker that is conserved in Gram-negative bacteria and that is selected from the group comprising Ecs0036, HI1576, EG10839 & EG11396, HI0019, or any of the sequences with SEQ ID NOs 63, 108, 112-116, 130-136, 138-144, 194-232, 238-239, 242-254, 256-325, 396, 400-403, 426-461.

The present invention thus provides for highly conserved molecular markers that can be used for detecting the molecular presence of micro-organisms, and in particular of bacteria, in samples and/or tissues, including in cultured samples which give a false-negative result using conventional detection techniques. The present conserved markers can also advantageously be used for detecting the molecular presence of micro-organisms, and in particular of bacteria, in samples from tissues showing bacterial background. In the latter case, the conserved molecular markers are preferably used in combination with specific

primers or probes that directly target a pre-defined panel of bacteria of interest and that exclude the "background flora". A suitable pre-defined panel of bacteria of interest may, for instance, include bacteria involved in community-acquired pneumonia, such as but is not limited to *Haemophilus influenzae*, *Legionella species*, *Staphylococcus aureus*, *Moraxella catarrhalis*, *Gram-negative enteric bacteria*.

It is further noted that the molecular identification of Gram phenotype is based on partially overlapping Gram-positive and Gram-negative markers. It must be born in mind that, unlike in the present invention, another conserved marker (16S) shows an extensive overlap between Gram-positive and Gram-negative bacteria. In the present case, using concomitantly both series of partially overlapping markers in a combined way makes it possible to cover a much broader spectrum of bacterial pathogens while defining also precisely the Gram phenotype of those pathogens. The strategy relies upon the molecular detection of gene preferentially present in Gram-positive or Gram-negative bacterial. Each series of markers allows therefore improving overall detection in their respective group (either Gram-positive bacteria for preferentially Gram-positive markers, or Gram-negative bacteria for preferentially Gram-negative markers). Considering the somehow overlapping specificity for both groups, (overlap within the Gram-positive specificity for Gram-negative markers and overlap within the Gram-negative specificity for Gram-positive markers), the power of the molecular discrimination is even increased for some bacteria targeted by both groups of markers. This combined strategy overcomes the potential lack of specificity obtained when using one single marker towards some species, as is for instance the case when using a 16S marker.

In addition, the use of different markers which are mapped on different loci in the bacteria also improves the quality of the diagnosis in that it can more easily circumvent false positive reactions due to accidental PCR contamination hampering the use of one particular marker.

Primers and probes derived from conserved molecular markers

In another embodiment, the invention relates to a primer pair (forward and reverse primers) suitable for amplifying a molecular marker that is conserved in Gram-positive bacteria. More preferably, the invention relates to a primer pair suitable for amplifying any of the conserved molecular marker sequences that are conserved in Gram-positive bacteria as defined herein, and that are preferably selected from the group comprising Spy0160, Spy1372, SpyM3_0902 & SpyM3_0903, and Spy1527, or any of the sequences with SEQ ID

NOs 1-62, 64-107, 109-111, 117-129, 137, 145-148, 150-193, 233-237, 240-241, 255, 326-395, 397-399, 404-425.

In another embodiment, the invention relates to a primer pair (forward and reverse primers) suitable for amplifying a molecular marker that is conserved in Gram-negative bacteria. More preferably, the invention relates to a primer pair suitable for amplifying any of the conserved molecular marker sequences that are conserved in Gram-negative bacteria as defined herein, and that are preferably selected from the group comprising Ecs0036, HI1576,, EG10839 & EG11396 and HI0019, or any of the sequences with SEQ ID NOs 63, 108, 112-116, 130-136, 138-144, 194-232, 238-239, 242-254, 256-325, 396, 400-403, 426-461.

The primers of the present invention include at least 15-mer oligonucleotide and are preferably 70%, 80%, 90% or more than 95% homologous to the exact complement of the target sequence to be amplified. Those primers are about 15 to 50 nucleotides long, and preferably about 15 to 35 nucleotides long. Of course, primers consisting of more than 50 nucleotides can be used.

The present invention also relates to a nucleic acid probe capable of hybridizing to a molecular marker that is conserved in Gram-positive bacteria. More preferably, the invention relates to a nucleic acid probe capable of hybridizing any of the molecular marker sequences that are conserved in Gram-positive bacteria as defined herein, and that are preferably selected from the group comprising Spy0160 (PurA), Spy1372 (PstI), SpyM3_0902 & SpyM3_0903, and Spy1527, or any of the sequences with SEQ ID NOs 1-62, 64-107, 109-111, 117-129, 137, 145-148, 150-193, 233-237, 240-241, 255, 326-395, 397-399, 404-425.

In another embodiment, the present invention also relates to a nucleic acid probe capable of hybridizing to a molecular marker that is conserved in Gram-negative bacteria. More preferably, the invention relates to a nucleic acid probe capable of hybridizing any of the molecular marker sequences that are conserved in Gram-negative bacteria as defined herein, and that are preferably selected from the group comprising Ecs0036, HI1576, EG10839 & EG11396 and HI0019, or any of the sequences with SEQ ID NOs 63, 108, 112-116, 130-136, 138-144, 194-232, 238-239, 242-254, 256-325, 396, 400-403, 426-461.

The probe of the present invention preferably includes at least 15-mer oligonucleotide and are preferably 70%, 80%, 90% or more than 95% homologous to the exact complement of the target sequence to be detected. Those probes are preferably about 15 to 50 nucleotides long. The primers and probes of the invention can be used, for diagnostic purposes, in investigating the presence or the absence of a target nucleic acid in a biological

sample, according to all the known hybridization techniques such as for instance dot blot, slot blot, hybridization on arrays including nanotools, real-time PCR, etc...

The probes of the invention will preferably hybridize specifically to one or more of the above-mentioned molecular marker sequences.

5 The primers of the invention may amplify specifically one or more of the above-mentioned marker sequences. The design of specifically hybridising probes is within the skilled person's knowledge. Also the design of primers which can specifically amplify certain sequences or molecular markers is within the skilled person's knowledge.

10 The nucleic acid probes of this invention can be included in a composition or kit which can be used to rapidly determine the presence or absence of pathogenic species of interest (see below).

Compositions

15 In another embodiment, the invention relates to a composition. In a preferred embodiment, the invention relates to a composition comprising at least one primer pair (forward and reverse primers) suitable for amplifying a conserved molecular marker that is conserved in Gram-positive bacteria and at least one primer pair (forward and reverse primers) suitable for amplifying a conserved molecular marker that is conserved in Gram-negative bacteria.

20 Preferably, the composition comprises at least one primer pair suitable for amplifying any of the molecular marker sequences that are conserved in Gram-positive bacteria and that are selected from the group comprising Spy0160, Spy1372, SpyM3_0902 & SpyM3_0903, and Spy1527, or any of the sequences with SEQ ID NOs 1-62, 64-107, 109-111, 117-129, 137, 145-148, 150-193, 233-237, 240-241, 255, 326-395, 397-399, 404-425, 25 and at least one primer pair suitable for amplifying any of the molecular marker sequences that are conserved in Gram-negative bacteria and that are selected from the group comprising Ecs0036, HI1576, EG10839 & EG11396 and HI0019, or any of the sequences with SEQ ID NOs 63, 108, 112-116, 130-136, 138-144, 194-232, 238-239, 242-254, 256-325, 396, 400-403, 426-461.

30 In yet another embodiment, the invention relates to a composition comprising at least one nucleic acid probe capable of hybridizing to a molecular marker that is conserved in Gram-positive bacteria, and at least one nucleic acid probe capable of hybridizing to a molecular marker that is conserved in Gram-negative bacteria. Preferably, the composition comprises at least one nucleic acid probe capable of hybridizing to a molecular marker that is 35 conserved in Gram-positive bacteria selected from the group comprising Spy0160, Spy1372,

SpyM3_0902 & SpyM3_0903, and Spy1527, or any of the sequences with SEQ ID NOs 1-62, 64-107, 109-111, 117-129, 137, 145-148, 150-193, 233-237, 240-241, 255, 326-395, 397-399, 404-425, and at least one at least one nucleic acid probe capable of hybridizing to a molecular marker that is conserved in Gram-negative bacteria selected from the group comprising Ecs0036, HI1576, EG10839 & EG11396 and HI0019, or any of the sequences with SEQ ID NOs 63, 108, 112-116, 130-136, 138-144, 194-232, 238-239, 242-254, 256-325, 396, 400-403, 426-461.

By "composition", it is meant that primers or probes complementary to bacterial DNA may be in a pure state or in combination with other primers or probes. In addition, the primers or probes may be in combination with salts or buffers, and may be in a dried state, in an alcohol solution as a precipitate, or in an aqueous solution.

Kits

In yet another embodiment, the invention relates to a kit for detecting and identifying one or more micro-organisms, preferably bacteria, in a sample, which comprises:

a) a composition comprising at least one primer pair (forward and reverse primers) suitable for amplifying a conserved molecular marker that is conserved in Gram-positive bacteria and at least one primer pair (forward and reverse primers) suitable for amplifying a conserved molecular marker that is conserved in Gram-negative bacteria; for amplifying polynucleic acids in said sample,

b) a composition comprising at least one nucleic acid probe capable of hybridizing to a molecular marker that is conserved in Gram-positive bacteria, and at least one nucleic acid probe capable of hybridizing to a molecular marker that is conserved in Gram-negative bacteria,

c) a buffer enabling hybridization reaction between the probes contained in said composition and the polynucleic acids present in said sample or amplified products therefrom or components necessary for producing the buffer,

d) a solution for washing hybrids formed under the appropriate wash conditions or components necessary for producing the solution, and

e) optionally a means for detection of said hybrids.

A kit according to the invention preferably includes all components necessary to assay for the presence of bacteria. In the universal concept, the kit includes a stable preparation of labeled probes, hybridization solution in either dry or liquid form for the hybridization of target and probe polynucleotides, as well as a solution for washing and

removing undesirable and nonduplexed polynucleotides, a substrate for detecting the labeled duplex, and optionally an instrument for the detection of the label.

In a preferred embodiment, the present kit comprises a composition which comprises at least one primer pair suitable for amplifying any of the molecular marker sequences that are conserved in Gram-positive bacteria selected from the group comprising Spy0160, Spy1372, SpyM3_0902 & SpyM3_0903, and Spy1527, or any of the sequences with SEQ ID NOs 1-62, 64-107, 109-111, 117-129, 137, 145-148, 150-193, 233-237, 240-241, 255, 326-395, 397-399, 404-425, and at least one primer pair suitable for amplifying any of the molecular marker sequences that are conserved in Gram-negative bacteria selected from the group comprising Ecs0036, HI1576, EG10839 & EG11396 and HI0019, or any of the sequences with SEQ ID NOs 63, 108, 112-116, 130-136, 138-144, 194-232, 238-239, 242-254, 256-325, 396, 400-403, 426-461.

In yet another preferred embodiment, the present kit comprises a composition which comprises at least one nucleic acid probe capable of hybridizing to a molecular marker that is conserved in Gram-positive bacteria selected from the group comprising Spy0160, Spy1372, SpyM3_0902 & SpyM3_0903, and Spy1527, or any of the sequences with SEQ ID NOs 1-62, 64-107, 109-111, 117-129, 137, 145-148, 150-193, 233-237, 240-241, 255, 326-395, 397-399, 404-425, and at least one at least one nucleic acid probe capable of hybridising to a molecular marker that is conserved in Gram-negative bacteria selected from the group comprising Ecs0036, HI1576, EG10839 & EG11396 and HI0019, or any of the sequences with SEQ ID NOs 63, 108, 112-116, 130-136, 138-144, 194-232, 238-239, 242-254, 256-325, 396, 400-403, 426-461.

In yet another preferred embodiment, the kit according to the present invention further comprises one or more genus-, species and/or strain-specific nucleic acid probes capable of hybridizing to a genus-, species and/or strain-specific bacterial polynucleotide sequence.

DNA chip

In another preferred embodiment, the present invention provides a DNA chip in which nucleic acid probes are immobilized on a solid support. The invention relates to the manufacturing of a solid support (array –DNA chip) on which several sets of nucleic acid probes are covalently bound or directly synthesized.

In a preferred embodiment, the invention relates to a DNA chip in which at least one of nucleic acid probe capable of hybridizing to a molecular marker that is conserved in Gram-positive bacteria, and at least one nucleic acid probe capable of hybridizing to a molecular marker that is conserved in Gram-negative bacteria, is immobilized on a solid support.

Preferably, the DNA chip comprises at least one nucleic acid probe capable of hybridizing to a molecular marker that is conserved in Gram-positive bacteria selected from the group comprising Spy0160, Spy1372, SpyM3_0902 & SpyM3_0903, and Spy1527, or any of the sequences with SEQ ID NOs 1-62, 64-107, 109-111, 117-129, 137, 145-148, 150-193, 233-237, 240-241, 255, 326-395, 397-399, 404-425, and at least one nucleic acid probe capable of hybridizing to a molecular marker that is conserved in Gram-negative bacteria selected from the group comprising Ecs0036, HI1576, EG10839 & EG11396 and HI0019, or any of the sequences with SEQ ID NOs 63, 108, 112-116, 130-136, 138-144, 194-232, 238-239, 242-254, 256-325, 396, 400-403, 426-461 immobilized on a solid support.

In yet another preferred embodiment, the DNA chip according to the present invention further comprises one or more genus-, species and/or strain-specific nucleic acid probes capable of hybridizing to a genus-, species and/or strain-specific bacterial polynucleotide sequence.

The DNA chip which is formed by arranging DNA fragments of variety of base sequences on the surface of a narrow substrate in high density is used in finding out the information on DNA of an unknown sample by hybridization between an immobilized DNA and unknown DNA sample complementary thereto. Examples of the solid carrier on which the probe oligonucleotides are fixed include inorganic materials such as glass and silicon and polymeric materials such as acryl, polyethylene terephthalate (PET), polystyrene, polycarbonate and polypropylene. The surface of the solid substrate can be flat or have a multiple of hole. The probes are immobilized on the substrate by covalent bond of either 3'end or 5'end. The immobilization can be achieved by conventional techniques, for example, using electrostatic force, binding between aldehyde coated slide and amine group attached on synthetic oligomeric phase or spotting on amine coated slide, L- lysine coated slide or nitrocellulose coated slide. The immobilization and the arrangement of various probes onto the solid substrate are carried out by pin microarray, inkjet, photolithography, electric array, etc.

The term "DNA chip" as used herein, is to be understood in its broadest sense, i.e. including nanochips or nanotools that are designed to recognize a specific pattern of nucleic acids through hybridization.

Assay

In another embodiment, the invention relates to an assay for detecting and identifying one or more micro-organisms, preferably bacteria, in a sample, characterized in that said assay comprises the use of at least two conserved molecular markers, and preferably

comprises the use of at least one molecular marker that is conserved in Gram-positive bacteria and at least one molecular marker that is conserved in Gram-negative bacteria.

In the prior art, ultimate molecular species identification results classically from sequence analysis of an amplification product and the comparison of this sequence with those which are available in public DNA database (for instance, GeneBank...). The sequence analysis requires nearly 24 hours to complete the various analytical steps: amplicon purification, cycle sequencing, reading and interpretation of the results.

The present invention provides a strategy which permits to significantly reduce the time requested for genera, species, and optionally strain, identification of bacteria in a sample compared to classical identification strategies as described above. More in particular, the present strategy preferably consists in amplifying a set of conserved genetic markers and either to hybridize produced amplicons on specific capture probes covalently bound on an array or, alternatively, to hybridize a specific probe during the amplification step (e.g. real-time PCR with Taqman or molecular Beacon probes). The result of the identification will include information regarding the Gram phenotype of bacteria present in the sample of interest (or a combination of both Gram phenotype in case of mixed infections with Gram-positive and Gram-negative), as well as information on genera and species to which they belong. The final results will integrate all the hybridization signals generated by the selected markers.

In a preferred embodiment, the method for detecting and identifying one or more micro-organisms, preferably bacteria, in a sample may comprise the following steps:

- a) If appropriate isolating and/or concentrating the DNA present in said sample;
- b) amplifying said DNA with
 - o at least one pair of (forward and reverse) primers suitable for amplifying a molecular marker that is conserved in Gram-positive bacteria, and
 - o at least one pair of (forward and reverse) primers suitable for amplifying a molecular marker that is conserved in Gram-negative bacteria,
- c) hybridizing the amplified DNA fragments obtained in step b) with genus-, and/or species-, and/or strain-specific primers or nucleic acid probes
- d) detecting the hybrids formed in step c) and
- e) identifying micro-organisms in said sample from the differential hybridization signals obtained in step d)

The present invention allows to detect the presence of bacteria in human, animal and/or environmental samples, and, at the same time, to identify those bacteria, including highly pathogenic ones. Such detection and identification system is based on the pattern of

hybridization of several combined DNA fragments. Identification relies upon concomitant signals generated by a panel of unrelated markers. The system provides discrimination based on the Gram-phenotype as well as genus- and species-specificity.

To provide nucleic acid substrates for use in the detection and identification of micro-organisms in clinical samples using the present assay, nucleic acid, preferably DNA, is extracted from the sample. The nucleic acid may be extracted from a variety of clinical samples, or environmental samples, using a variety of standard techniques or commercially available kits.

A second step is an amplification of the desired DNA region of the target DNA by PCR. Examples of the PCR include most typical PCR using the same amounts of forward and reverse primers, multiplex PCR in which a multiple of target DNAs can be amplified at once by adding various primers simultaneously, ligase chain reaction (LCR) in which target DNA is amplified using specific 4 primers and ligase and the amount of fluorescence is measured by ELISA (Enzyme Linked Immunosorbent Assay), and the other PCR such as Hot Start PCR, Nest-PCR, DOP-PCR (degenerate oligonucleotide primer PCR), RT-PCR (reverse transcription PCR), Semi-quantitative RT-PCR, Real time PCR, RACE (rapid amplification of cDNA ends), Competitive PCR, STR (short tandem repeats), SSCP (single strand conformation polymorphism), DDRT-PCR (differential display reverse transcriptase), etc.

A further step comprises the hybridization of the amplified DNA fragments obtained in step b) with specific primers or nucleic acid probes. The choice of the applied hybridization technique should not be considered as limitative for the present invention. Nanotools can also be designed to recognize a specific nucleic acid pattern with or without PCR amplification.

In one embodiment, step c) may include an identification by contacting the amplified DNA fragments obtained in step b) with a composition comprising at least one nucleic acid probe capable of hybridizing to a molecular marker that is conserved in Gram-positive bacteria, and at least one nucleic acid probe capable of hybridizing to a molecular marker that is conserved in Gram-negative bacteria. In such case, steps b) and c) of the above described method are performed subsequently. For instance, identification may be performed using a reverse hybridization procedure (dot blot, slot blot, hybridization on micro-, macro- or nano-arrays, etc....) In such case, hybridization of marked amplicons is performed on Gram-, genera- and species-specific nucleic acid probes bound covalently on the array (e.g. micro- or macro-arrays). While the result is visual, the reading can also be automated, facilitating therefore the use in the clinical practice.

In another embodiment, step c) may include the use of real-time PCR with specific probes (multiplex approach) which allows to have a specific result in a couple of hours. Simplex or multiplex PCR techniques in real-time include the use of specific acid probes on a DNA target during the PCR step (e.g. Taqman probes, molecular beacons or MGB (Minor Groove Binding) probes, etc...). In such case, steps b) and c) of the above described method are performed simultaneously. A significant advantage of using a real-time PCR technique is the increased speed, e.g. only a couple of hours are required for obtained final results. This is mainly due to the reduced cycle times, removal of separate post-PCR detection procedures, and the use of sensitive fluorescence detection equipment, allowing earlier amplicon detection. Another advantage of a real-time PCR technique is that it is a single tube procedure with the reading during the PCR and no manipulation required at the end of the procedure. This single tube procedure prevents therefore the risk of molecular contamination existing with other PCR procedures, including micro- and macro-array techniques. Preferably a nested real-time PCR strategy is used to increase the sensitivity of the method with a detection limit of one DNA copy in tissue samples.

The formed hybrids can be quantified by labeling the target with a fluorescence or radioactive isotope in accordance to conventional methods. The labeling may be carried out by the use of labeled primers or the use of labeled nucleotides incorporated during the polymerase step of the amplification.

According to a preferred embodiment of the present invention, the primers suitable for amplifying a molecular marker that is conserved in Gram-positive bacteria used in step b) of the above mentioned method preferably comprise primers suitable for amplifying a molecular marker selected from the group comprising Spy0160, Spy1372, SpyM3_0902 & SpyM3_0903, Spy1527, or any of the sequences with SEQ ID NOs 1-62, 64-107, 109-111, 117-129, 137, 145-148, 150-193, 233-237, 240-241, 255, 326-395, 397-399, 404-425.

According to another preferred embodiment of the present invention, the primers suitable for amplifying a molecular marker that is conserved in Gram-negative bacteria used in step b) of the above mentioned method preferably comprise primers suitable for amplifying a molecular marker selected from the group comprising Ecs0036, HI1576, EG10839 & EG11396 and HI0019, or any of the sequences with SEQ ID NOs 63, 108, 112-116, 130-136, 138-144, 194-232, 238-239, 242-254, 256-325, 396, 400-403, 426-461.

The following examples are meant to illustrate the present invention. **Examples 1-3** present and describe molecular marker sequences that have been characterized on a wide panel of clinical and reference bacterial genera species and bacterial strains and that allow the discrimination between Gram-positive and Gram-negative bacteria as well as genera and

species identification. **Example 4** illustrates the use of molecular markers according to the present invention for the detection and identification of *Bacillus* bacteria and for the discrimination between various *Bacillus* strains of the same species. **Example 5** illustrates nucleic acid probes according to the present invention.

5

Examples

Example 1 Characterization of molecular markers of genes enabling the identification of Gram-positive bacteria

The present example aims to test the Gram-positive specificity of several markers. The list of Gram-positive bacteria used in the present example (study of markers specificity) is given in **table 2A**.

10

Table 2A Gram-positive bacteria

genus	species	strain reference
<i>Bacillus</i>	<i>anthracis</i>	1978
<i>Bacillus</i>	<i>anthracis</i>	STERNE
<i>Bacillus</i>	<i>anthracis</i>	BUTARE
<i>Bacillus</i>	<i>anthracis</i>	1655H85
<i>Bacillus</i>	<i>anthracis</i>	CODA - CERVA
<i>Bacillus</i>	<i>anthracis</i>	2054H82
<i>Bacillus</i>	<i>cereus</i>	ATCC10987
<i>Bacillus</i>	<i>cereus</i>	ATCC 14579
<i>Bacillus</i>	<i>pumilus</i>	Clinical
<i>Bacillus</i>	<i>species</i>	Clinical
<i>Bacillus</i>	<i>thuringiensis kurstaki</i>	T03A016 HD_1
<i>Bacillus</i>	<i>thuringiensis israelensis</i>	4Q2_72
<i>Bacillus</i>	<i>mycoides</i>	MYC003
<i>Bacillus</i>	<i>mycoides</i>	NRS306
<i>Bacillus</i>	<i>weihenstephanensis</i>	WSBC10204
<i>Bacillus</i>	<i>halodurans</i>	DSMZ 497
<i>Bacillus</i>	<i>firmus</i>	DSMZ 12643
<i>Bacillus</i>	<i>megatherium</i>	DSMZ 1324
<i>Bacillus</i>	<i>pseudomycoïdes</i>	DSMZ 12442
<i>Clostridium</i>	<i>difficile</i>	DSMZ 1296
<i>Clostridium</i>	<i>perfringens</i>	DSMZ 756
<i>Enterococcus</i>	<i>faecium</i>	DSMZ 6177
<i>Enterococcus</i>	<i>faecalis</i>	DSMZ 2570
<i>Enterococcus</i>	<i>flavescens</i>	DSMZ 7370
<i>Enterococcus</i>	<i>durans</i>	DSMZ 20633
<i>Enterococcus</i>	<i>casseliflavus</i>	DSMZ 20680
<i>Enterococcus</i>	<i>gallinarum</i>	DSMZ 20628
<i>Enterococcus</i>	<i>hirae</i>	DSMZ 20160
<i>Enterococcus</i>	<i>raffinosis</i>	DSMZ 75633

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<i>Enterococcus</i>	<i>avium</i>	DSMZ 20679
<i>Enterococcus</i>	<i>villorum</i>	CODA - CERVA
<i>Lactococcus</i>	<i>lactis</i>	DSMZ 20481
<i>Listeria</i>	<i>monocytogenes</i>	DSMZ 20600
<i>Listeria</i>	<i>innocua</i>	DSMZ 20649
<i>Staphylococcus</i>	<i>aureus</i>	ATCC 35884
<i>Staphylococcus</i>	<i>epidermidis</i>	ATCC 14990
<i>Staphylococcus</i>	<i>hominis</i>	ATCC 27844
<i>Staphylococcus</i>	<i>haemolyticus</i>	ATCC 29970
<i>Staphylococcus</i>	<i>saprophyticus</i>	ATCC 15305
<i>Staphylococcus</i>	<i>xylosus</i>	ATCC 35663
<i>Staphylococcus</i>	<i>simulans</i>	ATCC 27848
<i>Staphylococcus</i>	<i>cohnii cohnii</i>	ATCC 35662
<i>Staphylococcus</i>	<i>capitis capitis</i>	ATCC 27840
<i>Staphylococcus</i>	<i>sciuri</i>	ATCC 29062
<i>Staphylococcus</i>	<i>warneri</i>	ATCC 27836
<i>Staphylococcus</i>	<i>lugdunensis</i>	ATCC 43809
<i>Staphylococcus</i>	<i>gallinarum</i>	ATCC C3572
<i>Staphylococcus</i>	<i>schleiferi schleiferi</i>	ATCC 43808
<i>Staphylococcus</i>	<i>capitis ureolyticus</i>	ATCC 49326
<i>Staphylococcus</i>	<i>cohnii urealyticum</i>	ATCC 49330
<i>Staphylococcus</i>	<i>auricularis</i>	ATCC 33753
<i>Staphylococcus</i>	<i>caseolyticus</i>	ATCC 13548
<i>Staphylococcus</i>	<i>intermedius</i>	ATCC 29663
<i>Streptococcus</i>	<i>pyogenes</i>	DSMZ 20565
<i>Streptococcus</i>	<i>agalactiae</i>	DSMZ 2134
<i>Streptococcus</i>	<i>pneumoniae</i>	DSMZ 20566
<i>Streptococcus</i>	<i>oralis</i>	DSMZ 20627
<i>Streptococcus</i>	<i>sanguinis</i>	DSMZ 20567
<i>Streptococcus</i>	<i>mitis</i>	DSMZ 12643
<i>Streptococcus</i>	<i>gordonii</i>	DSMZ 6777
<i>Streptococcus</i>	<i>canis</i>	DSMZ 20386
<i>Streptococcus</i>	<i>mutans</i>	DSMZ 20523
<i>Streptococcus</i>	<i>subspecies</i>	Clinical
<i>Streptococcus</i>	<i>bovis</i>	DSMZ 20480
<i>Streptococcus</i>	<i>thermophilus</i>	DSMZ 20617
<i>Streptococcus</i>	<i>suis</i>	DSMZ 9682

The following sequences have been characterized and used for multigenotypic identification of Gram-positive bacteria.

5 The **Spy0160 sequence** (marker I) from *Streptococcus pyogenes* (accession number: AE006485.1; position 3201 to 4030) is part of an open reading frame homologous for the gene *purA*. The *purA* protein plays an important role in the *novo* bacterial synthesis of purines. It catalyses the synthesis of adenylosuccinate starting from inosine monophosphate (IMP) and of aspartate, and using energy provided by the GTP. The first nucleotides alignments performed suggested the existence of conserved sequences similar to the

Spy0160 sequence in a few Gram-positive bacteria. These findings have been extended to a wide panel of bacteria that were available in our DNA bank and confirmed that this marker was present in almost all Gram-positive bacteria and was very helpful in discrimination of closely related Gram-positive species and in many cases could allow discrimination between strains of the same species

A second marker is the **Spy1372 sequence** (Marker II) from *Streptococcus pyogenes* (accession n° AE004092, position 1139277 to 1141010). The corresponding gene probably encodes an enzyme involved in the transport of sugar in bacteria. Indeed, this gene is homologous to gene ptsI of *Staphylococcus aureus* coding for a phosphoenol pyruvate phosphatase (accession n° NC_002758, from position 1137273 to 1138991). This gene is part of PTS operon (phosphotransferase system) including several genes coding for proteins involved in importation of sugar by bacteria (Plumbridge *et al*, 2002). The product of ptsI gene is a protein called Enzyme I, which may be phosphorylated by phosphoenol pyruvate. Phosphorylated Enzyme I can give its phosphate group to another protein of the PTS group through a cascade which leads to the entry of glucose in the bacterial periplasm (Stentz *et al*, 1997).

A third marker is the **SpyM3_0902 - SpyM3_0903 sequence** (Marker III) from *Streptococcus pyogenes* MGAS315 (accession n° AE014154, from position 40670 to 41160). This sequence is located downstream the gene encoding alpha-helicase and corresponds to the open reading frame of a hypothetical protein.

A fourth marker is the **Spy1527 sequence** (Marker IV) from *Streptococcus pyogenes* from position 1201 to 2464, including nucleotides 2465 to 2625 (accession n° AE006586). The Spy1527 sequence corresponds to the gene *typA*, coding for a putative GTP-binding protein (GTP-BP). The fragment from position 2465 to 2625 does not correspond to an open reading frame, but is a non-coding sequence.

A first analysis of some available complete bacterial genomes suggests that homologous sequences were present in most of those bacteria.

A further analysis has been performed on reference strains and on several hundreds clinical strains provided by Belgian hospitals. The conservation of targets of interest (*purA* and *ptsI* (i.e. Marker I and II)) has been confirmed in the genome of all these reference and clinical strains. This analysis confirmed the very little genomic variability of these sequences within a species of interest. This feature is crucial to allow the use of these marker sequences in a strategy of multigenotypic identification of Gram-positive bacteria.

Example 2 Characterization of molecular markers of genes enabling the identification of
Gram-negative bacteria

The present example aims to test the Gram-negative specificity of several markers. The list of Gram-positive bacteria used in the present example (study of markers specificity) is given

5 in **table 2B**.

Table 2B Gram-negative bacteria

genus	species	strain reference
<i>Acinetobacter</i>	<i>baumanii</i>	ATCC 19606
<i>Acinetobacter</i>	<i>calcoaceticus</i>	DSMZ 1139D
<i>Bordetella</i>	<i>parapertussis</i>	Clinical
<i>Bordetella</i>	<i>bronchiseptica</i>	Clinical
<i>Bordetella</i>	<i>pertusis</i>	Clinical
<i>Brucella</i>	<i>melitensis biovar 1</i>	16M
<i>Brucella</i>	<i>melitensis biovar 2</i>	63/9
<i>Brucella</i>	<i>abortus biovar 1</i>	544
<i>Brucella</i>	<i>abortus biovar 2</i>	86/8/59
<i>Brucella</i>	<i>canis</i>	RM6/66
<i>Brucella</i>	<i>ovis</i>	63/290
<i>Brucella</i>	<i>suis biovar 1</i>	1330
<i>Brucella</i>	<i>suis biovar 2</i>	686
<i>Burkholderia</i>	<i>cepacia</i>	ATCC 17770
<i>Citrobacter</i>	<i>freundii</i>	DSMZ 30039
<i>Cryptococcus</i>	<i>neoformans</i>	DSMZ 70219
<i>Enterobacter</i>	<i>cloacae</i>	ATCC 13047
<i>Enterobacter</i>	<i>aerogenes</i>	DSMZ 13048
<i>Escherishia</i>	<i>coli O157:H7</i>	DSMZ 8579
<i>Escherishia</i>	<i>coli K12</i>	DSMZ 6367
<i>Francisella</i>	<i>tularensis</i>	SVA / T7
<i>Haemophilus</i>	<i>influenzae</i>	DSMZ 9999
<i>Haemophilus</i>	<i>ducrei</i>	-
<i>Klebsiella</i>	<i>pneumoniae</i>	ATCC 13883
<i>Klebsiella</i>	<i>oxytica</i>	ATCC 43863
<i>Legionella</i>	<i>pneumophila</i>	DSMZ 7513
<i>Moraxella</i>	<i>catarrhalis</i>	DSMZ 11994
<i>Morganella</i>	<i>morganii</i>	ATCC 25830
<i>Neisseria</i>	<i>meningitidis groupe C</i>	ISP ???
<i>Neisseria</i>	<i>meningitidis groupe B</i>	clinical
<i>Pasteurella</i>	<i>multocida</i>	-
<i>Proteus</i>	<i>mirabilis</i>	ATCC 29906
<i>Proteus</i>	<i>vulgaris</i>	ATCC 13315
<i>Providencia</i>	<i>stuartii</i>	ATCC 29914
<i>Pseudomonas</i>	<i>aeruginosa</i>	DSMZ 50071

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<i>Pseudomonas</i>	<i>putida</i>	ATCC 12633
<i>Pseudomonas</i>	<i>syringae</i>	ATCC 39254
<i>Salmonella</i>	<i>enteritidis</i>	Clinical
<i>Salmonella</i>	<i>enterica hadar</i>	Clinical
<i>Salmonella</i>	<i>enterica brandenburg</i>	Clinical
<i>Salmonella</i>	<i>enterica derby</i>	Clinical
<i>Salmonella</i>	<i>enterica virchow</i>	Clinical
<i>Salmonella</i>	<i>enterica typhimurium</i>	Clinical
<i>Salmonella</i>	<i>enterica paratyphi B</i>	Clinical
<i>Serratia</i>	<i>liquefasciens</i>	ATCC 27592
<i>Serratia</i>	<i>marcescens</i>	ATCC 13880
<i>Shigella</i>	<i>sonnei</i>	Clinical
<i>Shigella</i>	<i>flexneri</i>	-
<i>Vibrio</i>	<i>parahaemolyticus</i>	-
<i>Vibrio</i>	<i>cholerae</i>	-
<i>Yersinia</i>	<i>pestis</i>	-

The following sequences have been characterized and used for multigenotypic identification of Gram-negative bacteria.

5 The **HI1576 sequence** (marker VI) from *Haemophilus influenzae* corresponds to the gene coding for phosphoglucose isomerase (accession n° U32831, from position 12660 to 13991) an enzyme playing a role in glucidic metabolism especially for glycolysis (Morris *et al*, 2001).

10 Another sequence is the **Ecs0036 sequence** (marker V) from *Escherichia coli* O157:H7 (accession n° AP002550; from position 35200 to 36200). It is believed that this sequence encodes the large carbamoyl-synthetase unit, an enzyme which catalysis the synthesis of carbamoyl phosphate, from glutamine, bicarbonate and two ATP molecules through a mechanism which requires several successive steps (Rauschel *et al*, 2001). The synthesized carbamoyl-phosphate contributes to *de novo* synthesis of pyrimidic bases in bacteria (Minic *et al*, 2001).

15 Another sequence is the **EG10839 & EG11396 (sfrB & yigC) sequence** (= marker VII) from *Escherichia coli* K12 (accession n° NC_000913; from position 4022578 to 4024071). The corresponding protein is not yet known. When considering the sequence of the gene, it is a putative flavoprotein reductase. A search in DNA databases allowed us to find homologous sequences in some bacteria.

20 The **HI0019** (= marker VIII) sequence from *Haemophilus influenzae* (accession n° U32687, from position 7501 to 8550). This sequence shares all the characteristics of a coding sequence. However, the product of this coding sequence does not match any known

protein. This sequence is homologous to the gene coding for the hypothetical protein yleA from *Pasteurella multocida* (accession n° AF23940) whose function is totally unknown.

Example 3 Additional molecular marker sequences

This example illustrates the determination of marker sequences homologous to the sequences Spy0160, Spy1372, SpyM3-0902 & SpyM3-0903, Spy1527, Ecs0036, HI1576, and EG10839 & EG11396 as defined above in other Gram-positive or Gram-negative bacteria. These marker sequences were obtained using sets of degenerated primers, which have been identified based on theoretical alignments of the above-defined marker sequence (see examples 1-2) with sequences available in DNA databases.

Table 3A-H represents some degenerated primer sequences that have been used to amplify homologous marker sequences present in other Gram-positive or Gram-negative bacteria. PCR amplification was done using the identified degenerated primers on bacterial DNA isolated from various other Gram-positive or Gram-negative bacteria. Amplification was done under conditions of low stringency. In **table 3A-H**, the conditions the PCR programs and applied temperatures are indicated.

Table 3A Target sequence: Homologs of Spy0160 (purA gene or Marker I) in Gram-positive bacteria

Primers	Sequence	Tm	Annealing temperature during the PCR	Amplicon size
GRP1-S	5'-YHTTTYGAAGGDGCDCAAGG-3' (SEQ ID NO: 462)	61°C	50°C	585 bp
GRP1-AS	5'-GRYCWGGMCCWACTGAGAA-3' (SEQ ID NO: 463)	59°C		

Table 3B Target sequence: Homologs of Spy1372 (pstI gene or Marker II) in Gram-positive bacteria

Primers	Sequence	Tm	Annealing temperature during the PCR	Amplicon size
GRP2-S	5'-CCNGCCATYTCWCCRCACAT-3' (SEQ ID NO: 464)	63°C	50°C	443 bp
GRP2-AS	5'-AMGARATGAAYCCRTTCYTDGG-3' (SEQ ID NO: 465)	64°C		

Table 3C Target sequence: Homologs of SpyM3_0902 & SpyM3_0903 (Marker III) in Gram-positive bacteria

Primers	Sequence	Tm	Annealing temperature	Amplicon size
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26

			during the PCR	
GRP3-S	5'-GACGGAMYTCTGGAGAGACC-3' (SEQ ID NO: 466)	57°C	48°C	around 600 bp
GRP3-AS	5'- GCRTAYTTDGTGCCATWCCAAA-3' (SEQ ID NO: 467)	59°C		

Table 3D Target sequence: Homologs of Spy1527 (typA gene-Marker IV) in Gram-positive bacteria

Primers	Sequence	Tm	Annealing temperature during the PCR	Amplicon size
GRP4-S	5'-GARCGTATYATGAAAATGGT-3' (SEQ ID NO: 468)	57°C	45°C	885 bp
GRP4-AS	5'-CATDCCYTCAGDCKCAT-3' (SEQ ID NO: 469)	59°C		

5 **Table 3E** Target sequence: Homologs of HI1576 (glucose-6-phosphate isomerase gene - marker VI) in Gram-negative bacteria

Primers	Sequence	Tm	Annealing temperature during the PCR	Amplicon size
GN-1-S	5'- TGGGTYGGYGGYCGTTACT-3' (SEQ ID NO: 470)	63°C	50°C	around 500 bp
GN-1-AS	5'- TCGGTYTGNGCRAAGAAGTT-3' (SEQ ID NO: 471)	64°C		

Table 3F Target sequence: Homologs of Ecs0036 (Carb-P, large subunit gene- or Marker V) in Gram-negative bacteria

Primers	Sequence	Tm	Annealing temperature during the PCR	Amplicon size
GN-2-S	5'-CSACNATYATGACYGAYCC-3' (SEQ ID NO: 472)	63°C	50°C	500-650 bp
GN-2-AS	5'-TCCATYTCRTAYTCYTTCCA-3' (SEQ ID NO: 473)	64°C		

10

Table 3G Target sequence: Homologs of EG10839 & EG11396 (sfrB & yigC or Marker VII) in Gram-negative bacteria

Primers	Sequence	Tm	Annealing temperature during the PCR	Amplicon size
GN-3-S	5'- AAYTTGGTRTACATRAACTG -3' (SEQ ID NO: 474)	63°C	50°C	Around 600 bp
GN-3-AS	5'- RVTGATYATGCGYTGCT-3' (SEQ ID NO: 475)	64°C		

Table 3H Target sequence: Homologs of HI0019 (yleA or Marker VIII) in Gram-negative bacteria

Primers	Sequence	T _m	Annealing temperature during the PCR	Amplicon size
GN-4-S	5'- GCCNGGGAADCCNACRAT -3' (SEQ ID NO: 476)	63°C	60°C	Around 500 bp
GN-4-AS	5'- GTNTCNRTNATGGAAGGCTG-3' (SEQ ID NO: 477)	64°C		

An example of a PCR amplification used to obtain marker sequences from bacteria is as follows: 10 ng of genomic DNA from each bacterial strain tested is added to a mixture containing 10 mM Tris HCl pH 9, 2.5 mM MgCl₂, 50 mM KCl, 0.1% Triton X-100 (v/v), 300 nM of each primer (forward and reverse; see **table 3** for primers used), 0.25 mM desoxynucleotides triphosphates (Roche Diagnostics, Mannheim, Germany), 2.5 U de Taq Polymerase Expand High Fidelity (Roche Diagnostics, Mannheim, Germany) in a final volume of 50 µl. Amplifications were carried out in a Mastercycler gradient (Applied Biosystem 2400, USA). An initial activation step of Expand High Fidelity (94°C for 3 min) is followed by 35 cycles (94°C for 40 s, annealing temperature equal to T_m -5 or -10 °C for 50 s, 72°C for 1 min) and a final extension for 10 min.

Amplified DNA fragments were run on a 2% agarose gel stained with ethidium-bromide and visualized on a UV transilluminator.

Figures 1-3 illustrate the amplification in some Gram-positive bacteria of molecular markers which are homologous to markers I to III respectively. **Figures 8 and 10** illustrate the amplification in some Gram-negative bacteria of molecular markers homologous to markers V (Ecs0036) and VI (HI1576) respectively. **Figures 4-7, 9 and 11-21** illustrate molecular marker sequences from different Gram-positive bacteria or Gram-negative bacteria.

Example 4 Use of an assay according to the invention for molecular identification of various *Bacillus* species and strains

The present example illustrates the use of an assay according to the invention for the molecular identification of various *Bacillus* species, including *Bacillus anthracis*, species that cannot be discriminated with ribosomal 16S rDNA gene (La Scola *et al*, 2003). **Table 4** summarizes the results obtained for the various *Bacillus* species with the current genotyping assay. The analyses were performed using the markers I, II and III. Marker I corresponds to the Spy0160 sequence, Marker II corresponds to the Spy1372 sequence, Marker III corresponds to the SpyM3_0902 & Spy M3_0903 sequence.

Primers were designed for these markers and with these primers DNA of *Bacillus* was amplified. Then, the obtained amplified sequences were sequenced and compared by alignment. **Table 4** indicates the number of modified nucleotides in the amplified marker sequences of these different *Bacillus* species and strains. The 16S ribosomal marker is not relevant in this context and cannot be used for identifying *Bacillus* species because the amplicons corresponding to each *Bacillus* species will give comparable nucleic acid sequences, with variations not exceeding 1% on the whole gene.

Table 4 Use of different molecular markers for the identification of *Bacillus* species

	Molecular marker	<i>B. cereus</i> 10987	<i>B. cereus</i> 14579	<i>B. thuringiensis</i> 4Q2-72 israelensis	<i>B. anthracis</i> 1978
<i>B. cereus</i> 10987	Marker III (SEQ ID NO: 168)		8	29	29
	Marker I (SEQ ID NO: 18)		1	23	21
	Marker II (SEQ ID NO: 70)		2	3	11
	16S		0	0	ND
<i>B. cereus</i> 14579	Marker III (SEQ ID NO: 169)	8		32	31
	Marker I (SEQ ID NO: 19)	1		22	20
	Marker II (SEQ ID NO: 71)	2		5	13
	16S	0		0	ND
<i>B. thuringiensis</i> 4Q2-72 israelensis	Marker III (SEQ ID NO: 170)	29	32		12
	Marker I (SEQ ID NO: 33)	23	22		30
	Marker II (SEQ ID NO: 80)	3	5		12
	16S	0	0		ND
<i>B. anthracis</i> 1978	Marker III (SEQ ID NO: 162)	29	31	12	
	Marker I (SEQ ID NO: 12)	21	20	30	
	Marker II (SEQ ID NO: 64)	11	13	12	
	16S	ND	ND	ND	

ND = not determined

This example shows unambiguously that the combined use of several unrelated molecular markers markedly improves bacterial species identification, as well as, to some extent, characterization of a well-determined strain within a particular species. The present

method is so specific that it can go beyond the species identification and discriminate strains of the same species.

Example 5 Nucleic acid probes according to the present invention

This example illustrates an oligonucleotide (nucleic acid probe) that has been designed from marker I of *Staphylococcus aureus* (SEQ ID NO: 23) 5'-gtgtaggctcctacattcgtttc-3' (SEQ ID NO: 478). This oligonucleotide is specific for *S. aureus* species and can therefore allow discrimination of this species with other bacteria whereas another nucleic acid probe, the oligonucleotide 5'-cattcgtttcaaaggtaatg-3' (SEQ ID NO:479) which is located on the same marker allows discrimination of different strains of *S. aureus* (i.e. strains MRSA MW2 and MRSA COL versus strains Mu-50 and N315). These multi-resistant strains carry different methicillin resistance cassette chromosome and their resistance patterns to antimicrobials agents are different.

The illustrated nucleic acid probes can for instance advantageously be used in an assay according to the present invention, on a DNA chip according to the present invention. The two oligonucleotides provided above can be considered as specific probes which can be bound on a biochip and therefore allow discrimination between various amplicons obtained from MRSA strains amplified with the primers of **table 3**.

Conclusion

The present invention demonstrates that multigenotypic molecular analyses according to Gram-, genus- species- and strain-specificity can be achieved by using concomitantly or sequentially a panel of distinct conserved molecular markers, either by conventional polymerase chain reaction PCR (with exploitation of single nucleotide specific polymorphism or SNP) , real-time PCR (with/without specific Taqman probes), or post-PCR reverse hybridization on solid support (micro-, macro- or nano-array). The analyses allow a fast and specific detection of bacterial DNA and a wide bacterial genotyping in human, animal or environmental samples.

The combined use of the herein described molecular markers allows rapid and specific molecular identification of a wide panel of bacteria in samples and/or tissues, even in samples showing a background bacterial flora. To the applicant's knowledge, there is no such diagnostic tool that is based on the use of a panel of various highly conserved bacterial molecular markers for detecting and identifying bacteria according to Gram-, genus-, species-, and to some extent also strain- classification. Compared to the existing typing systems, we believe that this is a major improvement, in view of the increased need for rapid

and multigenotypic bacterial diagnoses, especially when considering nosocomial infections and epidemic bacterial diseases occurring in a natural, accidental or criminal setting. To this respect, molecular typing of bacteria according to the Gram phenotype is of particular interest when appropriate antibiotherapy has to be rapidly started.

5

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Claims

1. An assay for detecting and identifying one or more micro-organisms in a sample, characterized in that said assay comprises the use of at least two conserved molecular markers.
5
2. Assay according to claim 1, characterized in that said micro-organisms are bacteria.
3. Assay according to claims 1 or 2, characterized in that said assay comprises the use of at least one molecular marker that is conserved in Gram-positive bacteria and at least one molecular marker that is conserved in Gram-negative bacteria.
10
4. Assay according to any of claims 1 to 3, characterized in that said molecular marker that is conserved in Gram-positive bacteria is selected from the group comprising the Spy0160, Spy1372, SpyM3_0902 and SpyM3_0903, and Spy1527 sequences.
15
5. Assay according to any of claims 1 to 3, characterized in that said molecular marker that is conserved in Gram-positive bacteria is selected from the group comprising the sequences with SEQ ID NOs 1-62, 64-107, 109-111, 117-129, 137, 145-148, 150-193, 233-237, 240-241, 255, 326-395, 397-399, 404-425.
20
6. Assay according to any of claims 1 to 3, characterized in that said molecular marker that is conserved in Gram-negative bacteria is selected from the group comprising the Ecs0036, HI1576, EG10839 and EG11396, and HI0019 sequences.
25
7. Assay according to any of claims 1 to 3, characterized in that said molecular marker that is conserved in Gram-negative bacteria is selected from the group comprising the sequences with SEQ ID NOs 63, 108, 112-116, 130-136, 138-144, 194-232, 238-239, 242-254, 256-325, 396, 400-403, 426-461.
30
8. Use of an assay according to any of claims 1 to 7 for diagnosing bacterial infection of a sample.
9. A primer pair suitable for amplifying a molecular marker that is conserved in Gram-positive bacteria as defined in claims 4 or 5.
35

10. A primer pair suitable for amplifying a molecular marker that is conserved in Gram-negative bacteria as defined in any of claims 6 or 7.

5 11. A nucleic acid probe capable of hybridizing to a molecular marker that is conserved in Gram-positive bacteria as defined in claims 4 or 5.

12. A nucleic acid probe capable of hybridizing to a molecular marker that is conserved in Gram-negative bacteria as defined in claims 6 or 7.

10

13. A composition comprising at least one primer pair suitable for amplifying a molecular marker that is conserved in Gram-positive bacteria as defined in claims 4 or 5, and at least one primer pair suitable for amplifying a molecular marker that is conserved in Gram-negative bacteria as defined in claims 6 or 7.

15

14. A composition comprising at least one nucleic acid probe capable of hybridizing to a molecular marker that is conserved in Gram-positive bacteria as defined in claims 4 or 5 and at least one nucleic acid probe capable of hybridizing to a molecular marker that is conserved in Gram-negative bacteria as defined in claims 6 or 7.

20

15. A kit for detecting and identifying one or more micro-organisms, preferably bacteria, in a sample, which comprises a composition according to claim 13 and/or claim 14.

25

16. A DNA chip in which at least one nucleic acid probe capable of hybridizing to a molecular marker that is conserved in Gram-positive bacteria as defined in claims 4 or 5, and at least one nucleic acid probe capable of hybridizing to a molecular marker that is conserved in Gram-negative bacteria as defined in claims 6 or 7, is immobilized on a solid support.

30

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Figure 1 Amplification of molecular marker I (pur A) in Gram-positive bacteria

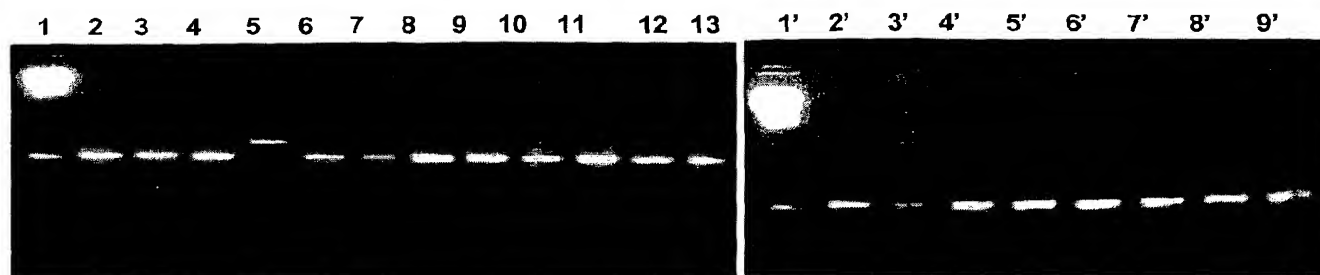
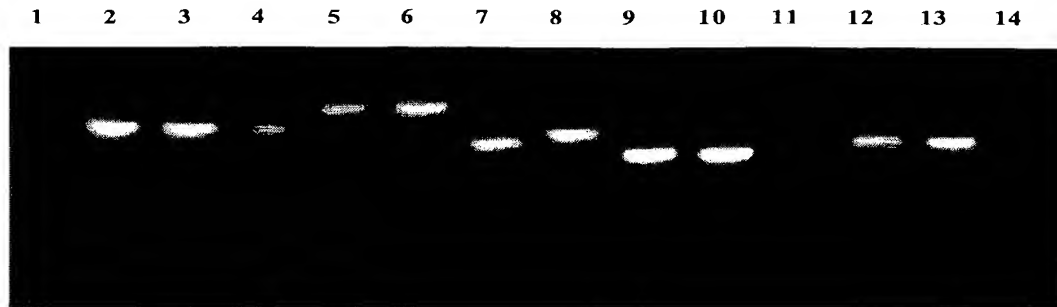
1 = DNA Ladder (λ /Hind III)2 : *Streptococcus pyogenes*3. *Streptococcus pneumoniae*4. *Streptococcus oralis*5. *Enterococcus hirae*6. *Enterococcus casseliflavus*7. *Streptococcus agalactiae*8. *Streptococcus sanguis*9. *Enterococcus faecalis*10. *Enterococcus gallinarum*11. *Enterococcus faecium*12. *Enterococcus flavescens*13. *Enterococcus durans*1' : DNA Ladder (λ /Hind III)2' : *Enterococcus raffinosus*3' : *Enterococcus villorum*4' : *Staphylococcus aureus*5' : *Staph. epidermidis*6' : *Staphylococcus hominis*7' : *Bacillus anthracis*8' : *Bacillus cereus*9' : *Bacillus megatherium*

Figure 2. Amplification of molecular marker II (ptsI) in Gram-positive bacteria

L = DNA ladder (123 bp)

1. *Bacillus anthracis*
2. *Bacillus cereus*
3. *Listeria monocytogenes*
4. *Bacillus subtilis*
5. *Streptococcus pneumoniae*
6. *Streptococcus pyogenes*
7. *Streptococcus agalactiae*
8. *Streptococcus mutans*
9. *Enterococcus faecalis*
10. *Staphylococcus aureus*
11. *Staphylococcus epidermidis*
12. *Bacillus thuringensis*
13. *Staphylococcus hominis*
14. *Enterococcus faecium*
15. *Clostridium perfringens*
16. *Bacillus mycoides*
17. Negative control
18. Negative control

Figure 3. Amplification of molecular marker III (SpyM3_0902- SpyM3_0903) in Gram-positive bacteria



1. DNA Ladder
- 2 : *Streptococcus pyogenes*
3. *Streptococcus pneumoniae*
4. *Enterococcus faecalis*
5. *Streptococcus agalactiae*
6. *Streptococcus sanguis*
7. *Enterococcus casseliflavus*
8. *Streptococcus oralis*
9. *Bacillus anthracis*
10. *Bacillus cereus*
11. *Enterococcus raffinosus*
12. *Enterococcus gallinarum*
13. *Enterococcus flavescens*
14. Negative control of PCR.

Figure 4: Marker I (PurA) sequences amplified from different Gram positive bacteria (SEQ ID NOs 1-62), and from a Gram-negative bacterium (SEQ ID NO: 63)

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GTCTGAGTATCAGGTATTACTAACCTCTCTCTGAATTCAATTGATGTTCTTTTCAGGGCTTGATACGGTGAAAATTT
GTGTGGCTTATGACCTTGATGGGAAACGTATTGACTATTACCCAGCAAGCCTTGAACAGCTAAAACGTTGTAAAC
CAATCTATGAAGAATTACCGGGCTGGTCTGAAGATATTACAGCTTGTCGTAGCTTAGATGATCTTCCAGAAAATG
CACGTAATTACGTTCCCGTGTTGGCGAATTGGTTGGTGTTCGTATTTCTACTTTNCTCAGTAGGNCCAGGTC

5. *Streptococcus sanguis* (SEQ ID NO. 5)**SSAN**

CTTTTTGAAGGGGCTCAAGGAGTTATGCTCGACATTGATCAAGGAACATACCCATTTGTAACATCTTCCAATCCA
GTAGCAGGTGGTGTCACAATTGGTTCGGGAGTTGGACCAAGTAAATTAATAAAGTAGTAGGTGTATGTAAAGCT
TACACTAGCCGTGTTGGTGATGGACCATTCCCAACAGAACTTTTTGATGAGGTTGGTGACCGTATTTCGTGAGATT
GGTAAAGAGTATGGTACAACGACCGTCTGCTCGCGTTGGATGGTTTGATTCTGTTGTTATGCGTCACAGC
CGTCGAGTATCAGGTATTACTAACCTCTCTCTGAATTCAATTGATGTTCTTTTCAGGGCTTGATACGGTGAAAATT
TGTGTGGCTTATGACCTTGATGGGAAACGTATTGACTATTACCCAGCAAGCCTTGAACAGCTAAAACGTTGTAAA
CCAATCTATGAAGAATTACCGGGCTGGTCTGAAGATATTACAGCTTGTCGTAGCTTAGATGATCTTCCAGAAAAT
GCACGTAATTACGTTCCCGTGTTGGCGAATTGGTTGGTGTTCGTATTTCTACTTTCTCAGTTGGGTCCAGACC

6. *Enterococcus faecium* (SEQ ID NO. 6)**EFCM**

TTCTTGAAGGGGCGCAAGGGGTTATGCTGGATATTGACCAAGGGACTTATCCATTTGTAACCTCTTCTAATCCA
GTTGCAGGGGAGTCACCATCGGTTCCGGTGTTGGTCCGAGCAAAATTGACAAGGTAGTTGGTGTCTGCAAGGCCT
ACACCAGTCGGGTCGGAGATGGACCATTCCCAACAGAGCTTTTTGATGAAGTTGGTGACCGCATTCGTGATATCG
GCCACGAATATGGCACTACCACTGGTCGCCACGTCGGGTAGGTTGGTTGACTCGGTTGTTATGCGCCATAGCC
GCCGTGTATCAGGGATTACCAATCTTTCGCTTAACTCCATCGATGTCTTGAGTGGTCTGGATACAGTGAAAATCT
GTGTAGCTTATGACTTGGATGGCCAAAGAATCGACCACTACCCAGCTAGTCTGGAACAGCTCAAGCGCTGCAAGC
CGATTTACGAAGAGCTGCCAGGCTGGTCAGAGGACATCACTGGAGTCCGCAGTCTGGAAGACTTGCCAGAAAATG
CCCGTAACTATGTTCCCGAGTGAGTGAGCTGGTTGGCGTTCGCATTTCTACCTTNCTCAGTAGGGCCAGACC

7. *Enterococcus durans* (SEQ ID NO. 7)**EDUR**

CTCTTTGAAGGGGCACAAGGTGTGATGTTGGATATCGATCAAGGAACGTATCCATTTGTGACTTCTTCTAATCCG
GTAGCTGGTGGTGTAAACGATCGGTAGTGGCGTTGGCCCTTCAAAGATCAATAAAGTCGTTGGTGTATGTAAAGCT
TATACTTCTCGTGTAGGAGATGGCCCATTTCCCAACAGAACTATTTGACGAAACAGGTCAACAAATCCGTGAAGTC
GGTCGTGAATATGGTACGACAACAGGTCGACCTCGTCGTGTCGTTGGTTTGATACAGTCGTGGTGCGCCATTCA
AAACGTGTATCAGGAATCACTAACCTATCATTGAATTCAATCGATGTATTAAGCGGACTAGAAACAGTAAAAATC
TGTACAGCGTATGAATTAGATGGAGAATTGATCTATCATTACCCAGCAAGCCTGAAAGAATTGAAACGTTGCAAA
CCAGTATACGAAGAACTTCTTGGTTGGTCTGAAGATATTACAGCATGTAAAACACTTGCTGAACTACCAGAAAAC
GCCCCTAACTATGTTAGACGTATCTCAGAGCCTGTAGGAGTCCGTATTTCAACATTCTCAGTAGGTCCAGACC

8. *Streptococcus pyogenes* (SEQ ID NO. 8)**SPYO**

CTATTTGAAGGGGCACAAGGGGTTATGCTTGATATTGACCAGGAACGTACCCATTTGTAACGTCTTCAAACCCAG
TTGCTGGTGGTGTAAACCATTTGGTTCTGGTGTGGCCCAATAAAATCAACAAAGTAGTTGGTGTCTGTAAAGCCT
ACACAAGCCGTGTCGGTGATGGGCCATTCCCTACAGAACTCTTTGATGAAGTGGGTGAGCGCATTCGTGAAGTGG
GTCATGAGTACGGGACAACGACCGGCCGTCCACGTCGTGTCGTTGGTTTGATTGGTTGTCATGCGCCACAGTC

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GTCGTGTATCAGGTATTACTAACCTCTCTCTGAATTCAATTGATGTTCTTTCAGGGCTTGATACGGTTAAGATTT
GTGTGGCTTATGACCTTGATGGGAAACGTATTGACTATTACCCAGCAAACCTTGAACAACCTCAAACGTTGCAAAC
CAATCTATGAAGAATTACCAGGCTGGCAAGAGGACATCACAGGTGTTTCGTAGCCTTGATGAGCTTCCTGAAAATG
CCCGCAACTACGTTTCGTTCGTGTTGGAGAATTGGTTGGCGTTCGCATTTCAACCTTCTCAGTTGGGCCAGACC

9. *Streptococcus pneumoniae***(SEQ ID NO. 9)****SPNE**

CTATTTGAAGGGGCTCAAGGTGTTATGCTAGATATCGACCAAGGTACTTATCCATTTGTTACGTCATCAAACCTT
GTAGCTGGTGGTGTGACAATTGGTTCTGGTGTCCGCTCCAAGCAAGATTGACAAGGTTGTAGGTGTATGTAAAGCT
TATACGAGTCGTGTAGGAGATGGTCCTTTCCCAACTGAGTTGTTTGATGAAGTGGGAGAACGTATCCGTGAAGTG
GGTCATGAATATGGTACAACAACCTGGTTCGTCCACGTCGTGTAGGTTGGTTTGACTCAGTTGTGATGCGTCATAGC
CGTCGTGTTTCTGGTATTACTAACCTTTCTTTGAACTCTATTGATGTTTTGAGCGGTTTGGATACTGTGAAAATC
TGTGTGGCCTATGATCTTGACGGTCAACGTATTGACTACTATCCAGCTAGTCTTGAGCAATTGAAACGTTGCAAG
CCTATCTATGAAGAGTTGCCAGGTTGGTCAGAAGATATTACCGGAGTTCGCAATTTGGAAGATCTTCCTGAGAAT
GCGCGTAACTATGTTTCGTTCGTGTGAGTGAATTGGTTGGCGTTCGTATTTCTACTTTTCTCAGTAGGTCCAGGCC

10. *Streptococcus oralis* (SEQ ID NO. 10)**SORA**

CTTTTCGAAGGTGCGCAAGGTGTCATGTTGGACATTGATCAAGGGACTTATCCATTTGTTACTTCTTCAAACCTT
GTCGCTGGTGGTGTGACGATTGGGTCTGGTGTGGTCCAAGTAAGATTGACAAGGTTGTAGGTGTCTGTAAAGCC
TACACAAGTCGTGTAGGAGATGGACCGTTCCCAACTGAATTATTTGATGAAGTGGGAGATCGCATCCGTGAAGTA
GGTCATGAATATGGTACAACAACCTGGTTCGTCCACGTCGTGTGGGTTGGTTTGACTCAGTTGTGATGCGTCACAGC
CGCCGTGTATCTGGGATTACCAATCTTTCAATTGAACTCTATAGATGTTTTGAGTGGTTTGGATACTGTGAAAATC
TGTGTGCGCTATGATCTTGATGGTCAACGTATTGATTACTATCCTGCTAGTCTTGAGCAGTTGAAACGTTGTAAG
CCAATCTACGAGGAATTGCCAGGTTGGTCAGAAGACATCACTGGAGTCCGTAATTTGGAAGACCTTCCTGAGAAT
GCACGCAACTATGTTTCGTTCGTGTAAGCGAGTTGGTTGGTGTTCGTATCTCAACTTTCTCAGTTGGGCCAGATC

11. *Staphylococcus hominis* (SEQ ID NO. 11)**SHOM**

CTCTTTGAAGGAGCGCAAGGAGTTATGTTAGATATCGACCATGGTACATATCCTTTTGTAACGTCAAGTAATCCT
GTGGCAGGTAATGTGACAGTAGGAACCTGGCGTGGGTCCAACCTTCGTATCTAAAGTGATTGGGGTATGTAAATCC
TATACATCTCGTGTAGGTGACGGCCCATTCCTACTGAATTATTCGACGAAGATGGTCATCATATTAGAGAAGTA
GGTCGTGAATATGGAACGACAACAGGACGTCCTCGTCGTGTAGGTTGGTTCGACTCAGTTGTATTACGTCACTCT
CGTCGTGTAAGTGGTATTACAGACTTATCTATTAACCTCAATTGACGTTTTAACAGGTTTAGATACGGTTAAATT
TGTACAGCTTATGAGTTAGATGGTGAAACAATCACAGAATATCCAGCAAACCTTAGACCAATTACGTCGTTGTAAA
CCAATTTTCGAAGAGTTACCTGGTTGGACGGAAGACATTACAGGTTGTCGTACATTAGAAGAATTACCTGAAAAC
GCACGTAAATACTTAGAACGTATTTCTGAATTATGTGGCGTTCATATTTCAATCTTCTCAGTAGGTCCAGGCC

12. *Bacillus anthracis* 1978 (SEQ ID NO. 12)

GCTTCANTCGACCCGGTACGTACCCGTTTCGTTACATCTTCTAACCCAATTGCTGGTGGTGTAAACAGTTGGAACCTG
GAGTTGGTCCTGCGAAAGTTACTCGCGTTGTAGGTGTATGTAAAGCATATACAAGCCGCGTTGGTGATGGTCCAT
TCCCTACTGAGCTTCATGACGAAATTGGTCATCAAATTCGTGAAGTTGGTCGTGAGTATGGAACGACAACCTGGTC
GTCCACGCCGCGTAGGTTGGTTTCGATAGCGTTGTTGTAAGACATGCACGTCGTGTTAGTGGTTTAAACAGATTTAT

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CATTAAACTCTATCGACGTTCTAACTGGTATTCCAACACTTAAATTTGTGTTGCTTACAAATGCGATGGGAAAG
TTATCGATGAAGTTCCAGCAAACCTTAAACATTTTAGCGAAATGTGAGCCTGTATACGAAGAGCTTCCAGGTTGGA
CAGAAGATATTACTGGTGTAAAGATCATTAGATGAGCTTCCTGAAAATGCACGAAAATACGTAGAACGTGTTTCTG
AGTTAACAGGAATTCAATTATCTATGTTCTCAGTG

13. *Bacillus anthracis* Butare (SEQ ID NO. 13)

GCTTGCTATCGACCCGGTACGTACCCGTTTCGTTACATCTTCTAACCCAATTGCTGGTGGTGTAAACAGTTGGAAC
GGAGTTGGTCCTGCGAAAGTTACTCGCGTTGTAGGTGTATGTAAAGCATATACAAGCCGCGTTGGTGATGGTCCA
TTCCCTACTGAGCTTCATGACGAAATTGGTCATCAAATTCGTGAAGTTGGTCGTGAGTATGGAACGACAACCTGGT
CGTCCACGCCGCGTAGGTTGGTTCGATAGCGTTGTTGTAAGACATGCACGTCGTGTTAGTGGTTTAAACAGATTTA
TCATTAAACTCTATCGACGTTCTAACTGGTATTCCAACACTTAAATTTGTGTTGCTTACAAATGCGATGGGAAA
GTTATCGATGAAGTTCCAGCAAACCTTAAACATTTTAGCGAAATGTGAGCCTGTATACGAAGAGCTTCCAGGTTGG
ACAGAAGATATTACTGGTGTAAAGATCATTAGATGAGCTTCCTGAAAATGCACGAAAATACGTAGAACGTGTTTCT
GAGTTAACAGGAATTCAATTATCTATGTTCTCGTG

14. *Bacillus anthracis* Sterne (SEQ ID NO. 14)

CTTCGACNCGGTACGTACCCGTTTCGTTACATCTTCTAACCCAATTGCTGGTGGTGTAAACAGTTGGAACCTGGAGTT
GGTCCTGCGAAAGTTACTCGCGTTGTAGGTGTATGTAAAGCATATACAAGCCGCGTTGGTGATGGTCCATTCCCT
ACTGAGCTTCATGACGAAATTGGTCATCAAATTCGTGAAGTTGGTCGTGAGTATGGAACGACAACCTGGTCGTCCA
CGCCGCGTAGGTTGGTTCGATAGCGTTGTTGTAAGACATGCACGTCGTGTTAGTGGTTTAAACAGATTTATCATT
AACTCTATCGACGTTCTAACTGGTATTCCAACACTTAAATTTGTGTTGCTTACAAATGCGATGGGAAAGTTATC
GATGAAGTTCCAGCAAACCTTAAACATTTTAGCGAAATGTGAGCCTGTATACGAAGAGCTTCCAGGTTGGACAGAA
GATATTACTGGTGTAAAGATCATTAGATGAGCTTCCTGAAAATGCACGAAAATACGTAGAACGTGTTTCTGAGTTA
ACAGGAATTCAATTATCTATGTTCTCAGTGGCCCC

15. *Bacillus anthracis* 1655H85 (SEQ ID NO. 15)

GGTNCGTACCCGTTTCGTTACATCTTCTAACCCAATTGCTGGTGGTGTAAACAGTTGGAACCTGGAGTTGGTCCTGCG
AAAGTTACTCGCGTTGTAGGTGTATGTAAAGCATATACAAGCCGCGTTGGTGATGGTCCATTCCCTACTGAGCTT
CATGACGAAATTGGTCATCAAATTCGTGAAGTTGGTCGTGAGTATGGAACGACAACCTGGTCGTCCACGCCGCGTA
GGTTGGTTCGATAGCGTTGTTGTAAGACATGCACGTCGTGTTAGTGGTTTAAACAGATTTATCATTAAACTCTATC
GACGTTCTAACTGGTATTCCAACACTTAAATTTGTGTTGCTTACAAATGCGATGGGAAAGTTATCGATGAAGTT
CCAGCAAACCTTAAACATTTTAGCGAAATGTGAGCCTGTATACGAAGAGCTTCCAGGTTGGACAGAAGATATTACT
GGTGTAAAGATCATTAGATGAGCTTCCTGAAAATGCACGAAAATACGTAGAACGTGTTTCTGAGTTAACAGGAATT
CAATTATCTATGTTCTCAGTGGCCCCNGGNCCNAN

16. *Bacillus anthracis* Coda-cerva (SEQ ID NO. 16)

GGTNCGTACCCGTTTCGTTACATCTTCTAACCCAATTGCTGGTGGTGTAAACAGTTGGAACCTGGAGTTGGTCCTGCG
AAAGTTACTCGCGTTGTAGGTGTATGTAAAGCATATACAAGCCGCGTTGGTGATGGTCCATTCCCTACTGAGCTT
CATGACGAAATTGGTCATCAAATTCGTGAAGTTGGTCGTGAGTATGGAACGACAACCTGGTCGTCCACGCCGCGTA
GGTTGGTTCGATAGCGTTGTTGTAAGACATGCACGTCGTGTTAGTGGTTTAAACAGATTTATCATTAAACTCTATC

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GACGTTCTAACTGGTATTCCAACACTTAAAATTTGTGTTGCTTACAAATGCGATGGGAAAGTTATCGATGAAGTT
CCAGCAAACCTAAACATTTTAGCGAAATGTGAGCCTGTATACGAAGAGCTTCCAGGTTGGACAGAAGATATTACT
GGTGTAAGATCATTAGATGAGCTTCCTGAAAATGCACGAAAATACGTAGAACGTGTTTCTGAGTTAACAGGAATT
CAATTATCTATGTTCTCAGTGGCCCCNNGGNCCCA

17. *Bacillus anthracis* 2054H82 (SEQ ID NO. 17)

NGCTTNAATCGACCCGGTACGTACCCGTTTCGTTACATCTTCTAACCCAATTGCTGGTGGTGTAAACAGTTGGAAC
GGAGTTGGTCCTGCGAAAGTTACTCGCGTTGTAGGTGTATGTAAAGCATATACAAGCCGCGTTGGTGATGGTCCA
TTCCCTACTGAGCTTCATGACGAAATTGGTCATCAAATTCGTGAAGTTGGTCGTGAGTATGGAACGACAACTGGT
CGTCCACGCCGCGTAGGTTGGTTTCGATAGCGTTGTTGTAAGACATGCACGTCGTGTTAGTGGTTTAAACAGATTTA
TCATTAAACTCTATCGACGTTCTAACTGGTATTCCAACACTTAAAATTTGTGTTGCTTACAAATGCGATGGGAAA
GTTATCGATGAAGTTCCAGCAAACCTAAACATTTTAGCGAAATGTGAGCCTGTATACGAAGAGCTTCCAGGTTGG
ACAGAAGATATTACTGGTGTAAAGATCATTAGATGAGCTTCCTGAAAATGCACGAAAATACGTAGAACGTGTTTCT
GAGTTAACAGGAATTCAATTATCTATGTTCTCAGT

18. *Bacillus cereus* ATCC 10987 (SEQ ID NO. 18) BCER10987

GNCNCGGTACGTACCCGTTTCGTTACATCTTCTAACCCAATTGCTGGCGGTGTAAACAGTTGGAACCTGGAGTTGGTC
CTGCGAAAGTTACTCGCGTTGTAGGTGTATGTAAAGCATATACAAGCCGCGTTGGTGATGGTCCATTCCCTACTG
AGCTTCATGATGAAATTGGTCATCAAATTCGTGAAGTTGGTCGCGAGTATGGAACGACAACTGGTCGTCCACGCC
GCGTAGGTTGGTTTCGATAGCGTTGTTGTAAGACATGCACGTCGTGTTAGTGGTTTAAACGATCTATCATTAAATT
CTATCGACGTTTTAACAGGTATTCCAACCTCTTAAAATTTGTGTAGCTTACAAATACAATGGCGAAGTTATTGATG
AAGTTCCAGCTAACTTAAACATTTTAGCGAAATGTGAGCCTGTATATGAAGAGCTTCCAGGTTGGGAAGAAGATA
TTACTGGTGTAAAATCATTAGATGAACTTCCTGAAAATGCACGAAAATACGTAGAACGTGTTTCTGAGTTAACAG
GAATTCAAATATCTATGTTCTCAGTAGNCCCC

19. *Bacillus cereus* ATCC 14579 (SEQ ID NO. 19) BCER14579

GGTCGTACCCGTTTCGTTACATCTTCTAACCCAATTGCTGGTGGTGTAAACAGTTGGAACCTGGAGTTGGTCCTGCGA
AAGTTACTCGCGTTGTAGGTGTATGTAAAGCATATACAAGCCGCGTTGGTGATGGTCCATTCCCTACTGAGCTTC
ATGATGAAATTGGTCATCAAATTCGTGAAGTTGGTCGCGAGTATGGAACGACAACTGGTCGTCCACGCCGCGTAG
GTTGGTTTCGATAGCGTTGTTGTAAGACATGCACGTCGTGTTAGTGGTTTAAACGATCTATCATTAAATTCTATCG
ACGTTTTAACAGGTATTCCAACCTCTTAAAATTTGTGTAGCTTACAAATACAATGGCGAAGTTATTGATGAAGTTC
CAGCTAACTTAAACATTTTAGCGAAATGTGAGCCTGTATATGAAGAGCTTCCAGGTTGGGAAGAAGATATTACTG
GTGTAAAATCATTAGATGAACTTCCTGAAAATGCACGAAAATACGTAGAACGTGTTTCTGAGTTAACAGGAATTC
AAATATCTATGTTCTCAGTNGGCCCC

20. *Bacillus megatherium* (SEQ ID NO. 20)

BMEG

CTATTCGAAGGGGCACAAGGTGTTATGTTAGATATCGATCAAGGAACATATCCATTGTTACATCTTCAAACCCA
GTAGCGGGTGGAGTAACAATTGGTTCTGGGGTAGGTCCATCTAAAATCAAACACGTTGTAGGTGTATCAAAAGCG
TATACAACTCGTGTGGTGACGGCCCTTTCCCAACTGAATTAACAAACGAAATCGGTGATCAAATCCGTGAAGTA
GGACGTGAATATGGTACAACAACCTGGTCGTCTCGCCGTGTAGGTTGGTTCGACAGTGTAGTTGTACGTCATGCT

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CGTCGCGTTAGTGGAATCACAGATCTATCTTTAACTCAATTGATGTATTAACGGGAATTGAGACATTAAAGATT
TGCGTAGCTTATCGTTATAAAGGGGAAGTTATGGAAGAATTCCCTGCTAGCTTAAAAACACTTGACAGAGTGCGAA
CCTGTATATGAAGAGCTTCCAGGTTGGACAGAAGATATTACGGGTGTGAAAACATTAGATGAGTTACCTGATAAC
GCTCGCCACTACTTAGAGCGCGTGTCTCAATTAACAGGTATTCCTTTATCTATTTTCTCAGTAGGTCCAGGCC

21. *Enterococcus casseliflavus* (SEQ ID NO. 21) ECAS

TATTCGAAGGNAGCTCAAGGCGTGATGCTGGATATCGACCAAGGAACCTATCCTTTCGTGACATCATCCAACCCC
GTTGCTGGAGGTGTCACCATCGGTAGTGGTGTGGGTCTTCAAAAATCAACAAAGTCGTTGGTGTCTGCAAAGCT
TACACCTCTCGGGTAGGAGATGGTCCTTTCCCAACGGAACGTGTTTGATGAAACAGGTGAACAAATTCGTAAGATC
GGTCGTGAATACGGAACAACGACAGGACGTCCTCGCCGTGTGGGCTGGTTTGATACCGTCGTGATGCGCCATTCA
AAACGGGTCTCAGGGATCACGAATCTATCCCTTAACTCGATCGATGTCTTGAGCGGCTTAGAAACCGTGAAGATC
TGTACGGCTTATGAACTAGACGGCGAATTGATCTATCATTACCCAGCAAGCTTGAAAGAGTTGAACCGCTGCAAA
CCAGTCTACGAAGAACTTCTTGGCTGGTCTGAAGACATTACTGGCTGCAAAACATTAGCAGATCTGCCAGAAAAT
GCACGCAATTACGTTCAACGCATCTCTGAATTAGTCGGTGTCCGCATTTTCGACCTTCTCAGTAGGTCCAGACC

22. *Enterococcus raffinosus* (SEQ ID NO. 22) ERAF

CTATTTGAAGGTGCTCAAGGCGTTATGCTGGATATTGATCAAGGAACCTATCCATTTGTTACTTCTTGAACCCA
GTTGCCGGTGGGGTAACTATCGGTAGTGGTGTAGGACCTGCTAAAATCGACAAAGTTGTCGGTGTGTTGTAAAGCC
TATACTTCACGCGTAGGTGATGGACCTTTCCTCAACTGAATTGTTTGATGAAGTTGGAGATCAGATTTCGTGAAGTC
GGTCGTGAATATGGAACGACTACTGGTCGTCCACGTCGTGTGGGCTGGTTTGACTCGGTTGTGATGCGTCATTCA
AAACGTGTTTCTGGGATTACGAATCTTCTTTAACTCGATTGATGTCTTGAGCGGTCTGGATACAGTGAAAATT
TGTACAGCGTATGAGCTGGACGGAGAACTAATTTACCATTATCCAGCAAGCCTAAAAGAATTAATTCGTTGTAAG
CCCGTTTATGAAGAACTACCTGGTTGGAGCGAAGATATTACAGGCTGCCGTGATTTAGCTGATCTACCGGAAAAT
GCGCGTAATTATGTACGTCGCGTTTCTGAACTTGTGGGTGTGCGTATCTCGACCTTCTCAGTTGGTCCTGGTC

23. *Staphylococcus aureus* (SEQ ID NO. 23) SAUR

CTATTTGAAGGGGCACAAGGTGTAATGTTAGATATCGACCATGGTACATATCCATTCGTTACATCAAGTAATCCA
ATTGCAGGTAACGTTACTGTTGGTACAGGTGTAGGTCCTACATTCGTTTCAAAGGTAATTGGTGTATGTAAAGCT
TATACATCACGTGTTGGTGTGATGGTCCATTCCCTACTGAATTATTCGATGAAGATGGACATCATATTAGAGAAGTT
GGTCGTGAATATGGTACAACAACAGGACGTCCACGTCGTGTAGGTTGGTTTGATTGAGTTGTATTACGTCACTCT
CGTCGTGTAAGTGGTATTACAGATTTATCTATTAACCTCAATCGATGTTTTAACAGGCCTAGACACAGTGAAAATC
TGTACAGCTTATGAATTAGACGGTAAAGAAATTACTGAGTACCCAGCAAACTTAGATCAATTAACCGTTGTAAA
CCAATCTTTGAAGAGTTACCAGGTTGGACAGAAGACGTAACAAGTGTGCGTACTTTAGAAGAATTACCTGAAAAT
GCACGTAAATATTTAGAGCGTATTTTCAGAATTATGTAATGTACAAATTTCTATCTTCTCAGTAGGTCCAGGCC

24. *Staphylococcus epidermidis* (SEQ ID NO. 24) SEPI

CTCTTCGAAGGTGCTCAAGGTGTCATGTTAGATATCGACCATGGTACATATCCATTCGTTACATCTAGTAATCCA
GTTGCAGGTAACGTTACAGTAGGTACAGGTGTTGGCCCTACATCAGTGTCTAAAGTGATTGGTGTATGTAAATCA
TATACATCTCGTGTAGGTGACGGTCCATTCCCAACTGAACTTTTTGATGAAGATGGCCACCATATTAGAGAAGTG
GGTCGTGAATATGGTACAACACTACTGGACGTCCACGTCGTGTAGGTTGGTTTCGACTCAGTTGTATTACGTCATTCA

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CGTCGTGTAAGTGGTATCACAGATCTTTCAATTAACCTCAATCGACGTTTTTAACAGGATTAGACACAGTTAAAATT
TGTAAGTGTACGAATTAGATGGTGAAAAAATTACTGAATACCCAGCAAACCTTAGATCAATTAAGACGTTGTAAA
CCTATCTTCGAAGAGCTTCCAGGTTGGACTGAAGACATTACAGGTTGTCGTAGTTTAGATGAACTTCCTGAGAAT
GCACGTAATTACTTAGAGCGTATTTTCAGAAATTATGCGGTGTCCATATTTCAATCTTCTCAGTAGGTCCTGGTC

25. *Streptococcus mitis* (SEQ ID NO. 25) SMIT

TATGGCTAGCNATAGACCAAGGTACGTATCCATTTGTTACGTCATCAAACCTGTGGCTGGTGGTGTACGATTG
GTTCTGGTGGTGGTCCAAGTAAGATTGACAAGGTTGTAGGTTTATGTAAAGCCTATACGAGTCGAGTAGGAGACG
GTCCTTTCCCAACTGAATTGTTTGATGAAGTGGGAGAACGTATCCGTGAAGTTGGTCATGAATATGGTACAACAA
CTGGTCGTCCACGTCGTGTGGGTTGGTTTGACTCAGTTGTGATGCGTCATAGTCGTGCTGTTTCTGGTATTACTA
ATCTTTTCATTGAACCTCTATCGATGTTTTGAGTGGTTTAGATACAGTGAAAATCTGTGTGGCCTATGATCTTGATG
GTCAACGTATTGACTACTATCCAGCTAGTCTTGAGCAATTGAAACGTTGCAAGCCTATCTATGAAGAGTTGCCAG
GTTGGTCAGAAGATATTACTGGAGTTCGTAATTTGGAAGATCTTCCTGAGAATGCGCGTAACCTATGTTTCGTGCTG
TGAGTGAATTGGTTGGCGTTCGTATTTCTACTTTCTCAGTAG

26. *Streptococcus species* (SEQ ID NO. 26) SSPE

ATGGCTTGCTATTGACCAAGGGTACATACCCATTTGTAACATCATCTAACCCAGTCGCTGGTGGTGTAAACAATCG
GTTCTGGTGGTGGTCCAAGTAAATCAACAAAGTTGTCGGTGTATGTAAAGCCTACACAAGCCGTGTTGGTGACG
GACCATTCCCAACTGAACTTTTAGACGAAGTTGGTGACCGCATCCGTGAAGTGGGTACGAATATGGGACAACAA
CTGGACGTCCACGTCGTGTTGGTTGGTTTGACTCAGTTGTTATGCGTCACAGCCGCCGCGTATCAGGTATCACAA
ACTTGTCACTTAACTCAATTGACGTTCTTTCAGGTCTTGATACGGTCAAATCTGTGTGGCATAACGACCTTGACG
GTCAACGTATCGACCACTACCCAGCAAGCCTTGAACAATTGAAACGTTGTAAACCAATCTACGAAGAATTGCCAG
GTTGGTCAGAAGACATCACAGGTTGCCGTAGCCTAGATGAACTTCCCGAAAATGCTCGTGACTACGTTCCGCCGTG
TTGGTGAACCTCGTTGGTGTTCGCATTTCAACATTCTCAGTTGGCCCC

27. *Streptococcus canis* (SEQ ID NO. 27) SCAN

TGGCTTGCNATCGACCAAGGTAACCTATCCATTTGTTACTTCTTCAAACCCAGTTGCTGGTGGGGTAACAATCGG
TTCAGGTGTTGGTCCAAGCAAGATCAATAAAGTTGTCGGTGTATGTAAAGCTTACACAAGCCGTGTTGGTGACGG
TCCGTTCCCAACAGAACTTCTAGATGAAGTTGGAGATCGTATCCGTGAAATTGGTCACGAATATGGTACAACAAC
TGGACGTCCACGTCGTGTTGGTTGGTTTGACTCAGTTGTTATGCGTCACAGCCGCCGCGTATCAGGTATCACAAA
CTTGTCACTTAACTCAATCGATGTTCTTTCAGGACTTGATACTGTTAAAATCTGTGTGGCATAACGACCTTGACGG
TCAACGTATCGACCACTACCCAGCAAGTCTTGAACAATTGAAACGTTGTAAACCAATCTACGAAGAATTGCCAGG
TTGGTCAGAAGACATCACAGGTTGCCGTAGCCTAGATGAACTTCCCGAAAATGCTCGTGACTACGTTCCGCCGTG
TGGTGAACCTCGTTGGTGTTCGCATTTCAACATTCTCAGTTGGCCCC

28. *Streptococcus mutans* (SEQ ID NO. 28) SMUT

TATGGCTTGCNATTGACCAAGGTAACCTATCCATTTGTAACCTTCATCAAATCCAGTTGCAGGTGGCGTTACCATC
GGATCTGGTGGTGGACCAAGTAAATCAATAAGGTTGTTGGTGTCTGCAAAGCCTATACCAGCCGTGTAGGTGAT
GGTCCTTTCCCAACAGAACTTTTTGACCAAACGGGAGAGCGCATTCGTGAAGTTGGGCATGAATACGGGACAACA
ACAGGGCGTCCGCGTCGAGTTGGTTGGTTTGACTCAGTTGTTATGCGTCACAGCCGCCGCGTATCAGGCATTACC

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AATTTATCTCTTAAGTGTATTGATGTACTTTTCAGGTCTTGATATCGTAAAAATCTGTGTAGCCTATGATTTGGAT
GGAAAACGGATTGATCACTACCCTGCCAGTCTCGAACAACCTCAAACGCTGTAAACCTATTTATGAAGAATTGCCG
GGCTGGTCTGAAGATATTACAGGGGTTCGCAGTTTAGAAGATCTTCCTGAAAATGCTCGTAATTATGTCCGCCGT
GTAAGTGAATTAGTTGGTGTTCGTATTTCTACTTTCTCAGTNGTCCCC

29. *Streptococcus gordonii* (SEQ ID NO. 29)

SGOR

TAATGCTAGCAATTGACCAAGGTACCTATCCATTTGTAACCTCATCTAATCCAGTTGCTGGTGGTGTAAACGATCG
GTTCTGGTGTGGGTCCCTAGCAAGATTGACAAAGTAGTGGGTGTTTGTAAGCCTATACAAGTCGTGTTGGTGATG
GTCCTTTCCCAACAGAGCTTTTCGATGAAGTAGGTGACCGCATTCGTGAGGTTGGTCATGAGTATGGTACAACAA
CAGGACGTCCGCGTCGAGTTGGTTGGTTTGACTCTGTTGTTATGCGCCATAGCCGCCGTGTATCTGGGATTACCA
ATCTTTTCGCTTAAGTCTATCGATGTTTTGAGCGGTCTGGATACAGTCAAGATCTGTGTAGCCTATGATTTGGATG
GCCAAAGAATCGACCACTATCCAGCTAGTTTGGAACAGCTTAAACGTTGTAAGCCGATTTACGAAGAGCTTCCTG
GATGGTCTGAAGATATTACTGGCGTTCGTAAGTTAGAAGATCTTCAGAAAATGCTCGCAACTATGTTTCGGCGAG
TAAGCGAGTTGGTTGGTGTACGTATTTCCACCTTCTCAGTTGGCCCC

30. *Bacillus species* (SEQ ID NO. 30)

BSPE

TATGGCTTGCAATTGACNCGGTACGTACCCATTCGTTACATCTTCTAACCCGATTGCGGGTGGTGTAAACAGTTGG
AACTGGAGTTGGTCCTGCGAAAGTTACTCGCGTTGTAGGTGTATGTAAAGCATATACAAGCCGTGTTGGTGACGG
TCCATTCCCTACTGAACTTAATGATGAAATTGGTCATCAAATTCGTGAAGTTGGTCGTGAGTACGGAACAACAAC
TGGTCGTCCGCGCCGCGTAGGTTGGTTCGATAGCGTTGTTGTAAGACATGCGCGTCGTGTTAGTGGTTTTAACGGA
TCTATCATTAAATTCTATCGACGTTTTAACAGATATTCGACTCTTAAAATTTGTGTTGCTTACAAATACAATGG
CGAAGTTATCGATGAAGTTCCAGCAAACCTAAACATTTTAGCAAAATGTGAGCCTGTATATGAAGAGCTTCCAGG
TTGGACAGAAGATATTACTGGTGTAATAATCATTAGACGAGCTTCCTGAAAATGCACGAAAATACGTAGAACGTGT
TTCTGAGTTAACAGGAATTCAATTATCTATGTTCTCAGTNGTCCCC

31. *Bacillus pumilus* (SEQ ID NO. 31)

BPUM

GTTATGGCTTGCTATTGATCAAGGGACATATCCATTTGTCACGTCATCTAACCAGTAGCTGGAGGAGTGACGAT
TGGTTCTGGCGTAGGACCAACAAAAATTCAACATGTGGTCGGCGTGTCAAAGCGTACACAACACGTGTTGGAGA
TGGCCCATTCGGACAGAACTCCATGATGAAATTGGCGATCAAATCCGTGAGGTTGGCCGTGAATACGGTACAAC
AACTGGACGTCCGCGCCGTGTTGGCTGGTTTGACAGTGTGCTTGTCCGTCATGCTCGACGTGTGAGCGGGATTAC
AGATCTATCTCTTAAGTCAATTGATGTACTGACAGGGATTGAAACATTGAAAATCTGTGTGCTTATAAATTGAA
CGGAGAAATCACAGAGGAATTCCCAGCAAGTCTAAATGAAGTAGCGAAATGTGAGCCTGTCTACGAAGAAATGCC
AGGATGGACAGAGGATATTACAGGCGTGAAGAATTTAAGCGAACTGCCTGAAAATGCCCGTCATTATTTAGAGCG
CATTTACAAATTAACAGGTATTCCACTTTCCATTTTCTCAGTTGNCCCC

32. *Enterococcus villorum* (SEQ ID NO. 32)

EVIL

TATCGACCAGGGACATATCCATTTGTTACTTCTTCCATCCAGTAGCAGGTGGTGTAAACAATTGGTAGTGGCGTTG
GTCCATCTAAATTAATAAAGTCGTCGGAGTATGTAAAGCTTATACTTCTCGTGTGGAGATGGCCCGTTCCCTA
CAGAATTATTTGATGAAACAGGGCAACAAATACGTGAAGTAGGTCGTGAATATGGCACAACAACAGGTGCTCCAC
GACGAGTTGGATGGTTTGATACGGTTGTTATGCGCCATTCAAACGTTGATCAGGTATTACAAATTTATCTCTTA

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ATTCGATTGATGTATTAAGCGGATTAGAAACAGTAAAAATTTGTACGGCCTATGAACTAGATGGTGAGCTGATTT
ATCATTACCCAGCAAGTTTGAAGAATTGAAACGTTGTAAACCAGTATATGAAGAACTACCTGGATGGTCTGAAG
ATATTACGAAATGCAAGACACTTTCTGAATTGCCAGAAAATGCACGTAACCTATGTAAGACGTATTTCTGAGCTTG
TAGGTGTACGCATCTCCACATTTCTCAGTGGNCCC

33. *Bacillus thuringiensis* serovar *israelensis* BTHUISR
(SEQ ID NO. 33)

CNCGGTACGTACCCGTTTCGTTACATCTTCTAACCCGATTGCGGGTGGTGTAACAGTTGGAACCTGGAGTTGGCCCT
GCGAAAGTTACTCGCGTTGTAGGTGTATGTAAAGCATATACAAGCCGTGTTGGTGACGGTCCATTCCCTACTGAA
CTTAATGATGAAATTGGTCATCAAATTCGTGAAGTTGGTCGTGAGTACGGAACAACAACCTGGTCGTCCGCGCCGC
GTAGGTTGGTTCGATAGCGTTGTTGTAAGACATGCGCGTCGTGTTAGTGGTTTAAACGGATCTATCATTAATTTCT
ATCGACGTTCTAACAGATATTCCAACCTCTTAAAATTTGTGTTGCTTACAAATACAATGGCGAAGTTATCGATGAA
GTTCCAGCAAACCTTAAACATTTTAGCGAAATGTGAGCCTGTATATGAAGAGCTTCCAGGTTGGACAGAAGATATT
ACTGGTGTAATAATCATTAGACGAGCTTCCTGAAAATGCAAGAAAATACGTAGAACGTGTTTCTGAGTTAACAGGA
ATTCAATTATCTATGTTCTCAGTGGCCCC

34. *Bacillus thuringiensis* serovar *kurstaki* BTHUKUR
(SEQ ID NO. 34)

GGTCGTATCCATTCGTTACATCTTCTAACCCAGTTGCTGGTGGTGTAACAATCGGTTCTGGAGTTGGTCCTTCTA
AAATCAATCGTGATAGTAGGCGTATGTAAAGCATATACAAGCCGTGTTGGTGACGGTCCATTCCCTACTGAACTTA
ATGATGAAATTGGCCATCAAATTCGTGAAGTTGGTCGTGAATATGGTACAACAACAGGTCGTCCACGTCGCGTAG
GTTGGTTTTGACAGCGTTGTTGTAAGACATGCACGCCGTGTGAGTGGTTTAAACAGATTTATCTTTAAACTCTATCG
ACGTATTAACAGGTATTCCAACCTGTGAAAATCTGTATTGCATATAAGTATAATGGAGAAGTTCTGGATGAAGTTC
CAGCAAACCTTAAACATTTTAGCAAATGTGAGCCTGTATATGAAGAGCTTCCAGGTTGGACAGAAGATATTACTG
GTGTAAAATCATTAGAGGAGCTTCCTGAAAATGCAAGACATTATGTAGAGCGTGTGTCTCAATTAACAGGTATCC
AATTATCTATGTTCTCAGTTGNCCCCC

35. *Bacillus mycoides* MYC003 (SEQ ID NO. 35) BMYC003

GGTNCGTACCCATTCGTTACATCTTCTAACCCGATTGCTGGTGGTGTAACAGTTGGAACCTGGAGTTGGTCCTGCG
AAAGTTACTCGCGTTGTAGGTGTATGTAAAGCATATACAAGCCGTGTAGGTGATGGTCCGTTCCCTACTGAGCTT
CATGATGAAATTGGTCATCAAATTCGTGAAGTTGGTCGTGAATACGGAACAACAACCTGGTCGTCCACGCCGCGTA
GGTTGGTTCGATAGCGTTGTTGTAAGACATGCACGTCGTGTTAGTGGTTTAAACAGATCTATCATTAATTTCTATC
GACGTTCTAACAGGTATTCCAACCTCTTAAAATTTGTGTTGCTTACAAATACAATGGCGAAGTTATCGATGAAGTT
CCAGCAAACCTTAAACATTTTAGCGAAATGTGAGCCTGTATATGAAGAGCTTCCAGGTTGGACAGAAGATATTACT
GGTGTAAGAGCATTAGACGAGCTTCCTGAAAATGCACGAAAATACGTAGAACGTGTTTCTGAGTTAACAGGAATT
CAATTATCTATGTTCTCAGTGGNCCCCCG

36. *Bacillus mycoides* NRS306 (SEQ ID NO. 36) BMYC306

CGGTNCGTACCCGTTTCGTTACATCTTCTAACCCGATTGCTGGTGGTGTAACAGTTGGAACCTGGAGTTGGTCCTGC
GAAAGTTACTCGCGTTGTAGGTGTGTGTAAAGCATATACAAGCCGTGTAGGTGATGGTCCATTCCCTACTGAGCT

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TCATGATGAAATTGGTCATCAAATTCGTGAAGTTGGTCGTGAGTATGGAACGACAACCTGGTCGTCCACGCCGCGT
AGGTTGGTTCGATAGCGTTGTTGTAAGACATGCACGTCGTGTTAGTGGTTTAAACAGATTTATCATTAAATTCTAT
CGACGTTCTAACAGGTATTCCAACCTCTTAAAATTTGTGTTGCTTACAAATACAATGGCGAAGTTATCGATGAAGT
TCCAGCAAACCTTAAACATCTTAGCGAAATGTGAGCCTGTATATGAAGAGCTTCCAGGTTGGGAAGAAGATATTAC
TGGTGTAATAATCATTAGACGAACTTCCTGAAAATGCAAGAAAATACGTAGAGCGTGTTTCTGAATTAACAGGAAT
CCAATTATCTATGTTCTCAGT

37. *Bacillus weihenstephanensis* (SEQ ID NO. 37) BWEI

TTTTTTTNGGAAGNGCGCAAGGTGTTATGCTTGATATCGACCACGGTACGTACCCGTTTCGTTACATCTTCTAACC
CAATTGCTGGTGGTGTAAACAGTTGGAACCTGGAGTTGGTCCTGCGAAAGTTACTCGCGTTGTAGGTGTATGTAAAG
CATATACAAGCCGTGTTGGTGATGGTCCATTCCCTACTGAACTTAATGATGAAATCGGTCACCAAATTCGTGAAG
TTGGTCGTGAATACGGAACAACAACGGGTCGTCCACGCCGTGTAGGTTGGTTCGATAGCGTTGTTGTAAGACATG
CACGTCGTGTTAGTGGTTTAAACAGATTTATCATTAAACTCTATCGATGTATTAACAGGTATTCCAACGTTTAAAA
TTTGTGTTGCTTACAAATGCAATGGCGAAGTTATCGATGAAGTTCCAGCTAACTTAAACATTTTAGCGAAATGTG
AGCCTGTATATGAAGAGCTTCCNGGTTGGACAGAAGATGTTACTGCTGTGAAATCATTGGATGAGCTTCCTGAAA
ATGCAAGAAAATACGTAGAGCGTGTTTTCTGAATTAACNGGAAGCCAATTNNCAAG

38. *Staphylococcus haemolyticus* (SEQ ID NO. 38) SHAE

CAAGGTGTCATGTTAGATATCGACCATGGTACATATCCTTTTCGTAACCTCAAGTAACCCGTGTTGCAGGTAATGTA
ACAGTTGGTACAGGTGTAGGCCCAACTTTTCGTATCTAAAGTGATTGGTGTATGTAAAGCATATACATCTCGTGTA
GGCGATGGTCCATTCCCTACAGAATTATTTGATGAAAATGGACATCATATTAGAGAAGTTGGTCGTGAATACGGT
ACAACAACAGGACGTCCACGTCGTGTAGGTTGGTTTACTCAGTTGTATTACGTCACTCTCGTCGTGTTAGTGGT
ATTACAGACTTATCTATTAACCTCTATCGACGTACTTACAGGTCTTGATACAGTGAAGATTTGTACTGCTTACGAA
TTAGATGGAGAAGAAATTACAGAATATCCTGCTAACTTAGATCAATTACGTCGTTGTAAACCAATCTTTGAAGAG
TTACCAGGATGGGAAGAAGATATCACTGGTTGCCGTACATTAGAAGAATTACCAGATAACGCACGTAAATACTTA
GAACGCATTTCTGAATTATGTAATGTACGTATTTCAATCTTCTCAGT

39. *Staphylococcus saprophyticus* (SEQ ID NO. 39) SSAP

GCAAGGTGTGATGTTAGATATCGACCATGGTACATATCCATTTCGTTTCATCAAGTAACCCAGTTGCAGGTAATGTG
ACTGTCGGTGGCGGTGTAGGTCCAACATTCGTCTCTAAAGTTATCGGTGTGTGTAAAGCCTATACATCACGTGTC
GGCGATGGTCCATTCCCAACAGAACTATTTGACGAAGATGGGCACCACATCCGTGAAGTAGGTCGTGAATACGGT
ACAACAACAGGACGTCCACGTCGTGTAGGTTGGTTTACTCAGTTGTATTACGTCACTCTCGTCGTGCAAGTGGT
ATTACAGATTTATCTATTAACCTCAATTGATGTATTAACAGGCCTTAAAGAAGTTAAAATCTGTACTGCTTATGAG
TTAGACGGTAAAGAAATTACGGAATACCCAGCTAACTTGAAAGACTTACAACGTTGTAAGCCAATTTTTTGAAACA
TTACCAGGTTGGACAGAAGATGTGACAGGTTGTCGTTTATTAGAAGAATTACCTAATAATGCGCGTAGATACTTA
GAACGTATTTCTGAATTATGTGACGTGAAGATTTCAATCTTCTCAGTTGGCCC

40. *Bacillus subtilis* (SEQ ID NO. 40) BSUB

CTCAAGGGGTATGCTTGATATTGACCAAGGGACATACCCGTTTGTCACTTCATCCAACCCGGTCGCCGGAGGGG
TGACGATCGGTTCAAGCGTAGGCCCGACAAAATCCAGCACGTCGTGCGTGTATCTAAAGCGTACACAACCCGTG

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TCGGTGACGGTCCTTTCCCGACTGAGCTGAAAGATGAAACCGGGGATCAAATCCGTGAAGTCGGACGCGAATACG
GCACAAACGACAGGCCGTCCGCGCCGTGTCGGCTGGTTTGACAGCGTTGTTGTCCGCCATGCCC GCCGCGTCAGCG
GAATCACAGATCTTTCTCTGAACTCAATCGATGTGCTGACTGGCATTGAAACATTGAAAATCTGTGTCGCTTACC
GCTACAAAGGTGAAGTGATTGAAGAATTC CGGCAAGTCTGAAAGCTCTCGCAGAGTGTGAACCGGTATATGAAG
AAATGCCTGGCTGGACGGAAGATATCACAGGCGCAAAAACATTAAGCGATCTTCCTGAAAATGCGCGCCATTATC
TGGAACGCGTGTCTCANCTGACAGGTATTCCGCTTTCTATTTTCTCAGTAGGTCCAGA

41. *Listeria monocytogenes* (SEQ ID NO. 41) IMON

TTTGGAAGGGGCGCAAGGGGTATGCTTGATATTGATCAAGGAACATATCCATTTGTAACCTCAAGTAACCCGAT
TGCTGGTGGCGTAACATATCGGTAGTGGTGTGGTCCTTCAAAAATCAATCATGTTGTTGGTGTGGCGAAAGCTTA
TACAACACGTGTTGGTGATGGTCCTTTCCCAACAGAATTATTTGATTCTATTGGTGACACTATTCGTGAAGTCGG
TCATGAATATGGTACAACGACTGGTCGTCCGCGTCGTGTAGGTTGGTTTGATAGCGTAGTGGTTCGTCATGCGCG
TCGTGTTAGTGGATTAACAGATTTATCGTTAACACTACTTGATGTTTTGACAGGAATTGAGACACTTAAAATCTG
TGTAGCTTACAAATTAGACGGAAAAACAATTACAGAGTTCCAGCAAGTTTGAAAGATTTAGCTCGTTGCGAACC
TGTTTATGAAGAACTTCCAGGCTGGACGGAAGATATTACTGGAGTTACATCACTAGATGATCTTCCAGTGAAC TG
CCGCCATTACATGGAGCGTATCGCCCAACTTACGGGAGTGCAAGTTTCTATGTTCTCAGTAGGTCCCAGACCA

42. *Lactococcus lactis* (SEQ ID NO. 42) LLAC

TNATGCTTGATATTGACNAGGAACATACCCATTTGTAACCTCTCAAACCCAGTAGCTGGTGGGGTAACGATTGGC
TCTGGTGTGGGTCCATCAAAAATTTCAAAGTTGTTGGTGTGTTGTAAAGCCTATACTTCACGTGTGGGTGATGGT
CCATTCCCAACAGAACTTTTTGATGAAGTTGGACATCAAATTCGTGAAGTAGGACATGAATATGGAACAACAACA
GGACGTCCACGTGCTGTTGGTTGGTTTGACTCAGTCGTAATGCGTCATGCAAACGTGTTTCTGGCTTGACAAAT
CTTAGCTTGAATTCAATTGACGTTCTCTCAGGACTTGAACAGTAAAAATTTGTGTTGCTTACGAACGTAGTAAT
GGTGAACAAATTACTCATTATCCAGCATCACTTAAGGAATTAGCAGATTGCAAACCAATCTATGAAGAATTGCCA
GGATGGTCTGAAGATATTACTTCATGCCGAACCTTTAGAAGAGTTACCAGAAGCTGCTCGTAACTATGTTCTGTCG
GTTGGTGAAC TAGTTGGCGTACGTATCTCGACTTTCTCAGTNGTCCCC

43. *Enterococcus hirae* (SEQ ID NO. 43) EHIR

CTTTTTGAAGGGGCGCAAGGGTAATGCTAGATATTGACCAAGGTACCTATCCATTTGTAACCTCATCTAATCCA
GTTGCTGGTGGTGTAAACGATCGGTTCTGGTGTGGGTCTAGCAAGATTGACAAAGTAGTGGGTGTTTGTAAGCC
TATACAAGTCGTGTTGGTGATGGTCCTTTCCCAACAGAGCTTTTCGATGAAGTAGGTGACCGCATTTCGTGAGGTT
GGTCATGAGTATGGTACAACAACAGGACGTCCGCGTCGAGTTGGTTGGTTTGACTCTGTTGTTATGCGCCATAGC
CGCCGTGTATCTGGGATTACCAATCTTTGCTTAACTCTATCGATGTGTTGAGCGGTCTGGATACAGTCAAGATC
TGTGTAGCCTATGATTTGGATGGCCAAAGAATCGACCACTATCCAGCTAGTTTGGAACAGCTTAAACGTTGTAAG
CCGATTTACGAAGAGCTTCCTGGATGGTCTGAAGATATTACTGGCGTTCTGTAAGTTAGAAGATCTTCAGAAAAT
GCTCGCAACTATGTTTCGGCGAGTAANCAGTTGGTTGGTGTACGTATTTCCACCTTCTCAGTAGGTCCAGACCA

44. *Enterococcus avium* (SEQ ID NO. 44) EAVI

CTTTTCGAAGGTGCGCAAGGTGTAATGCTGGATATTGATCAAGGGACTTATCCATTTGTTACCTCTTCTAATCCG
GTTGCCGGCGGTGTACAGATCGGTAGCGGTGTTGGACCATCGAAGATTGATAAAGTCGTAGGGGTATGTAAAGCT

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TATACATCACGCGTTGGTGATGGACCTTTTCCAACGGAATTATTTGACGAAGTCGGCGATCAGATCCGCGAAGTT
GGTCGTGAATATGGAACAACAACCTGGCCGTCCACGTCGAGTTGGCTGGTTTGAAGTCTGTGGTTATGCGGCACTCA
AAACGCGCTTCTGGGATTACCAATCTATCTTTGAACTCAATCGATGTGTTGAGCGGCTTGGAACGGTCAAGATT
TGTACCGCTTATGAGTTAGACGGAGAATTAATCTATCATTATCCAGCAAGCTTAAAGGAATTGAATCGCTGCAAA
CCAGTTTATGAAGAGCTACCTGGCTGGAGTAAGGATATTACTGGCTGTCGTGATT

45. *Streptococcus bovis* (SEQ ID NO. 45) SBOV

TTTTTGAAGGGGCTCAAGGTGTCATGCTTGATATTGACCAAGGTACATACCCATTTGTTACATCTTCAAACCCAG
TTGCTGGTGGTGTAACATATCGGTTCAAGTGTGGTCCAAGCAAGATCAACAAAGTTGTTGGTGTATGTAAAGCCT
ACACAAGTCGTGTTGGTGATGGTCCATTCCCAACAGAACTTCTAGACGAAGTTGGAGATCGTATCCGTGAAATCG
GTCACGAATATGGTACAACAACAGGACGTCCACGTCGTGTTGGATGGTTTGAAGTCAAGTGTAAATGCGTCACAGCC
GTCGCGTATCAGGTATCACAACCTTGTCACTTAACCTCAATCGACGTTCTTTTCAAGACTTGATACTGTAAAGTCT
GTGTGGCTTACGACCTTGATGGCCAACGTATCGACCACATCCAGCAAGTCTTGAACAATTGAAACGTTGTAAAC
CAATCTACGAAGAATTGCCAGGTTGGTCAGAAGACATCACAGGCTGCCGTAGCCTAGATGAGCTTCCAGAAAATG
CTCGTAACTATGTTTCGTGCTGTTGGTGAACCTGTTGGTGTTCGCATTTCAACATTCTCAGTTGGTCCAGGCCA

46. *Streptococcus thermophilus* (SEQ ID NO. 46) STHE

CTATTTGAAGGTGCGCAAGGAGTTATGCTTGATATTGACCAAGGAACATAACCCATTTGTAACGTCATCAAACCCA
GTTGCTGGTGGTGTTACAATTGGTTCTGGTGTGGGCCATCTAAAATTAATAAGGTTGTGGGTGTATGTAAGGCC
TATACAAGTCGTGTCGGCGATGGTCCTTTCCCAACTGAGTTGTTTGATGAAGTGGGTGAACGTATCCGTGAAGTT
GGCCATGAATATGGAACAACAACCTGGACGTCCACGTCGTGTGGGATGGTTTGAAGTCAAGTGTAAATGCGTCATAGC
CGTCGTGTATCAGGTATTACAAACCTTAGCTTGAAGTGTATCGACGTTCTTTCTGGTCTTGATACTGTGAAAAT
TGTGTAGCCTACGATCTTGATGGTGAGCGCATTTGATTACTATCCGGCTAGCCTTGAGCAATTGAAACGTTGTAAA
CCAATTTATGAAGAATTGCCAGGTTGGGAAGAGGATATTACAGGTTGCCGTAGTTTANATGAGCTTCTGAAAAT
GCCCCTAATTATGTTTCGTGCTGATTGGTGAGTTGGTCGGTATACNTATCTCTACCTTCTCAGTAGGCCNNACCA

47. *Streptococcus suis* (SEQ ID NO. 47) SSUI

CGAAGGACGCAAGGAGTTATGTTGGATATGACCAAGGTACCTATCCATTCGTTACTTCTTCAAACCCAGTTGCTG
GTGGTGTGACGATCGGTAGCGGTGTGCGCCCAAGCAAGATTGACAAGGTTGTTGGTGTATGTAAGGCCTACACTA
GCCGTGTTGGTGACGGACCATTTCCGACTGAATTGCACGATGAAATCGGAGACCGTATCCGCGAAATCGGTAAAG
AGTACGGTACGACAACCTGGCCGTCCACGCCGTGTCGGTTGGTTTGAAGTCAAGTGTAAATGCGCCATAGCCGCCGTG
TGTCAGGTATTACCAACTTGTCCCTCAACTCGATTGACGTCCTTGTGAGTCTTGGGACCTTGAAAATCTGCGTGG
CTTATGACTTGGATGGTGAGCGTATTGACCACTACCCAGCAAGTTTGGAGCAACTCAAACGTTGCAAACCAATCT
ACGAAGAAATGCCAGGTTGGTCTGAAGACATCACAGGTGTACGTAGCCTGGATGAATTGCCAGAAGCGGCTCGCA
ACTATGTTTCGTGCTATCAGCGAATTGGTAGGCGTTCGTATCTCAACCTTCTCAGTAGGTCCAGACC

48. *Bacillus pseudomycolides* (SEQ ID NO. 48) BPMS

CTATTTGAAGGGGCGCAAGGCGTAATGCTTGATATTGATCAAGGTACGTATCCATTCGTTACATCTTCTAACCCA
GTTGCTGGTGGTGTAACAATCGGTTCTGGAGTTGGTCCTTCTAAAATCAATCGTGTAGTAGGCGTATGTAAAGCA
TATACAAGCCGTGTTGGTGACGGTCCATTCCCTACTGAACTTAATGATGAAATTGGCCATCAAATTCGTGAAGTT

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GGTCGTGAATATGGTACAACAACAGGTCGTCCACGTCGCGTAGGTTGGTTTGACAGCGTTGTTGTAAGACATGCA
CGCCGTGTGAGTGGTTTAAACAGATTTATCTTTAACTCTATCGACGTATTAACAGGTATTCCAACGTGTAAGAAC
TGATTGCATATAAGTATAATGGAGAAGTTCTGGATGAAGTTCCAGCAAACCTAAACATTTTAGCAAAATGTGAG
CCTGTATATGAAGAGCTTCCAGGTTGGACAGAAGATATTACTGGTGTAAAATCATTAGAGGAGCTTCCTGAAAAT
GCAAGACATTATGTAGAGCGTGTGTCTCAATTAACAGGTATCCAATTATCTATGTTCTCAGTAGGGCCNGACCA

49. *Staphylococcus capitis capitis* (SEQ ID NO. 49) SCAPCAP

CTCTTCGAGGAGCTCAAGGTGTCATGTTAGACATCGACCATGGTACTTACCCATTTCGTTACGTCAAGTAACCCAG
TTGCTGGTAATGTCACAGTAGGTACAGGTGTAGGTCCTACATCAGTTTCTAAAGTCATCGGTGTATGTAAATCAT
ATACGTACAGTGTAGGTGATGGTCCATTCCCCACAGAATTATTCGATGAAGATGGTCATCACATTAGAGAAGTAG
GTCGTGAATATGGTACAACAACAGGACGTCCACGCCGTGTAGGTTGGTTTGACTCAGTGGTACTACGTCAATTCAC
GTCGCGTAAGTGGTATCACAGATCTTTCAATCAACTCTATCGACGTTTAAACAGGTTTAGATACAGTTAAAATTT
GTACAGCATATGAGTTAGATGGCGAAGAAATCACTGAATACCCAGCTAACTTAGATCAATTAAGACGCTGTAAAC
CAATCTTCGAAGAACTTCCAGGTTGGACAGAAGATATCACAGGGCTGCCGCAGTTTAGAAGAACTCCCTGAAAAT
GCNCNCCAAATACCTAGAGCGTATTTCAAATTTATGTGGCGTACNCATTTCAATCCTTCTCAGTAGGGGGCCCTGA
CCCC

50. *Staphylococcus sciuri* (SEQ ID NO. 50) SSCI

CTTTTTGAAGGTGCGCAAGGTGTTATGTTAGATATCGACCACGGTACATATCCATTTCGTTACTTCAAGTAATCCA
ATTGCAGGTAACGTTACAGTAGGTGGCGGTGTTGGTCCAACATACGTATCTAAAGTAATTGGTGTATGTAAAGCT
TATACATCTCGTGTAGGAGACGGTCCATTCCCAACAGAATTATTTGATGAAGATGGTCACCATATCCGTGAAGTA
GGTCGTGAATACGGTACAACAACCTGGAAGACCACGTCGTGTAGGTTGGTTTGACTCAGTAGTTCTACGTCACTCA
CGCCGTGTAAGTGGTATTACAGATTTATCAATCAACTCAATTGACGTATTAACAGGATTAAAAACAGTTAAATC
TGTAACAGCATACGAAATTGATGGTGTGAAATCACTGAATATCCAGCAAACCTAAACGAATTAGAACGTTGTAAA
CCAATCTTTGAAGAACTACCAGGTTGGGAAGAAGACATTACAGGATGCCGTTCACTAGAAGAATTACCAGATAAC
GCACGTCGTTTTTTTAAACGCATCTCTGAATTATGTANC GTTAAANTTCTATCTTCTCAGTAGGTCCAGGTC

51. *Staphylococcus warneri* (SEQ ID NO. 51) SWAR

CTTTTTGAAGGAGCGCAAGGTGTGATGTTAGACATCGACCACGGTACATATCCATTTCGTCACTTCAAGTAACCCA
GTAGCAGGTAACGTTACTGTAGGTACTGGTGTAGGTCCAACATACGTATCAAAGTCATTGGTGTATGTAAAGCT
TATACATCACGTGTTGGTGTAGGTCCATTCCCTACAGAATTATTTGATGAAGATGGTCATCACATTAGAGAAGTT
GGTCGTGAATACGGTACAACAACCTGGTCGTCCACGTCGTGTAGGTTGGTTCGACTCAGTAGTATTACGTCAATTC
CGCCGTGTAAGTGGTATTACAGACTTATCAATCAACTCAATTGATGTGTAACTGGCTTAGATACAGTTAAAATC
TGTAACAGCATATGAATTAGATGGTAAAGAAATTAAGTGAATATCCAGCTAACCTAGATCAATTACAACGTTGTAAA
CCAATCTTCGAAGAATTACCTGGTTGGACAGAAGATATTACAGGTTGCCGTACTTTAGAAGAGCTTCCTGAAAAT
GCACGCAAATATTTAGAACGTATTTCTGAATTATGTGGCGTACGTATTTCAATCTTCTCAGTTGGTCTCTGGCCAG
GGCGA

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52. *Staphylococcus lugdunensis* (SEQ ID NO. 52) SLUG

TTCTTTGAAGGAGCTCAAGGTGTTATGTTAGATATTGATCATGGTACATATCCTTTTCGTACATCAAGCAATCCT
GTAGCCGGCAATGTCACTGTTGGTACAGGTGTAGGTCCAACCTTCGTTTCTAAAGTAATTGGTGTGTGTAAAGCA
TACACATCTCGCGTAGGCGATGGTCCTTTCCCAACTGAACTATTTGATGAAGATGGGCACCATATTAGAGAGGTT
GGTCGTGAATATGGTACGACGACAGGACGTCCACGTGCGTGGGTTGGTTTGATTTCAGTCGTGCTACGTCACTCA
CGTCGTGTTAGTGGTATTACAGACTTATCTATTAACCTCTATTGATGTACTAACAGGTTTAGATACGGTAAAAATT
TGTACAGCTTATGAGTTAGATGGAGAAGAAATTACGGAGTATCCAGCTAACCTTGATCAATTAAACGTTGTAAA
CCAATCTTTGAAGAATTACCTGGTTGGACAGAAGATATTACAGGCTGTCGTTTCATTAGAAGCATTGCCTGATAAT
GCACGTCGCTATTTAGAACGTATTTTCAAGATTATGCGGCGTTCATATTTCAATTTTCTCAGTAGGGCCAGACCA

53. *Staphylococcus gallinarum* (SEQ ID NO. 53) SGAL

CTTTTTGAAGGTGCGCAAGGCGTTATGTTAGATATCGACCATGGTACATACCCATTTGTTACTTCTAGTAATCCA
GTTGCAGGTAACGTAACCTGTAGGTGGCGGTGTTGGACCAACATTCGTATCAAAGTAATTGGCGTATGTAAAGCC
TATACATCACGTGTTGGTGACGGCCCATTTCCCAACTGAATTATTTGATGAAGATGGACATCATATCCGTGAAGTT
GGCCGCGAATATGGTACAACAACAGGACGTCCACGTGCTGTGGGTTGGTTTGACTCTGTTGTATTACGTCATTCA
CGCCGTGCAAGTGGTATCACAGATTTATCTATCAACTCTATTGACGTATTAACAGGCTTTGAAAATGTTAAGATT
TGTACTGCATACGAATTAGATGGAGAAGAAATCACTGAATACCCAGCAAACCTTAAAGGACTTACAACGTTGTAAA
CCAATCTTTGAAACATTACCAGGTTGGACAGAAGATGTCACAAGCTGTCGTTCACTAGATGAATTACCAGATAAT
GCACGCAGATATTTAGAGCGCATTTCTGAACCATGTAACGTGAAGATTTCAATCTTCTCAGTAGGGCCAGACCA

54. *Staphylococcus schleiferi schleiferi* (SEQ ID NO. 54) SSCH

GACCTGGACCAACTGAGAAGATAGAAATATGGACGTTACATAATTCTGAAATACGCTCTAAGTAACGGCGTGCAT
TTTGTGGTAGTTCGTCTAACTACGTACACCTGTAATATCTTCAGTCCAACCTGGTAATGTTTCAAAGATAGGTT
TACAACGTTTTAAGTCGTTTAAAGTTTGCTGGGTATTCCGTAATCTCTTTCCATCTAATTCATAAGCTGTACAGA
TTTTAACCTCTTCTAAGCCAGTTAAGACGTCGATAGAGTTGATTGATAAATCTGTAATCCCACTTACACGACGAG
AGTGACGTAATACAACGGAGTCAAACCAACCTACACGGCGTGGACGACCTGTTGTTGTGCCATATTCACGTCCGA
TTTACGAATATGGTGCCCTTGTTTCATCAAATAATTCTGTTGGGAATGGCCCATCACCTACACGTGAAGTGTATG
CTTTACATACGCCAACTACTTTTGATACATTTGTTGGCCCTACACCAGCACCAACTGTCACGTTACCCGCTACAG
GGTACTTGATGTTACAAAAGGATATGTTCCGTGATCGATGTCTGACATCACCCCTTGAGCCCTTCAAAGAGA

55. *Staphylococcus capitis ureolyticus* (SEQ ID NO. 55) SCAPURE

GACCAGGCCCAACTGAGAAGATTGAAATGTGTACGCCACATAATTCTGAAATACGCTCTAGGTATTTGCGTGCAT
TTTCAGGGAGTTCTTCTAGACTGCGACAACCTGTGATATCTTCTGTCCAACCTGGAAGTTCTTCGAAGATTGGTT
TACAGCGTCTTAATTGATCTAAGTTAGCTGGGTATTTCAGTGATTTCTTCGCCATCTAACTCATATGCTGTACAAA
TTTTAACTGTATCTAAACCTGTTAAACGTCGATAGAGTTGATTGAAAGATCTGTGATACCACTTACGCGACGTG
AATGACGTAATACTACTGAGTCGAACCAACCTACACGGCGTGGACGTCCTGTTGTTGTACCATATTCACGACCTA
CTTCTCTAATGTGATGACCATCTTCATCGAATAATTCTGTAGGGAATGGACCATCACCTACACGTGACGTATATG
ATTTACATACACCGATGACTTTAGAACTGATGTAGGACCTACACCTGTACCTACTGTGACATTACCAGCAACTG
GGTACTTGACGTAACGAATGGATATGTACCGTGGTCGATGTCTAACATGACACCTTGCGCACCTTCAAATAAA

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56. *Staphylococcus cohnii urealyticum* (SEQ ID NO. 56)**SCAPURE**

CTCGTTGAAGGTGCACAAGGCGTTATGTTAGATATCGACCACGGTACATACCCATTCGTTACGTCAAGTAACCCA
GTTGCAGGTAATGTCACGTGTCGGTGGTGGTGGTGGTCCAACATACGTATCTAAAGTCATTGGCGTATGTAAAGCT
TATACATCACGTGTCGGTGATGGCCATTCCCAACAGAACTATTTGATGATGATGGACACCACATCCGTGAAATT
GGCCGTGAGTACGGTACAACACTACTGGACGTCCACGTTCGTGTAGGTTGGTTCGATTTCAGTTGTATTACGTCACTCT
CGTCGTGCGAGTGGTATTACTGATTTATCAATCAACTCTATCGATGTCTTAACAGGCCTTAAAGAAGTGAAGATT
TGTACGGCGTATGAATTGGACGGTAAAGAAATTACTGAATATCCAGCGAATTTAAAAGACTTACAACGTTGTAAG
CCAATCTTTGAAACATTACCTGGTTGGACAGAAGATGTTACAGGTTGTCGCTCATTAGATGAGCTGCCAGACAAT
GCACGTAGATATTTAGAACGTATCTCTGAATTATGTGACGTTCAAATTTCAATCTTCTCAGTAGGGCCTGACCA

57. *Staphylococcus xylosus* (SEQ ID NO. 57)**SXYL**

CTTTTTGAAGGTGCTCAAGGTGTAATGCTAGATATCGATCATGGTACTTACCCATTCGTTACTTCAAGTAACCCA
GTTGCCGGTAACGTTACTGTTGGTGGCGGTGTAGGTCCAACATTTCGTATCTAAAGTCATTGGTGTATGTAAGGCA
TATACATCACGTGTAGGCGATGGTCCTTTCCCAACTGAACTATTTGATGATGACGGGCACCATATCCGTGAAGTA
GGTCGTGAATACGGTACAACACTACAGGTCGTCCACGCCGTGTAGGTTGGTTCGATTTCAGTTGTATTACGTCACTCT
CGCCGTGCGAGTGGTATTACAGACCTATCAATCAACTCTATTGATGTGTTAACAGGTCTAAAAGAAGTTAAAATC
TGTAATGTCCTATGAGTTAGACGGTAAAGAAATCACTGAATATCCAGCAAACCTGAAAGACTTACAACGTTGTAAG
CCAATCTTTGAAACATTGCCTGGTTGGACAGAAGATGTAAGTGGTTGTCAATCATTAGATGAATTACCTGATAAT
GCACGTAGATACTTAGAACGTATATCTGAACTAAGTGATGTTAAGATTTCTATCTTCTCAGTAGGGCCAGATCA

58. *Staphylococcus simulans* (SEQ ID NO. 58)**SSIM**

CTATTTGAAGGAGCGCAAGGGGTATGTTAGACATCGACCATGGTACATACCCATTCGTTACATCAAGTAACCCG
ATTGCTGGTAACGTTACTGTGCGCGCGGTATCGGACCAACATCAGTATCTAAAGTAATCGGTGTATGTAAAGCG
TATACGTCACGTGTAGGTGATGGTCCATTCCCTACTGAATTATTCGATGAAGATGGTCATCATATCCGTGAAGTA
GGTCGTGAATATGGTACAACACTACAGGACGCCCACGTGTCGCTGGTTCGACTCAGTGGTATTACGTCATTCA
CGTCGTGTAAGTGGTATTACTGACTTATCTATCAACTCAATCGACGTTTTAACTGGTTTAGATACAGTTAAAATC
TGTGTTGCGTATGAGTTAGATGGTGAAGAAATCACTGAATACCCAGCAAACCTTAAACGCGTTGAACCGTTGTAAA
CCAATTTACGAAGAATTACCAGGTTGGTCTGAAGATATTACAGGCGTACAATCATTAGAAGAATTACCAGATAAC
GCACGTCGTTACTTAGAACGTATTTCTGAGTTATGTAACGTAGGTATCTCAATCTTCTCAGTTGGTCCAGGTCA

59. *Staphylococcus cohnii cohnii* (SEQ ID NO. 59) SCOHCOH

TATTTGAAGGTGCACAAGGAGTAATGCTTGATATCGATCATGGTACTTATCCGTTTCGTCACCTTCAAGTAACCCGA
TTGCCGGTAACGTAACAGTTGGTACTGGTGTAGGTCCAACGTTTGTAGATAAAGTTGTTGGTGTATGTAAAGCTT
ACACATCACGTGTAGGGGATGGACCATTCCCAACTGAATTATTTGATGAAGATGGTCATCATATTCGTGAAGTGG
GTCGTGAATATGGAACGACTACAGGACGTCCACGTGTCGTGTAGGTTGGTTTGAATCTGTTGTATTACGCCATTCTC
GCCGTGCAAGTGGTATTACGGACTTGTCAATTAACCTCTATTGACGTATTAACCTGGTTTAGAACTGTTAAGATTT
GTACAGCATATGAATTGGATGGAAAAGAGATTACAGAATATCCAGCGAATTTAAATGAACTAAATCGTTGTAAAC
CGATTTTCGAAGAATTACCAGGATGGACTGAAGATGTGACTTCATGTAAGTCATTAGACGAGCTACCTGATAACG
CACGCCGTTACTTAGAGCGTATTTCCGAGTTATGTAATGTTAAGATTTCTATCTTCTCAGTAGGTCCAGACCA

60. *Staphylococcus auricularis* (SEQ ID NO. 60) SAURICU

CTATTTGAAGGAGCTCAAGGTGTGATGTTAGATATCGACCATGGTACGTACCCATTTGTTACATCTAGTAACCCCT
GTTGCTGGTAACGTGACAGTGGGTGCAGGTGTAGGTCCAACGTTTGTCTCTAAAGTGATTGGTGTATGTAAAGCC
TATACATCACGTGTCGGTGATGGTCCATTCCCAACTGAATTATTTGATGATGATGGTCACCACATCCGTGAAGTC
GGACATGAATACGGTACAACAACAGGACGCCCCAAGACGTGTCGGTTGGTTCGACTCTGTGGTATTACGTCACTCT
CGCCGTGTGAGCGGTATTACAGACCTTTCTATTA ACTCTATTGATGTGTTAACTGGTTTANATACAGTTAAAATT
TGTACCGCATACGAATTAGATGGGGAAGAAATTACAGAGTACCCAGCAAACCTTAAACGATCTAAAACGCTGCAAA
CCAATCTTTGAAGAACTTCCAGGTTGGAACGAANATATTACAGGTTGCCGCAGCTTAGAAGAATTACCTGACAAT
GCACGTCACTACTTANAACGCATTGCANAACCTTTGTGACGTAAACATTTCAATCTTCTCAGTTGGGCCAGACCA

61. *Staphylococcus caseolyticus* (SEQ ID NO. 61) SCAS

CTTTTCGAAGGGGCGCAAGGAGTAATGCTTGATATCGATCATGGTACTTATCCGTTTCGTCACCTTCAAGTAACCCG
ATTGCCGGTAACGTAACAGTTGGTACTGGTGTAGGTCCAACGTTTGTAGATAAAGTTGTTGGTGTATGTAAAGCT
TACACATCACGTGTAGGAGATGGACCATTCCCAACTGAATTATTTGATGAAGATGGTCATCATATTTCGTGAAGTG
GGTCGTGAATATGGAACGACTACAGGACGTCCACGTGCTGTAGGTTGGTTTGACTCTGTTGTATTACGCCATTCT
CGCCGTGCAAGTGGTATTACGGACTTGTCAATTA ACTCTATTGACGTATTA ACTGGTTTAGAACTGTTAAGATT
TGTACAGCATATGAATTGGATGGAAAAGAGATTACAGAATATCTAGCGAATTTAAATGAACTAAATCGTTGTAAA
CCGATTTTCGAAGAATTACCAGGATGGACTGAAGATGTGACTTCATGTAAGTCATTAGACGAGCTACCTGATAAC
GCACGCCGTTACTTAGAGCGTATTTCCGAGTTATGTAATGTTAAGATTTCTATCTTCTCAGTTGGTCCAGACCA

62. *Listeria innocua* (SEQ ID NO. 62) LINN

CTTTTCGAAGGAGCACAAAGGGGTTATGCTTGATATTGATCAAGGAACATATCCATTTGTAACCTCAAGTAATCCG
ATTGCTGGTGGCGTAACAATTGGTAGCGGTGTTGGCCCATCGAAAATCAATCATGTTGTTGGTGTGCAAAAGCA
TATACAACCTCGTGTTGGAGATGGTCCTTTCCCAACTGAATTATTTGATTCTATTGGTGACACTATCCGTGAAGTT
GGCCATGAATATGGTACAAC TACTGGTCGTCCGCGTCGTGTAGGTTGGTTTGATAGCGTGGTTGTTTCGTATGCT
CGTCGTGTGAGCGGACTAACAGGTTTATCCTTAACGCTACTGGACGTTTTGACAGGGATTGAAACACTTAAAATC
TGTGTAGCGTACAAGTTAGACGGAAAAACAATTACAGAATTTCCCGCAAGCTTGAAAGACTTAGCTCGTTGTGAA
CCTGTTTATGAAGAACTGCCTGGTTGGACAGAAGATATTACTGAAGTGCAATCATTAGATGACCTACCAGTAAGT
TGTCGTCATTACATGGAACGCATTGCTCAACTTACAGGTGTGCAAGTTTCTATGTTCTCAGTAGGGCCTGATCA

63. *Escherichia coli* K12 (SEQ ID NO. 63) ECOK12

CTATTTGAAGGGGCGCAAGGAAAAAGGATTGTCGATGCATAACGCCTCCGGATTGACTCTGGCTTAAAGCGTAGT
CAGTGGAGGAGATAACAAATTCATTTTTACAAAACTTAAACATGAAGGGGGAGACGCTTCTCCCCCTTAGTTT
TCAGGCCTTCTCAAGCATGGCGTGCTTCTGCAGGCTCTGGTACTCAGCGTTAAGCTCATCAGACAATTTTCAAG
CTTATCGGCGTTGACGGTAATAACAGTCGGGCAATCATGGTGCCCACTCATCAAACATACTGCGGCTGTGCTAA
TGCTTCTTCAGCATGATGAAGAGCACTCCACTCTTCTGATCCAGATGAAGATTCAACCGCAGCGATTTATCGTG
CAGTTCGCGATT CAGTTTAAAAAAGTTATCTCGTAGATGATTGCTTTCGCTGACGGACATGTATCCTTTTGCCTT
TCTCAGTTGGGCCAGACCA

Figure 5. Molecular marker II (ptsI) sequences amplified from Gram positive bacteria (SEQ ID NOs: 64-107; SEQ ID NOs: 109-111, SEQ ID NOs: 117-129, SEQ ID NO: 137, SEQ ID NOs 145-148), from some Gram-negative bacteria (SEQ ID NOs 108, 112-116, 130-136, 138-144) and from the fungi *Cryptococcus neoformans* (SEQ ID NO: 149).

64. *Bacillus anthracis* 1978 (SEQ ID NO. 64)

ANTTNGGGCATGGGNCNTCTTTATNAGCAGCATCGATAACCATTTTTACAAGACGTAAAATAGATAGGTTATAT
GGTTGGTATAAGTAAGATACTTGTTCGTTTCATACGGTCTGCAGCCATTGTGTATTGAATTAAGTCATTTGTTCCG
ATAGAGAAGAAATCAACTTCTTTTGCGAATTGATCTGCTAATACTGCTGAAGCTGGGATTTCAACCATCATACCA
ACTTCAATAGAATCAGAAACAGTTGTACCCACTTCTACAAGTTTCGCTTTTTCTTCTAATAAGATCGCTTTTGCT
TGACGGAACATCATCAAGAGTTGCAATCATTGGGAACATAATTTTAAAGTTACCGTATACGCTAGCACGAAGTAAT
GCACGAAGTTGTGTACGGAACACATCTTGCTCATCAAGACATAAGCGAATTGCACGGTAGCCCANGAACGGATNT
TTTTCTTTAA

65. *Bacillus anthracis* butare (SEQ ID NO. 65)

NCTTGGCAGGGCCNTCTTNATNAGCAGCATCGATAACCATTTTTACAAGACGTAAAATAGATAGGTTATATGGTT
GGTATAAGTAAGATACTTGTTCGTTTCATACGGTCTGCAGCCATTGTGTATTGAATTAAGTCATTTGTTCCGATAG
AGAAGAAATCAACTTCTTTTGCGAATTGATCTGCTAATACTGCTGAAGCTGGGATTTCAACCATCATACCAACTT
CAATAGAATCAGAAACAGTTGTACCCACTTCTACAAGTTTCGCTTTTTCTTCTAATAAGATCGCTTTTGCTTGAC
GGAACATCATCAAGAGTTGCAATCATTGGGAACATAATTTTAAAGTTACCGTATACGCTAGCACGAAGTAATGCAC
GAAGTTGTGTACGGAACACATCTTGCTCATCAAGACATAAGCGAATTGCACGGTAGCCCAAGAACGGAT

66. *Bacillus anthracis* Sterne (SEQ ID NO. 66)

ACTGCGCATNNGCCTTCTTTATGAGCAGCATCGATAACCATTTTTACAAGACGTAAAATAGATAGGTTATATGGT
TGGTATAAGTAAGATACTTGTTCGTTTCATACGGTCTGCAGCCATTGTGTATTGAATTAAGTCATTTGTTCCGATA
GAGAAGAAATCAACTTCTTTTGCGAATTGATCTGCTAATACTGCTGAAGCTGGGATTTCAACCATCATACCAACT
TCAATAGAATCAGAAACAGTTGTACCCACTTCTACAAGTTTCGCTTTTTCTTCTAATAAGATCGCTTTTGCTTGA
CGGAACATCATCAAGAGTTGCAATCATTGGGAACATAATTTTAAAGTTACCGTATACGCTAGCACGAAGTAATGCA
CGAAGTTGTGTACGGAACACATCTTGCTCATCAAGACATAAGCGAATTGCACGGTAGCCCANGAACGGATNNTTT
NTCTTAA

67. *Bacillus anthracis* 1655H85 (SEQ ID NO. 67)

NNCNNGCATGGGCCNTCTTTATNAGCAGCATCGATAACCATTTTTACAAGACGTAAAATAGATAGGTTATATGGT
TGGTATAAGTAAGATACTTGTTCGTTTCATACGGTCTGCAGCCATTGTGTATTGAATTAAGTCATTTGTTCCGATA
GAGAAGAAATCAACTTCTTTTGCGAATTGATCTGCTAATACTGCTGAAGCTGGGATTTCAACCATCATACCAACT
TCAATAGAATCAGAAACAGTTGTACCCACTTCTACAAGTTTCGCTTTTTCTTCTAATAAGATCGCTTTTGCTTGA
CGGAACATCATCAAGAGTTGCAATCATTGGGAACATAATTTTAAAGTTACCGTATACGCTAGCACGAAGTAATGCA
CGAAGTTGTGTACGGAACACATCTTGCTCATCAAGACATAAGCGAATTGCACGGTAGCCCANGAACGGANCTTTT
TTCTTTA

68. *Bacillus anthracis* Coda-Cerva (SEQ ID NO. 68)

ANNTGGCATNGGNCTTCTTTATGAGCAGCATCGATAACCATTTTTACAAGACGTAAAATAGATAGGTTATATGGT
TGGTATAAGTAAGATACTTGTTTCGTTTCATACGGTCTGCAGCCATTGTGTATTGAATTAAGTCATTTGTTCCGATA
GAGAAGAAATCAACTTCTTTTGCGAATTGATCTGCTAATACTGCTGAAGCTGGGATTTCAACCATCATACCAACT
TCAATAGAATCAGAAACAGTTGTACCCACTTCTACAAGTTTCGCTTTTTCTTCTAATAAGATCGCTTTTGCTTGA
CGGAACATCAAGAGTTGCAATCATTGGGAACATAATTTTTAAGTTACCGTATACGCTAGCACGAAGTAATGCA
CGAAGTTGTGTACGGAACACATCTTGCTCATCAAGACATAAGCGAATTGCACGGTAGCCCAAGAACGGATCNTTT
NTCTT

69. *Bacillus anthracis* 2054H82 (SEQ ID NO. 69)

TTNNGGCATGGCGCCNTCTTNATNAGCAGCATCGATAACCATTTTTACAAGACGTAAAATAGATAGGTTATATG
GTTGGTATAAGTAAGATACTTGTTTCGTTTCATACGGTCTGCAGCCATTGTGTATTGAATTAAGTCATTTGTTCCGA
TAGAGAAGAAATCAACTTCTTTTGCGAATTGATCTGCTAATACTGCTGAAGCTGGGATTTCAACCATCATACCAA
CTTCAATAGAATCAGAAACAGTTGTACCCACTTCTACAAGTTTCGCTTTTTCTTCTAATAAGATCGCTTTTGCTT
GACGGAACATCAAGAGTTGCAATCATTGGGAACATAATTTTTAAGTTACCGTATACGCTAGCACGAAGTAATG
CACGAAGTTGTGTACGGAACACATCTTGCTCATCAAGACATAAGCGAATTGCACGGTAGCCCAAGAACGGATCTT
TTTCTTTA

70. *Bacillus cereus* ATCC 10987 (SEQ ID NO. 70)

GCCTTCTTTATGAGCAGCATCGATAACCATTTTTACAAGACGTAAAATAGATGGGTTATATGGTTGGTATAAGTA
TGATACTTGTTTCGTTTCATACGGTCTGCAGCCATTGTGTATTGGATTAAATCATTTGTTCCGATAGAGAAGAAGTC
AACTTCTTTTCGCGAATTGATCTGCTAATACTGCTGAAGCTGGGATTTCAACCATCATACCAACTTCAATAGAATC
AGAAACAGTTGTACCCGCTTCTACAAGTTTCGCTTTCTCTTCTAATAAAATCGCTTTTCGCTTGACGGAACATC
AAGAGTTGCAATCATTGGGAACATAATTTTTAAGTTACCGTATACGCTAGCACGAAGTAATGCACGAAGTTGTGT
ACGGAACACATCTTGCTCATCAAGACATAAGCGAATTGCACGGTATCCCAAGAACGGATCATTCTCGTTA

71. *Bacillus cereus* ATCC 14579 (SEQ ID NO. 71)

CCATTTCTTCTTTATGAGCAGCATCGATAACCATTTTTACAAGACGTAAAATAGATGGGTTATATGGTTGGTAT
AAGTATGATACTTGTTTCGTTTCATACGGTCTGCAGCCATTGTGTATTGGATTAAATCATTTGTTCCGATAGAGAAG
AAGTCAACTTCTTTTCGCGAATTGATCTGCTAATACTGCTGAAGCTGGGATTTCAACCATCATACCAACTTCAATA
GAATCAGAAACAGTTGTACCCGCTTCTACAAGTTTCGCTTTCTCTTCTAATAAAATTGCTTTTCGCTTGACGGAAC
TCATCAAGAGTTGCAATCATTGGGAACATAATTTTTAAGTTACCGTATACGCTAGCACGAAGTAATGCACGAAGT
TGTGTACGGAACACATCTTGCTCATCAAGACATAAGCGAATTGCACGATATCCCAAGAACGGA

72. *Listeria monocytogenes* (SEQ ID NO. 72)

CCCCTCTTTATGAGAAGCATCAATTACCATTTTTACTAAACGTAAGATGGATGGATTGTATGGTTGGTAAAGGTA
AGAAACGCGTTCGTTTCATACGGTCCGCAGCCATTGTATACTGAATTAAGTCATTTGTTCCGATAGAGAAGAAATC
AACTTCTTTTGCAAATTGATCAGCAAGAACTGCAGCGGCAGGAATTTCAATCATAATTCCAAGTTCGATGGAATC
AGATACTTCTGTTCCAGCAGCTTTTAGTTTTGCTTTCTCATCTAGTAAATATCACGTGCTTGACGGAATTCATT

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TACTGTTGCAATCATCGGGAACATAATTTTTAAGTTACCATATACACTTGCGCGAAGTAAGGCGCGAAGTTGCGT
ACGGAATAATTCTTCATTTCGCAAAACAAAGACGAATTGCGCGGAATCCCAAGAACGGATCNTTCTCCTTA

73. *Streptococcus pneumoniae* (SEQ ID NO. 73)

CGCGTGAGCTGCTTTGATCCATTGTTAATCAAGCGTAGGATTGATGGGTTGTATGGTTGGTAAAGGTATGAACT
TGTTTCGTTTCATACGGTCTGCTGCCATTGTATATTGGATCAAGTCATTTGTACCAATTGAGAAGAAGTCAACTTCT
TTAGCAAATTGGTCTGCAAGCATAGCCGCTGCAGGAATCTCGATCATGATACCAACTTGAATGTTATCCGCAACT
GCAACACCTTCAGCAAGAAGGTTTGCTTTTTCTTCATCAAAGACTGCTTTCGCTGCACGGAATTCTTTCAAGAGC
GCAACCATTGGGAACATGATACGCAATTGACCGTGAACAGACGCACGAAGAAGAGCACGGATTTGTGTGCGGAAC
ATAGCATCTCCAGTCTCAGAGATAGAGATACGAAGAGCACGGAATCCNANGAACGGATCCTTTTTCNTA

74. *Streptococcus pyogenes* (SEQ ID NO. 74)

TGCGCTGCTTTGATACATTGTTGATCAAACGTAATATTGATGGGTTGTATGGTTGGTAAAGGTATGATACTTGTT
CGTTCATACGGTCTGCTGCCATAGTGTATTGGATAAGGTCGTTTGTTCGAATTGAGAAGAAATCAACTTCCTTAG
CAAATTGGTCTGCAAGCATAGCAGCTGCAGGAATCTCAATCATGATACCAACTTGGATGTCATCAGCAACCGCAA
CGCCTTCTGCAAGCAAGTTTGCTTTTTCTTCGTCAAAGACTGCTTTTGCAGCACGGAATTCTTTAAGAAGCGCAA
CCATTGGGAACATAATACGAAGTTGTCCGTGAACAGAGGCACGAAGAAGCGCACGCATTTGTGTGCGGAACATGG
CATCCCCAGTTTCAGAGATGGAAATACGAAGAGCACGGAACCNAAGAACGGATCNTTTTTNCCNTA

75. *Streptococcus agalactiae* (SEQ ID NO. 75)

GAGCAGCTTTGATAACGTTGTTAATCAAACGAAGGATTGATGGATTGTATGGTTGATAGAGGTATGAACTTGCT
CATTCATACGGTCCGCAGCCATTGTGTATTGGATAAGATCATTAGTACCAATTGAGAAGAAATCAACTTCCTTTG
CAAATTGGTCTGCAAGCATAGCTGCCGCTGGGATTTCAATCATAATACCAACTTCAATGCCTTCAGCTACTGCTA
CACCGTCAGCTAACAAAGTTCGCTTTCTCTTCTTCAAATATAGCTTTAGCAGCACGGAATTCTTTAAGCAAAGCAA
CCATTGGGAACATGATGCGTAGCTGTCCATGAAGTGAAGCACGAAGAAGTGTCTCGGATTTGTGTGCGGAACATTG
CATCACCAGTTTCAGAAATTGAAATACGCAATGCACGGAATCCCAAGAACGGATCNTTTTTCNTA

76. *Streptococcus mutans* (SEQ ID NO. 76)

TGAGCAGCCTTAACCCATGATCAACCAAGCGAAGAATGGATGGATTATAAGGTTGGTAGAGGTATGATACTTGTT
CATTCATACGGTCAGCAGCCATGGTGTATTGAATAAGGTCATTTGTACCGATTGAGAAGAAATCAACTTCCTTAG
CAAATTGGTCAGCCAACATTGCAGCTGCAGGAATTTCAATCATGATACCAACTTGGATATCATCTGAAACAGCAA
CGCCTTCAGCTTTAAGATTAGCCTTTCTTCTTCCAGAATACCTTTAGCTTTACGGAACTCATTGAGCAAAGCTA
CCATTGGGAACATGATACGCAACTGACCATGAACAGAAGCACGCAAAAGGGCACGCAACTGTGTGCGGAACATCT
GATTGCCTGTTTCTGAGATTGAAATACGAAGTGCACGAAAACCAAGAACGGATCATTCTCTTA

77. *Enterococcus faecalis* (SEQ ID NO. 77)

CGTCGTGTGCTGCATCAATTACATTTTTTAATTAAACGTAAGATTGATGGGTTGTATGGTTGGTATAAGTAAGAAA
CGCGTTTCGTTTCATACGGTCTGCCGCCATTGTGTATTGGATTAAGTCGTTGGTTCCAACACTAAAGAAGTCTACTT
CTTTGGCAAATTTATCAGCTAATACGGCAGCTGCTGGAATTTCAATCATAATACCTACTTGGATATCGTTTGAAA
CTTCAACACCTTCGTTGACTAATTTTTGTTTTCTTCGCTTCAAAGATTGCTTTCGCTGCTCTAAATTCTTTCAAAG

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TAGCAACCATTGGGAACATGATACGTAAGTTACCATGAACAGACGCACGTAATAATGCACGCATTTGTGTACGGA
ACATGCCGTCACCTAGTTCTGATAAGCTAATACGTAATGCACGGTAACCCAAGAACGGATNATTCTCGTA

78. *Staphylococcus aureus* (SEQ ID NO. 78) SAUR

NNCCNTCTTATGTGACGCTTCAATAACTTGTTTAACTAAACGTAAGATTGAAGGGTTATATGGTTGGTATAGAT
ATGATACACGCTCTGACATACGGTCAGCAGCTAATGTGTATTGAATTAAATCATTTGTACCGATACTGAAGAAAT
CTACTTCTTTAGCAAAGACATCAGCTAATGCTGCTGTTGCAGGTATCTCTACCATGATTCTAATTCTATATCAT
CCGAAATGTCATGACCTTCATTTTTTAAGGTTTTCTTTTTCTTCTAATAATATAGCTTTTGCTTCTCTAAATTCGT
TAATTGTTGCAACCATTGGGAACATGATATTTAACTTACCATAAACTGATGCACGTAATAATGCACGTAGCTGTG
GTCTGAAAATATCTTGTGCGCAAGGCATAAACGAATCGCACGGTAACCCAAGAACGGATCCNTTNTCCTTAA

79. *Staphylococcus epidermidis* (SEQ ID NO. 79) SEPI

CTTCTTTATGAGAAGCTTCAATAACTTGTTTAACTAATCGTAAAATTGAAGGATTATATGGTTGATATAAGTATG
AAACTCGTTTCAGACATACGGTCAGCAGCTAATGTGTATTGAATTAAGTCATTTCGTTTCTATACTAAAGAAATCTA
CTTCTTTAGCAAATACATCAGCAAGTGCCGCGGTAGCTGGAATTTCAACCATAATACCTAATTCAATATCATCTG
AAACTTCGTAACCTTCGCGAAGAAGATTTTCTTCTCTTCAAGAAGCATTGATTTAGCGTCACGGAATTCCTTAA
TTGTTGCTACCATTTGGGAACATAATATTCAATTTCCCATAGACTGAAGCACGTAGTAATGCACGTAATTGTGGTC
TAAAGATTTCCGGCTGTGCTAAACATAAACGTATCGCACGATAACCCAAGAACGGATCNTTCTNCGTA

80. *Bacillus thuringiensis* serovar *israelensis* BTHUISR
(SEQ ID NO. 80)

CTTTATGAGCAGCATCGATAACCATTTTTTACAAGACGTAAAATAGATGGGTTATATGGTTGGTATAAGTATGATA
CTTGTTTCGTTTCATACGGTCTGCAGCCATTGTGTATTGGATTAAATCATTCGTTCCGATAGAGAAGAAATCAACTT
CTTTCGCGAATTGATCTGCTAATACTGCTGAAGCTGGGATTTCAACCATCATACCAACTTCAATAGAATCAGAAA
CAGTTGTACCCGCTTCTACAAGTTTCGCTTTCTCTTCTAATAAAATCGCTTTCGCTTGACGGAACCTCATCAAGAG
TTGCAATCATTGGGAACATAATTTTTAAGTTGCCGTATACGCTAGCACGAAGTAATGCACGAAGTTGTGTACGGA
ACACATCTTGCTCATCAAGACATAAGCGAATTGCACGGTATCCCAAGAACGGATCATTCTCNTTA

81. *Bacillus thuringiensis* serovar *kurstaki* BTHUKUR
(SEQ ID NO. 81)

GCCATTTTCCTTCTTTATGAGCAGCATCGATAACCATTTTTTACAAGGCGTAAAATAGATGGATTATACGGTTGGT
ATAAGTAAGATACACGTTTCATTCATACGGTCTGCAGCCATTGTGTATTGGATTAGGTCGTTTGTTCGATAGAGA
AGAAATCAACTTCTTTTGCAAACCTGATCTGCTAATACTGCAGAAGCGGGAATTTCTACCATCATACCTACCTCAA
TAGCATCAGAAACAGTTGTACCAGCTTGAACAAGTCTTTCTTTCTTCTAATAAAATTGCTTTTGCTTGACGGA
ATTCATCAAGAGTTGCAATCATTGGGAACATAATTTTTAAATTACCATATACGCTTGACGAAGCAATGCACGAA
GTTGTGTACGGAACACATCTTGTCTTCAAGGCATAAGCGAATCGCACGGTAACCCAAGAACGGA

82. *Staphylococcus hominis* (SEQ ID NO. 82) SHOM

CNCCNNCCTTATGAGGAAGCTTCAATAACCTGTTTAACTAAACGTAATAATTGCTGGATTATATGGTTGATATAAA
TATGAAACACGTTTCAGACATACGATCAGCTGCCATAGTATATTGAATTAAGTCATTAGTTTCTATACTAAAGAAA

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TCTACTTCTTTAGCAAAGATATCAGCTAACGCAGCAGTAGAAGGAATCTCTACCATGATACCTACTTCGATATCA
TCAGCAACTTCTTGTCTTCGCTAGTTAATTTATCTTTTTCTTCTAAAAGAATAGCTTTAGCATCTCTAAACTCT
TTAATAGTAGCTACCATTTGGGAACATAATATTTAATTTACCATAAGCAGATGCGCGTAATAACGCACGTAATTGT
GTTCTGAAGATGTCTTGTGATCTAAGCACAAACGAATTGCACGATAACCCANGAACGGATTCATNTCNTA

83. *Enterococcus faecium* (SEQ ID NO. 83)**EFCM**

CGCGTGTGCTGCATCAATTACATTTTTGATCAAACGTAAAATTGATGGGTATATGGTTGGTACAAGTAAGAAAC
GCGTTCGTTTCATACGGTCTGCTGCCATTGTGTATTGAATCAAATCGTTCGTACCTACAGAGAAGAAATCTACTTC
TTTTGCAAACCTGTCTGCTAAGACTGCTGCTGCTGGAATCTCGATCATGATGCCGACTTGGATCGTATCAGATAC
TTCCTTGCCTTCACTGATCAATTTTTGTTTTCTTCTTCAAAGATCGTTTTGCTGCGCGGAATTCTTTGAGTGT
AGCTACCATAGGGAACATGATACGTAAGTTACCATGAACAGATGCACGAAGCAATGCACGCATTTGTGTACGGAA
CATTTTCGTGCGCTTGTTCAGATAAACTGATACGCAATGCACGATATCCCAAGAACGGATCATTCTCCTTA

84. *Clostridium perfringens* (SEQ ID NO. 84) CPER

CNTGTTTGTGAGCTCCATCTATTGTCAATTTTGATTAATCTTAATACAGCTGGATGCATTGGATTGTAAAGGTATG
ATACCTTTTCACTCATTCTGTGAGCAGCTAATGTATATTGTATTAAATCGTTAGTTCCTATTGAGAAGAAATCAA
CATGCTTAGCTAATTCATCAGCATAAACTGCTGCAGCTGGGATTTCAACCATGATACCCATTGAATTGAATCTG
AGTATGCTATACCTTCTGCTTTTAACTCAGCTTTCGATCTTCAACAAATGCTTTAGCTTGTGGAATTCTTCTA
ATCCTGAAATCATTTGGGAACATTACTGCAAGATTTCCATAAACAGAAGCTCTTAATAAAGCTCTTATTTGAACTC
TAAAGATATCTTTTCTGTCTAAGCATAATCTTATAGCTCTGTATCCCAAGAACGGATCNNTNNTCNTTAA

85. *Bacillus mycoides* MYC003 (SEQ ID NO. 85) BMYC003

CTTTATGAGCAGCATCGATCACCATTTTTACAAGACGTAAAATTGATGGGTATATGGTTGGTATAAGTAAGATA
CACGTTTCGTTTCATACGGTCTGCAGCCATTGTGTATTGGATTAAGTCATTTGTTCCGATAGAGAAGAAATCGACTT
CTTTTGCGAATTGATCTGCTAATACTGCTGAAGCTGGAATTTCAACCATCATACCAACTTCAATAGAATCAGAAA
CAGTTGTACCCGCTTGGACAAGTCTTTCTTTCTTCTAATAAAAATCGCTTTCGCTTGACGGAATTCATCAAGAG
TTGCAATCATCGGGAACATAATTTTAAAGTTACCGTATACGCTAGCACGAAGTAATGCACGAAGTTGTGTACGGA
ACACATCTTGTCTTCAAGGCATAAGCGAATTGCACGGTATCCCAAGAACGGATCNTTCTCNTTA

86. *Bacillus mycoides* NRS306 (SEQ ID NO. 86) BMYC306

GCCATTTTCCTTCTTTATGAGCAGCATCGATAACCATTTTTACAAGACGTAAAATAGATGGGTATATGGTTGGT
ATAAGTAAGCTACTTGTTCGTTTCATACGGTCCGCAGCCATTGTGTATTGGATTAAATCATTTGTTCCGATAGAGA
AGAAATCAACTTCTTTTGCGAATTGATCTGCTAATACTGCAGAAGCTGGAATTTCAACCATCATACCAACTTCAA
TAGAATCAGAAACAGTTGTACCCGCTTCTACAAGTTTTGCTTTCTTCTAATAAGATTGCTTTTCGCTTGACGGA
ACTCATCAAGAGTTGCAATCATTGGGAACATAATTTTAAAGTTACCGTATACGCTAGCACGAAGTAATGCACGAA
GTTGTGTACGGAACACATCTTGCTCATCAAGACATAAGCGAATTGCACGGTATCCCAAGAACGGATCATTCTCTT

A

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87. *Streptococcus oralis* (SEQ ID NO. 87)

SORA

CNNTTTCCTTCGCGTGAGCTGCTTTGATAACGTTGTTGATCAGCGTAGGATTGATGGGTTGTATGGTTGGTAAA
GGTATGAAACTTGCTCGTTCATACGGTCTGCTGCCATTGTGTATTGGATCAAGTCGTTTGTACCAATTGAGAAGA
AGTCAACTTCTTTAGCAAATTGGTCTGCAAGCATTGCTGCTGCAGGAATTTTCGATCATGATACCAACTTGGATAT
TATCCGCAACTGCAACACCTTCAGCAAGAAGGTTTGCTTTTTCTTCGTCAAAGACTGCTTTTCGCTGCACGGAATT
CTTTCAAGAGCGCAACCATTTGGGAACATGATACGTAATTGACCGTGAACAGACGCACGAAGAAGAGCACGGATTT
GTGTGCGGAACATAGCATCTCCAGTCTCAGAGATAGAGATACGAAGAGCACGGAATCCNAAGAACGGATCNTTTC
TCTTA

88. *Enterococcus hirae* (SEQ ID NO. 88)

EHIR

CNATTTACCTTCGCATGCGCTGCATCGATCACGTTTTTAATCAAACGTAGGATTGATGGGTTGTAAGGTTGATAC
AAGTATGAAACACGTTTCGTTTCATACGGTCAGCTGCCATAGTGTATTGGATCAAGTCATTTCGTTCTACTGAGAAG
AAGTCAACTTCTTTAGCAAACCTTGTCAGCTAAGACAGCTGCTGCTGGAATTTTCGATCATGATGCCGACTTGGATC
GTATCAGATACTTCCACGCCTTCATTCAATAATTTTGTGTTTTCTTCGTTCAAAGATTGCTTTTGCAGCACGGAAT
TCTTTAAGAGTCGCTACCATTGGGAACATGATACGTAAGTTCCATGAACAGATGCACGTAATAATGCGCGCATT
TGCGTACGGAACATTTTCGTCACCTTGTTCTGACAAGCTGATTGCTAATGCACGATAGCCCAAGAACGGATCNTTN
TCCTTA

89. *Enterococcus avium* (SEQ ID NO. 89)

EAVI

CNATTTNCCTTCGCGTGCGCTGCATCAATCACGTTTTTGATTAAGCGTAGAATTGATGGGTTATATGGTTGGTAA
AGGTAAGAAACGCGTTTCGTTTCATACGGTCAGCTGCCATCGTGTATTGAATTAAGTCATTTGTTCCGATACTGAAG
AAATCAACTTCTTTGGCAAACCTTGTCAGCTAGTACAGCTGCAGCTGGAATTTTCGATCATGATTCGACTTGGATC
GTATCAGAAACTTCCACGCCTTCTTTAACCAATTTTCTTTTTCTTCGTTGAACATTTTCTTCGCTGCACGGAAT
TCTTTTAATGTCGCAACCATTTGGGAACATGATGCGTAAGTTACCATGAACAGAAGCGCGCAACAATGCACGTAAT
TGTGTACGGAACATGTCATCGCCTAGTTCGGATAGACTAATACGCAATGCACGATAACCCAAGAACGGATCNTTT
TTCTTAA

90. *Staphylococcus saprophyticus* (SEQ ID NO. 90)

SSAP

TCGTAAGAAGCTTCTATTACTTGTTTTACTAAACGTAATATTGAAGGATTATATGGTTGATACAAGTAAGAAACA
CGTTCCTGACATTCTATCAGCAGCCATTGTATATTGAATTAATCATTCGTTCTTATACTGAAGAAATCAACTTCT
TTAGCAAATACATCTGCCAACGCAGCAGTAGAAGGAATTTCTACCATAATACCAAGTTCGATATCATCAGAACT
TCAATGCCTTCATTTGTTAAGTTATCTTTTTCTTCAAGTAACAATGCTTTAGCATCACGGAACCTTGGATTGTA
GCTACCATAGGGAACATGATATTCAATTTACCAAAAGCAGATGCACGTAATAATGCACGCAACTGTGGTCTGAAA
ATATCAGGTTGATCTAGGCATAAACGGATAGCACGGTAACCCAAGAACGGATCATTCTCTTA

91. *Staphylococcus haemolyticus* (SEQ ID NO. 91)

SHAE

GAAGCTTCATGACTTGTTTAACCAAGCGTAAAATAGCTGGGTTATAAGGTTGGTATAAGTATGAAACGCGTTCTG
ACATACGGTCAGCTGCCATAGTATATTGAATTAATCATTAGTACCAATACTGAAGAAATCCATTTCTTTAGCAA
AGATATCAGCTAAAGCAGCTGTAGATGGAATCTCAACCATGATACCTAACTCAATTTTCATCAGAAACGTCATGAC
CATCATTTTTAAGATTTTCTTTTTCTTCTAACAGAATGGCTTTAGCATCACGGAATTCATTGATTGTAGCTACCA

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TTGGGAACATAATGTTTAATTTACCGTAAGCTGACGCGCGTAATAATGCACGTAATTGTGTTCTGAAAATATCTT
GTTGATCTAAGCATAGACGAATTGCTCTGTAACCCAAGAACGGNTCNTTCTCTTA

92. *Enterococcus flavescens* (SEQ ID NO. 92) EFLA

NGCATGCGCTGAGTCGATCACGTTTTTGGATCAAACGTAAAATTGATGGGTTGTATGGTTGGTACAAGTAAGACAC
GCGCTCGTTCATGCGGTCTGCAGCCATTGTGTATTGGATCAAGTCATTGGTACCAATACTGAAGAAGTCAACTTC
CTTCGCAAACCTGTCTGCTAAGACAGCAGCTGCTGGAATTTTCGATCATGATTCCGACTTGGATCTCGTTAGAAAC
CTCAACGCCTTCGTCAATCAATTTTTGACGCTCTTCTTCATACATTTTCTTCGCAGTACGGAACCTCTTTCAATGT
TGCCACCATTGGGAACATGATACGTAAGTTGCCGTGAGCAGAAGCACGTAACAACGCACGAAGTTGGGTACGGAA
CATGTCATCCCCAAGTTCAGATAAGCTGATACGCAATGCACGATAGCCCAAGAACGGATATTNNTCNTA

93. *Enterococcus casseliflavus* (SEQ ID NO. 93) ECAS

GCGCTGAGTCGATACGTTTTTGGATCAAACGTAAAATTGATGGGTTGTATGGTTGGTACAAGTAAGACACGCGCTC
GTTTCATGCGGTCTGCAGCCATGGTGTATTGGATCAAGTCATTGGTACCAATACTGAAGAAGTCAACTTCCTTCGC
AACTTGTCTGCTAAGACAGCAGCTGCTGGAATTTTCGATCATGATTCCGACTTGGATCTCGTTAGAAACCTCAAC
GCCTTCGTCAATCAATTTTTGACGCTCTTCTTCATACATTTTCTTCGCAGTACGGAACCTCTTTCAATGTTGCCAC
CATTGGGAACATGATACGTAAGTTGCCGTGAGCAGAAGCACGTAACAACGCACGAAGTTGGGTACGGAACATGTC
ATCCCCAAGTTCAGATAAGCTGATACGCAATGCACGATAGCCCAAGAACGGATNATTTNTCTTA

94. *Enterococcus gallinarum* (SEQ ID NO. 94) EGAL

ACCTTNGCATGTGCTGAATCGATTACGTTTTTGGATCAACGTAGAAATAGATGGGTTATATGGTTGGTAAAGATATG
AACTTGTTCATTCATACGGTCTGCAGCCATTGTGTATTGGATCAAGTCATTGGTACCAATACTGAAGAAGTCTA
CTTCCTTGGCAAATTTGTCAGCTAAGACAGCTGCTGCAGGAATTTTCGATCATGATACCTACTTGAATATCTTCAG
AGACGGTTACGCCTTCATCGATCAATTTTTGACGTTCTTCTTCGTACATTTTTTTTCGCAGCACGGAACCTCTTCA
ATGTTGCCACCATTGGGAACATAATCCGCAAGTTTCCGTGAGCAGAAGCACGTAACAGCGCACGAAGTTGTGTAC
GGAACATGCCGTCACCCAACCTCAGACAACTGATACGCAATGCACGATAGCCCAAGAACGGATCTTTNTCCNTTA

95. *Enterococcus raffinosus* (SEQ ID NO. 95) ERAF

NTGTGCTGCATCAATGACGTTTTTAATCAAACGTAAAGATTGATGGGTTATATGGTTGATACAGGTATGAAACGCG
TTCGTTTCATACGGTCAGCAGCCATTGTGTATTGAATCAAGTCGTTTGTTCGGATACTAAAGAAGTCAACTTCTTT
TGCAAACCTTGTCAGCTAGAACAGCTGCGGCAGGGATCTCGATCATGATTCCGACTTGAATCGTATCAGAAACCTT
CACGCCTTCGTTAACAAGCTTTTCTTTTTCTTCGTTGAACATTTTCTTCGCTGCACGGAACCTCTTTTAATGTTGC
AACCATTGGGAACATGATGCGTAAATTGCCATGAAGTGAAGCGCGTAACAATGCACGTAAGTGTGTACGGAACAT
ATCGTCGCCTAATTCAGATAAACTGATACGCAATGCACGATAACCCAAGAACGGATNNTTCTNCGTAA

96. *Enterococcus villorum* (SEQ ID NO. 96) EVIL

GGNCTCTCGTCGTNAGCTGCATCAATCACGTTTTTGGATTAAACGTAAAATTGATGGGTTATAAGGTTGGTATAAG
TATGAAACGCGTTCGTTTCATACGGTCAGCTGCCATAGTGTATTGAATCAAATCATTTGTTTCTTACTGAGAAGAAG
TCAACTTCCTTCGCAAACCTGTCAGCTAAAACAGCAGCTGCAGGAATTTCAATCATAATGCCGACTTGGATCGTA
TCAGATACTTCCACGCCTTCATTCAATAACTTTTGTTCATCTTCAAAGATTGCTTTTGCCCCACGGAATTCT

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TTAAGTGTGCCACCATTGGGAACATGATACGTAAGTTACCGTGAACGGATGCACGCAATAACGCACGCATTTGT
GTACGGAACATTTTCGTCTCCTTGTTTCAGAAAGACTGATACGTAATGCACGATATCCNANGAACGGNTTATTTTTC
NTA

97. *Clostridium difficile* (SEQ ID NO. 97) CDIF

TTTNNGGANGGCNTCTNTTCGTANGCATTGTCTATANCAGTCTTTATAAGTCTTAAAACAGCTGGATNAAATTGAT
TGTAAGNTAACTTATCTTTTGATTCACTTCTATCAACTGCACAAGTGTATTGAATTAAATCATTAGTTCCTATAG
AGAAGAAATCTACGTGTTTAGCCAATACATCAGATATCACAGCAGCAGATGGAACCTTCTATCATCATACCAATTT
CTACATCTTTAGCATAAGCCACACCTTCAGAATCAAGTTCTGCTAAAACCTTCTTTTACAACCTTCTTTAGCTTGTA
ACAACCTCTTCTAAAGATGAAATCATTTGGGAACATGATTCTTAATCTTCCATGAACACTAGCTCTATATAAGCTC
TCAATTGAGTCTTAAATATATCTTTTCTATCTAGGCAAAGTCTTATTGCTCTGTAACCCAAGAACGG

98. *Streptococcus mitis* (SEQ ID NO. 98) SMIT

NGCGTGAGCTGCCTTGATAACGTTGTTGATCAAGCGAAGGATTGATGGGTTATATGGTTGGTAAAGGTATGAAAC
TTGCTCGTTCATACGGTCTGCTGCCATTGAGTATTGGATCAAGTCGTTTGTTCGAATTGACATGAAGTCTACTTC
TTTTGCAAATTGGTCTGCAAGCATCGCTGCTGCAGGGATTTCATCATGATACCAACTTGGATATCATCCGCAAC
TGCAACACCTTCAGCAAGAAGGTTTGCTTTTCTTCTTCATAAACTGCTTTGGCTGCACGGAATTCTTTCAAAAG
AGCAACCATTGGGAACATGATACGCAATTGACCATGAACAGAAGCACGAAGAAGAGCACGGATTTGTGTACGGAA
CATTGCATCTCCAGTTTCAGAAATAGAGATACGAAGGGCACGGAATCCNAAGAACGGATATTTTTCNTA

99. *Bacillus halodurans* (SEQ ID NO. 99) BHAL

NCCTTCGCTATGAGCTGCTTTAATAACCATATCGACGAGGCGTAAAATCGCAGGGTGGTATGGCTGATACAGGTA
GGAGACTCGCTCATTCATGCGGTCAGCAGCCATCGTATATTGAATTAAGTCGTTTCGTTCCGATACTGAAAAAGTC
TACTTCTTTTGCAAAAAGATTAGCCGCTACCGCCGTCGATGGGATTTCTACCATGATTCCCACTTCAATTGAATC
GGATACGTCCACTCCTTCACTAAGAAGCTTGTCTTTTCTCTTGCATGATCGCTTTTGCTTGGCGAAGCTCTTC
AAGGGTGGCGATCATTGGAAACATCACCTTTAAGTTACCGTATGTGCTTGCGCGAAGCAAGGCACGGAGTTGGGT
CCGGAAAATATCTTGTTTTTCAAGGCACAGACGAATCGCCCGAAACCNAAGAACGGATNNTTNTTCNTAA

100. *Bacillus weihenstephanensis* (SEQ ID NO. 100) BWEI

NTGAGCAGCATCGATAACCATTTTACAAGACGTAAAATAGATGGGTTATATGGTTGGTATAAGTAAGCTACTTG
TTCGTTTCATACGGTCTGCAGCCATTGTGTATTGGATTAAGTCATTTGTTCCAATAGAGAAGAAATCAACTTCTTT
TGCGAACTGATCAGCTAATACTGCTGAAGCTGGAATTTCAACCATCATACCAACTTCAATAGAATCAGAAACAGT
TGTACCCGCTTTAACAAGTCTTTCTTTCTTCTAATAAGATTGCTTTTCGCTTGACGGAACCTCATCAAGAGTTGC
AATCATTGGGAACATAATTTTAAAGTTACCGTATACGCTAGCACGAAGTAATGCACGAAGTTGTGTACGGAACAC
ATCTTGCTCATCAAGACATAAGCGAATTGCACGGTATCCCAAGAACGGATCNTTCTCNTTA

101. *Streptococcus species* (SEQ ID NO. 101) SSPE

CNNANTTNCCTTCGCGTGAGCTGCTTTGATAACGTTGTTAATCAACGAAGGATTGATGGGTTGTATGGTTGGTAA
AGGTATGAAACTTGTTTCGTTTCATACGGTCAGCAGCCATTGTGTATTGGATAAGGTGCTTTGTTCGGATTGAGAAG
AAGTCAACTTCTTTGCAAATTGGTCAGCAAGCATAGCTGCAGCTGGGATTTCAATCATGATACCAACTTGGATA

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TCATCTGAAACGGCAACACCTTCAGCTTTAAGGTTTGCTTTTTCTTCATCAAAGATTGCTTTAGCAGCACGGAAT
TCTTTAAGAAGAGCAACCATTGGGAACATGATACGAAGTTGTCCGTGTACAGATGCACGAAGAAGTGCACGGATT
TGTGTACGGAACATTGCATTTCTGTCTGAGATAGAAATACGAAGTGCACGGAATCCNAAGAACGGATCCTTT
TTCCTTAA

102. *Streptococcus gordonii* (SEQ ID NO. 102) SGOR

NTGCCTTCGCATGAGCCGCCCTTGATAACATTGTTGATCAAGCGAAGGATAGATGGGTTATAAGGTTGATAGAGGT
AAGAGACTTGTTTCATTCATCCGGTCAGCTGCCATAGTGTACTGGATCAAGTCGTTGGTACCAATTGAGAAGAAGT
CAACTTCCTTGGCAAATTGATCCGCCAACATAGCTGCTGCTGGAATTTCAATCATGATACCCACTTGAATGTTAT
CCGCTACAGCAACACCTTCAGCTTGCAATTTTCGCTTTTTCTTCTTCGTAACTGCTTTAGCCTTACGGAATTCTG
TTAGAAGGGCTACCATTGGGAACATGATACGTAATTGTCCATGTACAGACGCACGTAAGAGAGCGCGGATTGTG
TACGGAACATAGCATTACCAGTTTCAGAGATAGAGATACGCAAAGCACGGAAGCCNAAGAACGGTCNTTTT

103. *Streptococcus canis* (SEQ ID NO. 103) SCAN

CNCGTGAGCTGCTTTGATAACGTTGTTAATCAAACGAAGGATTGATGGGTTGTATGGTTGGTAAAGGTATGAAAC
TTGTTTCGTTTCATACGGTCAGCAGCCATTGTGTATTGGATAAGGTCGTTTGTTCGATTGAGAAGAAGTCAACTTC
TTTCGCAAATTGGTCAGCAAGCATAGCTGCAGCTGGGATTTCAATCATGATACCAACTTCGATATCATCTGAAAC
GGCAACACCTTCAGCTTTAAGGTTTGCTTTTTCTTCATCAAAGATTGCTTTAGCAGCACGGAATTCTTTAAGAAG
AGCAACCATTGGGAACATGATACGAAGTTGTCCGTGTACAGATGCACGAAGAAGTGCACGGATTTGTGTACGGAA
CATTGCATTTCTGTCTTGAGATAGAAATACGAAGTGCACGGAATCCNAAGAACGGTCNTTTTCTCTAA

104. *Bacillus pumilus* (SEQ ID NO. 104) BPUM

CNTACGCTGCTTCATAACAAGCGTAATCAAACGTAAATCGCTGGATTGTAAGGCTGGTAAAGATAAGACACTCG
TTCGTTTCATTTCGATCAGCAGCCATTGTGTATTGAATCAAATCATTTGTTCCAATACTGAAGAAATCAACTTCTTT
TGCGAATTGGTCTGCGATGACAGCGGTTGATGGAATTTCTACCATTATACCGATTTCAATGGAATCGGATACGTC
TGTACCAGCGGCAACCAATGCTTCTTTTTCTTCAAGTAAATGGCTTTTGCTTCTCTAAATTCTGATAATGTGCG
GATCATAGGGAACATGATTTTCAAGTTTCCATATGTACTTGCACGAAGTAAGGCGCGTAGTTGTGTTCTGAAAAT
CTCCTGTTCTTCGAGGCAAAGGCGGATCGCTCTAAAGCCNAAGAACGGATNTTTTCTNTTAA

105. *Bacillus species* (SEQ ID NO. 105) BSPE

TGAGCGCATCGATAACCATTTTTACAAGACGTAAATAGATGGGTTATATGGTTGGTATAAGTATGATACTTGTT
CGTTCATACGGTCTGCAGCCATTGTGTATTGGATTAAATCATTTGTTCCGATAGAGAAGAAGTCAACTTCTTTCG
CGAATTGATCTGCTAATACTGCTGAAGCTGGGATTTCAACCATCATACCAACTTCAATAGAATCAGAAACAGTTG
TACCCGCTTCTACAAGTTTCGCTTCTCTTCTAATAAAATTGCTTTTGCTTGACGGAACCTCATCAAGAGTTGCAA
TCATTGGGAACATAATTTTAAAGTTACCGTATACGCTAGCACGAAGTAATGCACGAAGTTGTGTACGGAACACAT
CTTGCTCATCAAGACATAAGCGAATTGCACGGTATCCCAAGAACGGATCCNTTNTNCTTTAA

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106. *Lactococcus lactis* (SEQ ID NO. 106) LLAC

GTGAGCTGCTTTGATNCATTGTTAATCAAACGAAGGATTGATGGATTGTAAGGTTGGTAAAGGTAAGAACTTGT
TCATTCATACGGTCTGCAGCCATTGTATATTGGATGAGGTCGTTTGTACCAATTGAGAAGAAATCAACTTCCTTA
GCAAATTGGTCTGCAAGCATTGCTGCTGCTGGAATTTCAATCATGATACCTACTTCGATACCATCTGCAACTGGA
ACACCTTCAGCAATCAATTTTGGCTTTTTCTTCGTCATAAATCTTCTTAGCTGCACGGAACCTCAGTTACGAGAGCA
ACCATTGGGAACATGATACGAAGTTGTCCGTGTACAGAAGCACGCAAGAGTGCACGCAATTGTGTACGGAACATT
CCGTCACCAGCTGTTGAAAGGCTGATACGAAGTGCACGCCATCCCANGAACGGTNNTTTTTNTTTTAA

107. *Bacillus firmus* (SEQ ID NO. 107) BFIR

TCCAGGANGGGTTCNTCNTANGCTGCGTCAATTACCATTTTAACTAAACGCAGGATTGCAGGATTATACGGCTG
GTAAAGGTAAGAAACACGCTCATTTCATGCGGTCTGCAGCCATTGTGTACTGAATTAGATCATTAGTGCCAACACT
GAAGAAATCGACTTCTTTAGCAAACCTGATCAGCCATAACAGCAGTTGAAGGAATTTCAACCATAATTCCAATTC
AATGTTGTGCGCAACCTCTGCTCCTTCGCTCACAAGCTTTTGTCTTTCTTCTTCAAGGATTGCTTTGCCCTGACG
GAATTCTTCAAGAGTGGCAATCATAGGGAACATGATTTTAAGGTTTCATAGGTGCTTGCTCTTAATAAAGCCCT
TAATTGCGTCCTGAACATATCCTGTCTTCCAGACACAGACGAATCGCCCGGAAGCCCAAGAACGGATTTCATTNT
CTTA

108. *Haemophilus influenzae* (SEQ ID NO. 108) HINF

TGAGAGGCATCAATCACTTGTTTAAATTAACCAAGCACAGAGGGGTGCATCGGATTATAAAGATGGGAAATAAAC
TCATTACCGCGATCTACAGCCAAAGTATATTGAGTTAAATCGTTAGTACCGATACTAAAGAAATCCACTTCTTTT
GCTAAAAATTTGCATTTACTGCGGCAGAGGGGGTTTCGACCATTACACCAACTTGGATATTATTATCAAACAGT
CTCCCCCTCTTCACGTAATTCGCTTTTAAATGTTTCAATAACCGCTTTTAATTCCCGAATTTCTTCTACAGAAATA
ATCATCGGGAACATTACCGCCAATTTACCAAAAGCTGAAGCACGTAACACCGCGCGTAATTGTGCATTTAAAATT
TCACGACGATCTAATGCAATGCGAATCGCACGCCATCCCAAGAACGGATNNTTTTTTCTT

109. *Streptococcus bovis* (SEQ ID NO. 109) SBOV

TGAGCTGCTTTGATAACGTTGTTAATCAAACGAAGGATTGATGGGTTATATGGTTGGTAAAGGTATGAACTTGT
TCATTCATACGGTCAGCAGCCATTGTGTATTGGATAAGGTCGTTTGTTCGATTGAGAAGAAGTCAACTTCTTTT
GCAAATTGGTCAGCAAGCATAGCTGCAGCTGGGATTTCAATCATGATACCAACTTGGATATCATCTGAAACGGCA
ACACCTTCAGCTTTAAGGTTAGCTTTTTCTTCATCAAAGATTGCTTTAGCAGCACGGAATTCTTTAAGAAGTGCA
ACCATTGGGAACATGATACGAAGTTGTCCGTGTACAGATGCACGAAGAAGTGCACGGATTTGTGTACGGAACATT
GCATTTCTGTCTTCTGAGATAGAAATACGAAGTGCACGGAATCCNAAGAACGGTCNNTTTTTNCTTA

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110. *Enterococcus durans* (SEQ ID NO. 110) EDUR
TGTGCTGCATCAATCACGTTTTTGGATCAAACGTAAAATTGAAGGGTTATAAGGTTGATACAAGTAAGATACACGT
TCGTTTCATGCGGTCAGCTGCCATTGTGTATTGAATCAAGTCATTTCGTACCTACTGAGAAGAAGTCAACTTCCTTC
GCAAACCTTATCTGCTAAGACAGCTGCTGCAGGGATTTCAATCATGATGCCGACTTGGATCGTATCAGATACTTCC
ACGCCTTCGCTCACTAATTTTTGTTTTCTTCTTCAAAGATTGCTTTCGCTGCACGGAATTCTTTAAGAGTCGCT
ACCATTGGGAACATGATGCGTAAGTTTCCATGAACAGATGCACGTAACAATGCGCGCATTTGTGTACGGAACATT
TCGTACCTAATTCAGACAAGCTGATACGTAGCGCACGATAGCCCAAGAACGGATNNTTTTTCCCTTAA

111. *Streptococcus sanguis* (SEQ ID NO. 111) SSAN
CGCATGAGCTGCCTTGATAACATTGTTAATCAAGCGAAGGATAGATGGATTGTAAGGTTGATAGAGGTAAGAGAC
TTGCTCATTTCATCCGGTCAGCCGCCATAGTGTACTGAATCAAGTCGTTAGTACCAATTGAGAAGAAGTCTACTTC
CTTGGCAAATTGATCCGCCAACATAGCTGCTGCTGGGATTTCAATCATGATACCCACTTGGATATTATCTGCTAC
TGCAACGCCTTCAGCTTGCAGCTTAGCTTTTTCTTCGTCATAAACCGCTTTAGCTTTGCGGAATTCTGTCAGAAG
GGCCACCATTGGGAACATGATACGCAATTGTCCATGTACAGAAGCACGCAAGAGAGCGCGGATTTGTGTACGGAA
CATAGCATCGCCAGTTTCAGAGATAGAGATACGCAAAGCACGGAAACCAAAGAACGGTNNTTTTTNTCTTTAAAA

112. *Enterobacter cloacae* (SEQ ID NO. 112) ECLO
TCCTTTACCTTCTGCATGAGAGCATCAATAACTTGCTTGATCAAGTTCAGTACGGACGGTGACATTGGCTGGTAG
AGATGTGAAATCATATCATTACCACGGTCAACTGCCAGGGTGTACTGCGTTAAATCATTGGTGCCGATACTAAAG
AAATCAACTTCTTTGGCTAAATGACGCGCAATGGTCGCGGCTGCTGGTGTTCACCATTTACGCCGATCTCAATT
GACTCGTCAAATGCTTTACCTTCGTCACGCAATTCCTGTTTGTAGATCTCGATCTCTTTCTTCAGTGCACGCACT
TCTTCAACAGAGATGATCATCGGGAACATAATGCGCAGCTTACCGAAAGCAGAGGCACGCAGAATCGCACGCACC
TGGTCACGCAGGATTTCTTTACGATCCATGGCGATACGCACTGCACGCCAGCCCAAGAACGGATNNTTTTTTCTT
TAA

113. *Serratia liquefaciens* (SEQ ID NO. 113) SLIQ
NTGNCTTCTGCATGAGNATGCATCAATAACCTGTTTGATCAGGCCAAGCACTGATGGGGACATCGGGTTATAGAG
ATGAGAAATCAGCTCATTGCCGCGATCTACCGCCAGAGTATACTGGGTTAGATCGTTTGTCCCAATACTAAAGAA
GTGCACTTCTTTGCGCAGGTGATGAGCAATCACTGCCGCGGCCGGTGTTCACCATTTACGCCCACTTCAATGGT
CTCGTCAAAGGCCCTTGGATTCTTCACGCAGCTGCGCCTTCAGCGTCTCGATTTACCTTTTCAGATCGCGGACTTC
TTCCACGGAAATGATCATCGGGAACATGATGCGCAGTTTGCCGAACGCGGAAGCGCGCAGGATGGCGCGCAGTTG
CGCGTGCAGGATTTCTCTGCGGTCCATGGCGATACGAATCGCGCGCCAGCCNAAGAACGNNTNTTTTTTANTTTA

114. *Proteus mirabilis* (SEQ ID NO. 114) PMIR
GTGTGATGCATCAATCACCTGTTTAATCAGATTAAGTACAGCAGGTGACATTGGATTATATAGATGAGATATCAG
CTCATTTCACGGTCTACAGCCAGAGTATATTGTGTTAGATCGTTAGTCCCAATACTGAAAAAGTCAACTTCTTT
TGCCATATGGCGAGCCATAACAGCCGCTGCTGGCGTTTCAACCATAACACCGACTTCGATAGATTCATCAAAAGG
CTTATTTTCTTCACGAAGCTGGCTTTTTCAGTATTTCAAGTTCCGCTTTCAATGCTCGGATCTCTTCAACAGAGAT
AATCATTGGAAACATAATACGTAGTTTACCAAAGCAGACGCTCTTAAGATAGCACGTAATTGTGGATGAAGGAT
CTCTTTGCGGTCAAGACAAATACGAATTGCACGCCAACCCAAGAACGGATCNNTTTNTCCTT

115. *Providencia stuartii* (SEQ ID NO. 115)**PSTU**

GCCTCTGCATGTGATGCATCAATGACTTGCTTAATCAGTTCAATACAGCAGGCGACATTGGATTGTAGAGGTGAG
AAATCAGCTCATTACCACGGTCAACAGCTAGAGTATATTGAGTGAGATCGTTTCGTCCCAATACTGAAAAAGTCAA
CTTCTTTTGCTAAATGATGAGCAATAACCGCTGCGGCAGGGGTTTCCACCATGACACCAACTTCGATTGATTCAT
CAAAGGCTTTGCCTTCTTCACGTAATTGACCTTTTAGCATCTCAAGTTCTGCTTTTAGTTTCGGAACCTTCCTCAA
CGGAAATAATCATCGGGAACATAATACGCAGTTTACCAAAACTTGAGGCTCTTAAATAGCTCTTAACTGAGAAT
GTAGAATTTCTTTGCGATCAAGGCAAATACGAATTGCCCGCCAGCCCAAGAACGGT

116. *Proteus vulgaris* (SEQ ID NO. 116)**PVUL**

CCTTCTGCATGTGATGCATCAATAACCTGTTTTATCAGGTTAAGTACTGCTGGTGACATTGGATTATACAGATGA
GATATCAGCTCATTTCACGGTCTACAGCCAGAGTATATTGTGTTAGATCGTTAGTCCCAATACTGAAAAAGTCA
ACTTCTTTTGCCATGAGACGTGCCATTACGGCCGCCGAGGGGTTTCAACCATGACACCGACTTCGATAGACTCA
TCGAAAGTTTTGTTTTCTGCACGAAGCTGGCTTTTCAGTATTTCAAGTTCTGCTTTCAATGCGCGAATCTCTTCA
ATAGAGATAATCATTGGAAACATAATGCGTAGTTTACCAAAAGCAGATGCTCTTAAGATAGCACGTAATTGCGAA
TGAAGGATCTCTTTACGGTCAAGACAAATACGAATTGCTCTCCAACCCAAGAACGGTCNNTTTTTTTCTTA

117. *Staphylococcus simulans* (SEQ ID NO. 117) SSIM

TTCTCCGCACATACCTGTCCATTTACCTTCAGCATGAGACGCTTCGATAACACGTTGTACCAAGCGTAAAAATAGC
TGGGTTATATGGTTGGTATAAATAAGACACACGTTCTGACATACGGTCAGCTGCCATTGTATATTGGATTAAGTC
ATTTGTTCCGATACTGAAGAAGTCTACTTCTTTTCGCAAAGACATCAGCAAGTGCTGCTGTGATGGAATTTCAAC
CATGATACCGACTTCGATATCATCTGAAACTTCAACACCTTCATTTTTAAGGTTTTGACGTTCTTCTTCTAATAA
TGCTTTTCGCATCACGGAATTCTTGAATTGTCGCAACCATTGGGAACATAATGTTTAATTTTCCGTATACTGAAGC
ACGTAATAACGCGCGTAATTGCGGACGGAAAATTTCTGGTTGTGCTAAGCACAAGCGGATTGCACGATAACCCAA
GAACGGAT

118. *Staphylococcus sciuri* (SEQ ID NO. 118)**SSCI**

CTCCGCACATACCAGTCCATTTACCTTCTTTATGAGAAGCTTCAATTACTTGCTTAACCTAAGCGAAGAATTGCAG
GGTTATATGGTTGGTATAAGTAAGAAACACGCTCAGACATACGGTCAGCAGCCATTGTATATTGGATTAAATCAT
TCGTACCAATACTGAAGAAATCAACTTCTTTAGCAAAGATGTCTGCAAGTGCTGCAGTAGATGGAATTTCTACCA
TAATACCGATTTTCGATATCATCCGCAACGTTAACACCTTCAGAACTAATTTTTCTTTTTCTCAAGTAAGATTG
CTTTAGCATCTCTAAATTCTTTAATAGTTGCAATCATAGGGAACATGATATTTAACTTACCAAATTCAGATGCGC
GTAATAAAGCTCTTAATTGTGTTCTAAAGATTTTCAGTTTGATCTAAACATAAACGAATCGCTCTATATCCCAAGA
ACGG

119. *Staphylococcus capitis capitis* (SEQ ID NO. 119) SCAPCA

TCCGCACATACCAGTCCATTTACCTTCTTTATGAGAAGCTTCAATGACTTGCTTAACAAGACGTAATATAGATGG
GTTATATGGTTGATATAAATAAGATACACGCTCTGACATACGATCAGCAGCTAGTGATATTGAATTAAATCATT
TGTACCAATACTAAAGAAATCTACTTCCTTCGCAAAGACATCTGCTAATGCAGCAGTTGCTGGAATTTCAACCAT
GATACCTAATTCAATATCATCAGAAATGTCATAACCTTCATTTTCAAGGTTTTTCTTTTCTCTAAAAGAATTGC

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TTTGGCATCACGGAATTCTTTAATAGTAGCAACCATTTGGGAACATGATATTTAATTTACCGTAAGCAGATGCACG
TAATAATGCACGTAATTGCGGTCTAAAAATATCTTGTTGAGCTAAACATAAACGAATTGCTCTATAACCCAAGAA
CGGA

120. *Staphylococcus warneri* (SEQ ID NO. 120) SWAR

CCGCACATACCAGTCCATTTACCTTCTTTGTGAGAAGCTTCAATGACTTGTTTTACTAAGCGTAAAATTGAAGGG
TTGTATGGTTGATATAAGTAAGATACACGTTTCAGACATACGGTCAGCTGCTAATGTGTATTGGATTAAGTCATTT
GTACCAATACTAAAGAAATCTACTTCTTTAGCAAATACATCAGCTAATGCTGCTGCTGCTGGTATTTCAACCATG
ATACCTAACTCAATATCTTCAGAACTTCATAACCTTCATTTTGAAGATTTCTTTTTCTTCTAATAACATTGCT
TTAGCATCACGGAATTCCTTGATAGTTGCTACCATTGGGAACATGATATTTAATTTACCATAAACTGATGCACGT
AATAACGCGCGTAATTGTGGTCTGAAAATATCAGGTTGAGCTAAGCAAAGACGAATCGCTCTGTATCCCAAGAAC
GGATCATTCTCTTA

121. *Staphylococcus cohnii urealyticus* (SEQ ID NO. 121) SCOHURE

CCGCACATTCCAGTCCATTTGCCTTCTTTATGAGAAGCATCAATCACTTGTTGCACTAAACGTAAAATTGCTGGA
TTGTATGGTTGATACAAGTAAGATACTCGCTCTGACATACGATCCGCGGCCATTGTATATTGAATTAATCGTTC
GTTCCGATGCTGAAGAAATCTACTTCTTTAGCAAAAACATCTGCTAATGCTGCAGTTGAAGGAATTTCTACCATG
ATACCAACTTCTATATCATCAGATACTTCAATACCTTCATTTGTTAAATTTCTTTTTCTTCTAATAACAATGCT
TTCGCATCACGGAATTCCTTAATTGTGCTACCATTGGGAACATAATATTTAAATTTCCATAAGCTGACGCACGT
AATAAAGCACGCAATTGCGGTCTGAAAATGTGAGGTTGATCTAAACATAAACGAATCGCACGGTATCCCAAGAAC
GGNT

122. *Staphylococcus schleiferi scheiferi* (SEQ ID NO. 122) SSCH

CCGCACATACCTGTCCATTTACCTTCTTTATGAGATGCTTCAATTACTTGCTTAACTAAGCGTAAAATTGAAGGA
TTGTAAGGTTGGTAAAGATATGATACACGTTCTGACATACGGTCAGCTGCCATCGTATATTGAATTAAGTCATTC
GTTCCAATACTAAAGAAGTCAACTTCTTTAGCAAAAACATCAGCTAAAGCTGCTGTAGATGGAATTTCCACCATA
ATACCTAACTCAATATCATCGCTAACTTCAACGCCTTCTTGTTTTAAGTTTTCTTTTTCTTCAAGAAGAAGCGCT
TTTGCATCGCGGAATTCCTTAATCGTCGCAACCATTGGGAACATAATGTTTCAGTTTTCCGTAAGTTGAAGCGCGT
AATAACGCTCTTAATTGTGGACGGAAAATTTAGGTTGATCTAAACAAAGACGAATTGCACGGTATCC

123. *Staphylococcus intermedius* (SEQ ID NO. 123) SINT

CCGCACATACCTGTCCATTTGCCCTCTTGGTGAGAAGCGTCAATCACTTGTTTAATTAAACGTAAGNATTGATGG
ATTATATGGTTGGTAAAGATAAGATACACGTTCTGACATACGGTCTGCAGCCATTGTGTATTGAATTAATCGTT
TGTACCGATACTGAAGAAATCCACTTCTTTGCAAATACATCTGCAAGTGCGGCTGTTGCAGGGATTTCAACCAT
GATACCTANTTCGATATCGTCGCTCACTTCTACGCCTTCTTGTTTCAAGTTTTCTTTTTCTTCAAGAAGTAACGC
TTTCGCATCACGGAATTCCTGAATCGTTGCCACCATTGGGAACATAATATTCAATTTACCGTATGCTGAAGCTCT
TAATAATGCACGTAATTGTGGACGGAAAATTTAGGTTGATCTAAACATAAACGAATCGCACGGTAACCCAAGAA
CGGATTCAT

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124. *Staphylococcus cohnii cohnii* (SEQ ID NO. 124) SCOHCOH

CCGCACATCCCTGTCCATTTACCTTCTTTATGACTGGCATCAATAACTTGTTTCATCAGTCTAAGAATCGCTGGG
TTATAAGGCTGGTAAAGATAAGAGACGCGTTCATCATACGGTCTGCAGCCATCGTATATTGAATAAGATCATTC
GTACCGATACTAAAGAAATCAACCTCTTTCGCAAAGATATCGGCCATTGCTGCTGTAGAAGGAATCTCTACCATG
ATGCCAAGCTCGATATCGTCAGCAACTTTAACTTTATCTGCAATTAAATTGGCTTTCTCTTCTTCTAAGATTGCT
TTCGCATCACGGAATTCGTTGATAGTCGCAATCATCGGGAACATGATGCTCAGTTTACCGTGGATGGATGCACGT
AATAACGCACGAAGCTGTGTTCTAAAGATATCCTGCTGATCCAGACAAAGTCGAATCGCACGGTATCCAANGAAC
GGNTTCAT

125. *Staphylococcus capitis uralyticus* (SEQ ID NO. 125) SCAPURA

CCGCACATACCAGTCCATTTACCTTCTTTATGAGAAGCCTCTATTACTTGCTTAACAAGACGTAAAATAGAAGGA
TTATATGGTTGATATAAAATAAGATACACGTTCTGACATACGATCAGCAGCTAGTGTGTATTGAATTAAGTCATTA
GTACCGATACTAAAGAAGTCTACTTCCTTCGCAAAGACATCTGCTAATGCAGCAGTTGCTGGAATTTCAACCATG
ATACCTAATTCGATATCGTCAGAAATGTCATAACCTTCATTTTCAAGGTTTTCTTTCTTCTAAAAGAATCGCT
TTAGCATCACGGAATTCCTTGATAGTAGCAACCATTTGGGAACATGATATTTAATTTACCGTAAGCAGATGCACGT
AATAATGCACGTAATTGCGGTCTGAAAATATCTTGTTGCGCTAAACATAAACGAATTGCTCTATAACCCAAGAAC
GGNTTCATNTCTTA

126. *Staphylococcus gallinarum* (SEQ ID NO. 126) SGAL

CCGCACATACCTGTCCATTTACCTTGTTTAACTAAACGTAAAATTGAAGGATTATATGGTTGATACAAGTATGAT
ACACGTTCTGACATTCTATCTGCAGCCATAGTGTATTGAATTAAATCATTTGTACCGATACTAAAGAAGTCAACC
TCTTTAGCAAATACATCAGCTAAAGCTGCTGTAGAAGGAATTTCTACCATGATACCTAATTCGATATCATCAGAT
ACTTCAACACCTTCTTGTTAAATTGTCTTCTCTTCAAGAAGTAATGCTTTGGCATCACGGAATCTTGAATT
GTAGCAACCATTTGGGAACATGATATTTAACTTACCGAATGCAGATGCGCGTAATAATGCACGCAATTGCGGTCTG
AAAATATCAGGTTGATCCAAGCATAAACGTATCGCACGATATCCCAAGAACGGATTTCATNTCTTA

127. *Staphylococcus auricularis* (SEQ ID NO. 127) SAURICU

CCGCACATGCCAGTCCATTTACCTTCTTTATGAGAAGCTTCGATGACTTGTTTGCTCAACCAAGCGTAAAATAGC
TGGATTATATGGTTGATAAAGGTATGATACGCGTTCTGACATGCGGTCTGCAGCCATTGTATATTGAATTAAGTC
GTTTGTACCGATACTAAAGAAGTCGACTTCTTTCGCAAAGACATCTGCTAAAGCAGCTGTTGATGGAATTTGAC
CATAATACCTAATTCATATCATCTGAGACTTCAACTCCCTCTTGTTCTAAGTTTGCTTTTTCTTCTTCCAACAA
TGCTTTAGCATCACGGAATTCCTGAATTGTGCAACCATTTGGGAACATGATATTGAGTTTTCCGTACGTAGATGC
ACGTAATAATGCACGTAATTGTGGACGGAAAATATCAGGTTGATCTAAGCATAAACGAATCGCACGATAACCCAA
GAACGGATTTCAT

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128. *Staphylococcus caseolyticus* (SEQ ID NO. 128) SCAS

CCGCACATCCCTGTCCATTTACCTTCTTTATGACTGGCATCAATAACTTGTTTGATCAGTCTAAGAATC
GCTGGGTTATAGGGCTGGTAAAGATAAGAGACGCGTTCATCATAACGGTCTGCAGCCATCGTATATTGA
ATAAGATCATTTCGTACCGATACTAAAGAAATCAACCTCTTTTCGCAAAGATATCGGCCATTGCTGCTGTA
GAAGGAATCTCTACCATGATGCCAAGCTCGATATCGTCAGCAACTTTAACTTTATCTGCAATTAAATTG
GCTTTCTCTTCTCTAAGATTGCTTTTCGCATCACGGAATTCGTTGATAGTCGCAATCATTGGGAACATG
ATGCTCAGTTTACCGTGGATGGATGCACGTAATAACGCACGAAGCTGTGTTCTAAAGATATCCTGCTGA
TCCAGACAAAGTCGAATCGCACGGTATCCAAAGAACGGATTCA

129. *Staphylococcus xylosus* (SEQ ID NO. 129) SXYL

TGTGAAGCTTTAATCACTTGTTTTACTAAACGTAAAATTGAAGGATTGTATGGTTGATACAAGTAAGAAACACGC
TCAGACATACGATCAGCAGCCATTGTATATTGAATCAAATCATTTGTACCAATACTAAAGAAATCAACTTCTTTA
GCAAATACATCTGCTAAAGCAGCAGTTGATGGTATCTCTACCATAATACCTAATTCAATATCGTCAGATACTTCA
ATGCCCTTCGTTTGTTAAATTCTCTTTTTCTTCCAATAATAATGCTTTTGCATCTCGAAACTCTTTAATTGTGGCA
ACCATTGGGAACATGATATTTAATTTACCGTAAGTAGACGCACGTAACAATGCTCTTAATTGTGGTCTGAAAATA
TCAGGTTGATCTAAGCATAAACGAATTGCACGATATCCCAAGAACGGATCATTTTTTCGTAA

130. *Klebsiella pneumoniae* (SEQ ID NO. 130) KPNE

CCGCACATGCCAGTCCATTTACCTTCAGCGTGAGAAGCATCAATAACTTGCTTAATCAGATTCAGTACAGACGGT
GACATCGGCTGGTAAAGATGTGAAATCATATCATTACCACGGTCAACTGCCAGAGTATATTGCGTTAAATCATTG
GTGCCGATACTAAAGAAATCAACTTCTTTGGCCAGATGACGAGCAATAGTCGCCGAGCCGGTGTTCACCATC
ACGCCGATCTCAATGGATTTCGTCAAATGCTTTACCTTCGTCACGCAGTTTCTGTTTGTAGATTTGATCTCTTTC
TTCAGCGCACGCACTTCTTCAACAGAGATGATCATCGGGAACATAATGCGCAGCTTACCGAAAGCGGAGGCGCGC
AGGATGGCGCGAACCTGGTCGCGCAGGATCTCTTTACGATCCATCGCAATACGCACGGCAGCCAGCCNAAGAAC
GGAT

131. *Salmonella typhimurium* (SEQ ID NO. 131) STPM

CCGCACATGCCAGTCCATTTACCTTCTGCATGAGAAGCATCAATAACTTGCTTGATCAAGTTCAGTACGGACGGT
GACATTGGCTGGTAAAGGTGTGAAATCATATCATTACCACGGTCAACTGCCAGGGTGTACTGCGTTAAATCATTG
GTGCCGATACTAAAGAAATCAACTTCTTTGGCTAAATGACGCGCAATTGTGCGCGCAGCCGGTGTTCACCATC
ACGCCAATCTCAATGCTTTTCGTCAAATGCTTTACCTTCGTCACGCAGTTTCTGTTTGTAGATTTCAATCTCTTTG
CGCAGCGCGCGAACTTCTTCAACAGAGATGATCATCGGGAACATAATGCGCAATTTACCGAAAGCGGAGGCACGC
AGAATCGCGCGAACCTGGTCACGCAGGATCTCTTTGCGATCCATGGCGATACGCACGGCGCGCCAGCCNANGAAC
GGAT

132. *Escherichia coli* O157 :H7 (SEQ ID NO. 132) EC0157

CCTGCCATTTACCGCACATGCCAGTCCATTTGCCTTCAGCATGAGAAGCATCAATAACTTGCTTGATCAAGTTC
AGCACGGACGGTGACATTGGCTGGTAAAGGTGTGAAATCATATCATTACCACGGTCAACTGCCAGAGTGTACTGC
GTAAATCATTGGTGCCGATACTAAAGAAATCAACTTCTTTGGCTAAATGACGTGCAATTGTTGCGGCAGCCGGT
GTTTCCACCATTAACGCCGACTTCAATTGACTCGTCAAACGCTTTACCTTCGTCGCGCAGTTTCTGTTTGTAGATT

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TCGATCTCTTTGCGCAGTGCACGCACTTCTTCAACAGAGATGATCATCGGGAACATAATGCGCAATTTACCGAAA
GCCGAGGCACGCAGGATAGCGCGGAGCTGATCGCGCAGGATCTCTTTACGATCCATTGCGATACGGATAGCGCGC
CAGCCAAAGAACGGGTTCATTTCTTA

133. *Escherichia coli* K12 (SEQ ID NO. 133) ECOK12

TCCTGCCATTTCTCCGCACATGCCAGTCCATTTGCCTTCAGCATGAGAAGCATCAATAACTTGCTTGATCAAGTT
CAGCACGGACGGTGACATTGGCTGGTAAAGGTGTGAAATCATATCATTACCACGGTCAACTGCCAGAGTGACTG
CGTTAAATCATTGGTGCCGATACTAAAGAAATCAACTTCTTTGGCTAAATGACGTGCGATTGTTGCGGCAGCCGG
TGTTTCCACCATTACGCCGATTTCAATTGACTCGTCAAACGCTTTACCTTCGTGCGCAGTTCTGTGTTGTAGAT
TTCGATCTCTTTGCGCAGTGCACGCACTTCTTCAACAGAGATGATCATCGGGAACATAATGCGCAATTTACCGAA
AGCCGAGGCACGCAGGATAGCGCGGAGCTGATCGCGCAGGATCTCTCTACGATCCATCGCGATACGGATAGCGCG
CCAGCCCAAGAACGGATTTCATTTCTT

134. *Citrobacter freundii* (SEQ ID NO. 134) CFRE

TCCCGCCATTTCTCCGCACATGCCAGTCCATTTGCCTTCAGCATGAGAAGCATCAATAACTTGCTTGATCAGCGT
CAGCACAGATGGCGACATCGGTTGGTAAAGGTGTGAAATCATATCATTACCACGGTCAACTGCCAGGGTGTACTG
CGTTAAATCATTGGTGCCGATACTAAAGAAATCAACTTCTTTGGCTAAATGACGCGCAATTGTTGCCGCAGCCGG
TGTTTCCACCATCAGCCCAATCTCAATGCTCTCGTCAAATGCTTTACCTTCGTGCGCAGTTCTGTGTTGTAGAT
TTCAATCTCTTTGCGCAGTGCACGCACTTCTTCAACAGAGATGATCATTGGGAACATAATGCGCAGTTTACCGAA
AGCAGAGGCGCGCAGAATCGCGCGAACCTGGTCACGCAGGATCTCTTTACGATCCATGGCGATACGCACGGCAG
TCAGCCCAGGAATGGGTTCATCTCTT

135. *Pseudomonas putida* (SEQ ID NO. 135) PPUT

TCCCGCCATTTCTCCGCACATGCTCACTGGCTTGCCTTCACCATGGGCATCGCGCACCAACCGTGCTCAAGGCTTG
CAGCTCCGCCGGGTGCAGGTAGTCGTACAGGTGGCAACCCGCGGGTTGTTGCGGTCCACCGCCAGCAGGTACTG
GGTCAGGTGCTTGGAGCCGACCGACAGGAAATCCACCTGCCGCGCCAGTTCTTGGTCTGGTACACCGCCGCAGG
TATTTCCACCATCAGCCCCACCGGCGGCATCGGCACATCGGTGCCTTCGTACGCACCTCGCCCCAGGCGCGGTG
GATCAGGTGCAGCGCTTCTTCCAGCTCGTGGATGCCGGAATCATCGGCAGCAGGATGCGCAGGTTGTTACAGCC
CTCGCTGGCCTTGAGCATGGCGCGAGTCTGCACCAGGAAGATTTCCGGGTGGTCGAGGGTGACGCGGATGCCGCG
CCAGCCTAAGAATGGATTTCATCTCGT

136. *Shigella sonnei* (SEQ ID NO. 136) SSON

CCGGCCATTTACCACACATGCCAGTCCATTTGCCTTCAGCATGAGAAGCATCAATAACTTGCTTGATCAAGTTC
AGCACGGACGGTGACATTGGCTGGTAAAGGTGTGAAATCATATCATTACCACGGTCAACTGCCAGAGTGACTGC
GTTAAATCATTGGTGCCGATACTAAAGAAATCAACTTCTTTGGCTAAATGACGTGCAATTGTTGCGGCAGCCGGT
GTTTCCACCATTACGCCGATTTCAATTGACTCGTCAAACGCTTTACCTTCGTGCGCAGTTCTGTGTTGTAGATT
TCGATCTCTTTGCGCAGTGCACGCACTTCTTCAACAGAGATGATCATCGGGAACATAATGCGCAATTTACCGAAA
GCCGAGGCACGCAGGATAGCGCGGAGCTGATCGCGCAGGATCTCTTTACGATCCATCGCGATACGGATAGCGCGC
CAGCCCAGGAACGGATTTCATCTCTTA

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137. *Listeria innocua* (SEQ ID NO. 137)**LINN**

TCCTGCCATTTCTCCGCACATACCAGTCCATTTGCCCTCTTTATGAGAAGCATCAATTACCATTTTTACTAAGCG
TAAAATAGATGGATTGTATGGTTGGTAAAGGTAAGAAACGCGTTCATTCATACGGTCAGCAGCCATTGTATACTG
AATCAAGTCATTTGTTCCGATTGAGAAGAAATCAACTTCTTTTGCAAATTGATCAGCTAAAACCTGCAGCAGCAGG
AATTTCAATCATAATTCCAAGTTCGATGGAATCAGATACTTCTGTTCCAGCAGCTTTTAGTTTCGCTTTTTTCATC
TAGTAAAATATCGCGCGCTTGGCGGAATTCATTTACTGTTGCAATCATCGGGAACATAATTTTAAAGTTACCATA
TACACTTGCGCGAAGTAGAGCGCGAAGTTGTGTACGGAATAATTCTTCATTCGCAAAACAAAGACGAATCGCAGC
GAATCCTAAGAACGGGTTTCATTTCTG

138. *Serratia marcescens* (SEQ ID NO. 138)**SMAR**

TTCTNNGANGGACTCTNTCNTAAANAGCATCAATAACCTGTTTGATCAGGCCAAGCACTGATGGGGACATCGGGT
TATAGAGATGAGAAATCAGCTCGTTGCCGCGATCTACCGCCAGAGTATACTGGGTTAGATCGTTTGTCCCAATAC
TAAAGAAGTCGACTTCTTTTCGCCAGGTGGTGAGCGATGACCGCCGCGAGCCGGTGTTCACCATCACGCCCACCT
CGATGCTCTCGTCAAACGCCTTGCTTCTTCGCGCAGCTGCGCCTTCAGCGTCTCGATTTTCGCCTTTCAGATCGC
GCACTTCTTCCACGGAGATGATCATCGGGAACATGATGCGCAGTTTACCGAACGCCGAGGCGCGCAGGATGGCGC
GCAGCTGGGCGTGAGGATTTACGCGCGGTCCATCGCGATGCGGATGGCGCGCCAGCCNAAGAACGGATTTCATTN
TCTTA

139. *Salmonella enterica* hadar (SEQ ID NO. 139)**SHAD**

CCGCACATGCCAGTCCATTTACCTTCTGCATGAGAAGCATCAATAACTTGCTTGATCAAGTTCAGTACGGACGGT
GACATTGGCTGGTAAAGGTGTGAAATCATATCATTACCACGGTCAACTGCCAGGGTGTACTGCGTTAAATCATTG
GTGCCGATACTAAAGAAATCAACTTCTTTGGCTAAATGACGCGCAATTGTGCGCCGAGCCGGTGTTCACCATC
ACGCCAATCTCAATGCTTTCGTCAAATGCTTTACCTTCGTACGCAGTTCCTGTTTGTAGATTTCAATCTCTTTG
CGCAGCGCGCGAACTTCTTCAACAGAGATGATCATCGGGAACATAATGCGCAATTTACCGAAAGCGGAGGCACGC
AGAATCGCGCGAACCTGGTCACGCAGGATCTCTTTGCGATCCATGGCGATACGCACGGCGCGCCAGCCNAAGAAC
GGAT

140. *Salmonella enteritidis* (SEQ ID NO. 140)**SENT**

CCGCACATGCCAGTCCATTTACCTTCTGCATGAGAAGCATCAATAACTTGCTTGATCAAGTTCAGTACGGACGGT
GACATTGGCTGGTAAAGGTGTGAAATCATATCATTACCACGGTCAACTGCCAGGGTGTACTGCGTTAAATCATTG
GTGCCGATACTAAAGAAATCAACTTCTTTGGCTAAATGACGCGCAATTGTGCGCCGAGCCGGTGTTCACCATC
ACGCCAATCTCAATGCTTTCGTCAAATGCTTTACCTTCGTACGCAGTTCCTGTTTGTAGATTTCAATCTCTTTG
CGCAGCGCGCGAACTTCTTCAACAGAGATGATCATCGGGAACATAATGCGCAATTTACCGAAAGCGGAGGCACGC
AGAATCGCGCGAACCTGGTCACGCAGGATCTCTTTGCGATCCATGGCGATACGCACGGCGCGCCAGCCNAAGAAC
GGAT

141. *Salmonella enterica* Brandenburg (SEQ ID NO. 141) SBRA

CCGCACATGCCAGTCCATTTACCTTCTGCATGAGAAGCATCAATAACTTGCTTGATCAAGTTCAGTACGGACGGT
GACATTGGCTGGTAAAGGTGTGAAATCATATCATTACCACGGTCAACTGCCAGGGTGTACTGCGTTAAATCATTG
GTGCCGATACTAAAGAAATCAACTTCTTTGGCTAAATGACGCGCAATTGTGCGCCGAGCCGGTGTTCACCATC

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ACGCCAATCTCAATGCTTTTCGTCAAATGCTTTACCTTCGTACGCAGTTCCTGTTTGTAGATTTCAATCTCTTTG
CGCAGCGCGCGAACTTCTTCAACAGAGATGATCATCGGGAACATAATGCGCAATTTACCGAAAGCGGAGGCACGC
AGAATCGCGCGAACCTGGTCACGCAGGATCTCTTTGCGATCCATGGCGATACGCACGGCGCGCCAGCCNAAGAAC
GGAT

142. *Salmonella enterica* derby (SEQ ID NO. 142) SDER

CCGCACATGCCAGTCCATTTACCTTCTGCATGAGAAGCATCAATAACTTGCTTGATCAAGTTCAGTACGGACGGT
GACATTGGCTGGTAAAGGTGTGAAATCATATCATTACCACGGTCAACTGCCAGGGTGTACTGCGTTAAATCATTG
GTGCCGATACTAAAGAAATCAACTTCTTTGGCTAAATGACGCGCAATTGTCGCCGCAGCCGGTGTTCACCATC
ACGCCAATCTCAATGCTTTTCGTCAAATGCTTTACCTTCGTACGCAGTTCCTGTTTGTAGATTTCAATCTCTTTG
CGCAGCGCGCGAACTTCTTCAACAGAGATGATCATCGGGAACATAATGCGCAATTTACCGAAAGCGGAGGCACGC
AGAATCGCGCGAACCTGGTCACGCAGGATCTCTTTGCGATCCATGGCGATACGCACGGCGCGCCAGCCNAAGAAC
GGAT

143. *Salmonella enterica* virchow (SEQ ID NO. 143) SVIR

CCGCACATGCCAGTCCATTTACCTTCTGCATGAGAAGCATCAATAACTTGCTTGATCAAGTTCAGTACGGACGGT
GACATTGGCTGGTAAAGGTGTGAAATCATATCATTACCACGGTCAACTGCCAGGGTGTACTGCGTTAAATCATTG
GTGCCGATACTAAAGAAATCAACTTCTTTGGCTAAATGACGCGCAATTGTCGCCGCAGCCGGTGTTCACCATC
ACGCCAATCTCAATGCTTTTCGTCAAATGCTTTACCTTCGTACGCAGTTCCTGTTTGTAGATTTCAATCTCTTTG
CGCAGCGCGCGAACTTCTTCAACAGAGATGATCATCGGGAACATAATGCGCAATTTACCGAAAGCGGAGGCACGC
AGAATCGCGCGAACCTGGTCACGCAGGATCTCTTTGCGATCCATGGCGATACGCACGGCGCGCCAGCCNAAGAAC
GGAT

144. *Salmonella enterica* paratyphi B (SEQ ID NO. 144) SPTB

CCGCACATGCCAGTCCATTTACCTTCTGCATGAGAAGCATCAATAACTTGCTTGATCAAGTTCAGTACGGACGGT
GACATTGGCTGGTAAAGGTGTGAAATCATATCATTACCACGGTCAACTGCCAGGGTGTACTGCGTTAAATCATTG
GTGCCGATACTAAAGAAATCAACTTCTTTGGCTAAATGACGCGCAATTGTCGCCGCAGCCGGTGTTCACCATC
ACGCCAATCTCAATGCTTTTCGTCAAATGCTTTACCTTCGTACGCAGTTCCTGTTTGTAGATTTCAATCTCTTTG
CGCAGCGCGCGAACTTCTTCAACAGAGATGATCATCGGGAACATAATGCGCAATTTACCGAAAGCGGAGGCACGC
AGAATCGCGCGAACCTGGTCACGCAGGATCTCTTTGCGATCCATGGCGATACGCACGGCGCGCCAGCCNAAGAAC
GGAT

145. *Streptococcus thermophilus* (SEQ ID NO. 145) STHE

CCGCTCATACCAGCCCCATTTACCTTCAGCGTGAGCTGCCTTAATAACGTTGTTAATCAAGCGAAGGATTGATGGG
TTATATGGTTGGTAAAGGTATGAAACTTGTTTCATTACACGGTCAGCAGCCATTGTGTATTGGATAAGGTCGTTT
GTACCAATTGAGAAGAAATCAACTTCTTTAGCAAATTGGTCAGCAAGCATTGCTGCAGCTGGGATTTCAATCATG
ATACCTACTTCGATGTCGTTTGCAACGGCAACACCTTCAGCAACCAATTTAGCTTTTTCTTCTTCAAGAATACCT
TTAGCAGTACGGAACCTCAGTCAACAAAGCAACCATTGGGAACATGATACGCAATTTACCGTGAACAGATGCACGA
AGCAAGGCACGTAATTGAGTACGGAACATTTGGTTACCAGTTTCAGAGATAGAAATACGTAATGCACGGTAACCC
AAGAACGG

146. *Streptococcus suis* (SEQ ID NO. 146) SSUI

GCCCACATACCAGCCCATTTACCTTCTGCGTGTGCAGCCTTGATAACATTGTTAATCAAGCGAAGGATTGATGGG
TTATATGGTTGGTAGAGGTATGAAACTTGTTTCATTTCATACGGTCTGCAGCCATTGTGTACTGGATAAGGTCGTT
GTACCGATTGAGAAGAAGTCAACTTCTTTGGCAAATTGGTCTGCAAGCATTGCTGCTGCAGGGATTTCAATCATG
ATACCAACTTGGATATCATCCGCAACTGCTACACCTTCAGCCAACAAGTTTGCTTTTTCTTCATCAAGGATTGCT
TTTGCTGCACGGAATTCAGTCAACAAGGCAACCATTGGGAACATGATACGAAGTTTACCATGTACTGATGAACGA
AGAAGGGCACGCAACTGAGTGCAGAACATTTGGTTACCAGTCTCAGAGATAGAGATACGAAGGGCACGGAAACCN
AAGAA

147. *Bacillus pseudomycoïdes* (SEQ ID NO. 147) BPMS

CCGCACATACCAGCCCATTTTCCTTCTTTATGAGCAGCATCGATAACCATTTTTACAAGGCGTAAAATAGATGGA
TTATACGGTTGGTATAAGTAAGATACACGTTTCATTTCATACGGTCTGCAGCCATTGTGTATTGGATTAGGTCGTTT
GTTCCGATAGAGAAGAAATCAACTTCTTTTGCAAAGTCTGCTAATACTGCAGAAGCGGGAATTTCTACCATC
ATACCTACCTCAATAGCATCAGAAACAGTTGTACCAGCTTGAACAAGTCTTTCTTTCTTCTAATAAAATTGCT
TTTGCTTGACGGAATTCATCAAGAGTTGCAATCATTGGGAACATAATTTTTAAATTACCATATACGCTTGCACGA
AGCAATGCACGAAGTTGTGTACGGAACACATCTTGTCTTCAAGGCATAAGCGAATCGCACGGTAACCCAAGAA

148. *Staphylococcus lugdunensis* (SEQ ID NO. 148) SLUG

CCGCACATACCAGTCCATTTACCTTCTTTATGAGAAGCTTCAATCACTTGTTTCACTAGACGTAAAATAGCTGGA
TTATATGGTTGATAAAGGTATGATACACGTTCTGACATGCGGTCAGCAGCCATTGTGTATTGAATCAAATCATTA
GTACCGATACTGAAGAAATCAACTTCTTTAGCAAAGATATCAGCTAATGCAGCTGTTGATGGGATTTCTACCAT
ATTCCGAGCTCGATATCATCTGACACGTCATGTCCTTCATTTTTTAGATTTTCTTTTCTTCTAAAAGAAGCGCT
TTGGCATCTCTAAACTCATTAATAGTAGCAACCATTTGGGAACATAATATTTAATTTTTCCATATGCTGAAGCACG
CAAAAGAGCGCGCAACTGTGGTCTGAAAATATCAGGTTGATCTAAGCACAAATCGAATCGCACGGTAACCNAAAGAA

149. *Cryptococcus neoformans* (SEQ ID NO. 149) CNEO

CGACAGTTATGACCGACCCGGATCTTCTGTGATGGATTTGAGTAAGAGCATATATGCTGGGACCCGAAAGATGGT
GAACTATGCCTGAATAGGGCGAAGCCAGGGGAAACTCTGGTGGAGGCTCGTAGCGATTCTGACGTGCAAATCGAT
CGTCGAATTTGGGTATAGGGGCGAAAGACTAATCGAACCATCTAGTAGCTGGTTCCTGCCGAAGTTTCCCTCAGG
ATAGCAGAAACTCGCATCAGTTTTATGAGGTAAAGCGAATGATTAGAGGCCTTGGGGACGAAACGTCCTTAACCT
ATTCTCAAACCTTTAAATGTGTAAGAAGCACTTGTCACCTTAATTGGACGAGCGCATGCGAATGAGAGTTTCTAGTG
GGCCATTTTTGGTAAGCAGAACTGGCGATGCGGGATGAACCGATCGCGAGGTTAAGGTGCCGGAATACACGCTCA
TCAGACACCACAAAAGGTGTTAGTTCATCTAGACAGCAGGACGGTGGCCATGGAAGTCGGAATCCGCTAAGGAGT
GTGTAACAACCTCACCTGCCGAATGAACTAGCCCTGAAAATGGATGGCGCTCAAGCGTGTTACCCA

Figure 6. Molecular marker III (SpyM_0902 & SpyM_0903) sequences amplified from Gram positive bacteria (SEQ ID NOs 150-180).

150. *Streptococcus thermophilus* (SEQ ID NO. 150) *STHE*
TTGNAACGGCTTATGCTGTAGNACAAGNACACCGAAGGGGCAAGGGATAAGACCCGAAACTCTCAGGTAAAAGGA
CAGAAAGCATTGAATGTTTTTAACTTTCAGTAATAGCTTTGTACTTTCAGAGGTCTGGTTAAGCCAAACCTCTTT
TTGATGTCTCGGTCTAAGGAGATTTTAAACGCATGTTAGACTTTTTCACTTCCATTGATGACTTTGTATGGGGAC
CTCCCCCTTCTTGTCTTCTTGTAGGAAGTGGTATCTACCTTACAATCCGTCTTGGACTTTTGCAAATCATTCGTC
TGCCTAAAGCCTTTAACTTATCTTTGCTGAAGATAAAGGAGAGGGTGATATTTCTAGTTTTGCAGCCCTTGCCA
CAGCACTTGCTGCAACTGTTGGTACTGGTAACATTGTTGGTGTTCGACAGCCATTAAGACTGGTGGGCCTGGTG
CTCTTTTCTGGATGTGGATTGCTGCTTTCT

151. *Enterococcus villorum* (SEQ ID NO. 151) *SVIL*
CCGAAGGGGCAAGGGATAAGACCCGAAACTCTCAGGTAAAAGGACAGAAAGCATTGAATGTTTTTAACTTTCAGT
AATAGCTTTGTACTTTCAGAGGTCTGGTTAAGCCAAACCTCTTTTTGATGTCTCGGTCTAAGGAGATTTTAAACG
CATGTTAGACTTTTTCACTTCCATTGATGACTTTGTATGGGGACCTCCCCCTTCTTGTCTTCTTGTAGGAAGTGG
TATCTACCTTACAATCCGTCTTGGACTTTTGCAAATCATTCGCTGCTTAAAGCCTTTAACTTATCTTTGCTGA
AGATAAAGGAGAGGGTGATATTTCTAGTTTTGCAGCCCTTGCCACAGCACTTGCTGCAACTGTTGGTACTGGTAA
CATTGTTGGTGTTCGACAGCCATTAAGACTGGTGGGCCTGGTGCTCTTTTCTGGATGTGGATTGCTGCTTTCTT
TGGAATG

152. *Streptococcus pyogenes* (SEQ ID NO. 152) *SPYO*
TTANAGGCGCCGAGGGGCAAGGCATACTGCTCAATCTCTCAGGCAAAAGGACAGAAGGTAAAATACAAACACCAT
TAAGAACAGTCTTAGTCTTTTTTGTGTTTGCTGTTTTATCATTTGCTTCAGAAGTTGTCTCAAAGAAAGAGATAGC
TTTTTCTTTTGGCGTCTTCGATGACTTTTAGGAGAGAAAAGATGATAGCACTCGTTAAATTAATTGATAACCTTG
TTTGGGGACCGCCCCTCTTAATTTTATTGGTTGGGACGGGGATTTACCTTACCAGTCATTTAGGATTAATTCAAA
TCTTAAACTACCAAGAGCCTTTAAACTCATTTTTTTCAGATGACGAAGGACATGGAGATATTTATCCTTTGCTG
CTCTTGCAACTGCCCTTGCCGCTACTGTGGAAGTGGTAACATTGTTGGGGTTGCCACTGCTATCAAGTCTGGTG
GTCCTGGAGCGCTCTTTTGGATGTGGGTTGCCGCTTTTTTTGGAATGG

153. *Streptococcus mutans* (SEQ ID NO. 153) *SMUT*
GCGCCGAGGGGCAAGGCTGTTTGCTCAAACTCTCAGGCAAAAGGACAGAAAAGAAAAAGAATTTTTAATGTTG
AAACAATTCTTATCTTCTAACTCTAGAGGTATCGTCAAGTATTGACAACCTCTTTTTTGATTTCCATTTTCGGTTT
ATGAGGAGAAAAGTTTATATGTTAACATTTTTTAAAGCTCTAGACAGCTTTGTCTGGGGTGTTCCCTATTAGTT
CTTTTAGTCGGTACTGGAATTTATTTGAGTACTCGCTTAAGATTATTGCAGGTATTGAACTCCCTTTAGCCTTT
AAACTCATCTTTGCCGAGGACAAAGGGGAAGGTGATATTTGAGTTTTGCGGCTTTAGCTACTGCTCTTGCTGCC
ACTGTTGGAAGTGGAAATATCGTTGGTGTTCGCACTGCAATCAAAGCTGGCGGTCCGGGAGCACTCTTTTGGATG
TGGATAGCAGCTTTTTTTGGAATGGC

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154. *Streptococcus agalactiae* (SEQ ID NO. 154) SAGA

AAGTAGCAACATCTTTGTATTGACACCAAGNATGTGCTCTAGGCGCCGAAGGGGCAAGAAGAGTAAAACAACTCC
TCCAATCTCTCAGGCAAAAGGACAGAAGCTAAAAGCCAATATTAATAATGAGTAGTAAGCTTATTAAGTTTACTA
CTACCTTTATTTGTGCGCTTTTGTAGCTAGCATCTTTCAGAAGTTATCTCTTTTAGAGATAACTTTTTTCGTTTCA
TTACAGAATCCATAGGTATGTCATGTATCAAAGGAGAACATATGCTAACACTTTTTACTCATATCAATAGCTTCG
TTTGGGGTCCACCTTTACTTGCTTTATTAGTCGGAACAGGTATTTACCTATCATTTTCGCTTAGGTTTTGTTCAAT
TGAGACAACCTTTCTAGAGCTTTCAAATTGATTTTCCGAGAAGATAACGGACAAGGGGATATTTCAAGTTATGCTG
CTCTTGCAACTGCTCTTGCTGCAACGGTAGGGACAGGTAATATCGTTGGTGTGGCTACGGCTATTAAATCTGGAG
GACCAGGAGCTTTGTTTTGGATGTGGGTAGCCGCCTTTTTTGAATGGCCC

155. *Streptococcus sanguis* (SEQ ID NO. 155) SSAN

TAGAACCGCTCAAACCTCTCAGGTAAAAGGACAGAGCGAAGAGGCAGGGATTTCCCTACTCCAGCACATCCAGGAG
TACATGTTTTGCATGTGCTCTTTCTTTTCTCGGTGTGAAAGGAGCTTATATCATGTTGGAAATATTGAATCGT
CTGGATTCTTTTGTGTTGGGGTCCGCCCCCTGCTCATTTTGTGTTGGTACTGGTATCTATCTCAGTCTGCGTCTG
GGCTTGCTGCANATTTTTCGACTTCCTCGTGCCTTTTCGGCTAATCTTTGTATCGGACGAGGAGCATCAGGGCGAT
GTCTCTAGCTTTGCGGCTCTCTGTACGGCTCTAGCCGCGACTGTGGGAACGGGAAATATCATCGGAGTGGCAACT
GCCATTAAAACCGGTGGACCGGGGGCGCTCTTCTGGATGTGGGTGGCTGCTTTCTTTGGAATGGC

156. *Streptococcus oralis* (SEQ ID NO. 156) SORA

GGGCAAGGCAGGTAACCTGCTCAAACCTCTCAGGTAAAAGGACAGAGCTAGGATAGACCGCTTTTTGGCATTATCT
AAGCATTCCAGAGTACATGTATCTTGCATGTACTCTTTCTTTTGGGGTTGAAAGATAGGAGAAGGACATGTTAGA
ATTGCTTAAAGCGCTTGATGCTTTTGTGTTGGGGGCTCCCCTCTTGATCTTATTGGTCGGAACGGGTATCTATTT
GACCATCCGACTGGGCTTTTGCAGGTACTCGTCTCCCTAAGGCCTTTCAGTTGATCTTTACCAAGGACAAGGG
GCACGGCGATGTGTGAGCTTTGCTGCTCTCTGTACGGCTCTAGCAGCCACAGTTGGTACGGGAAATATCATCGG
GGTAGCGACAGCCATTAAGGTTGGAGGACCAGGGGCCCTCTTTTGGATGTGGATGGCGGCCTTCTTTGGAATGGC

157. *Streptococcus suis* (SEQ ID NO. 157) SSUI

TTTTGGCCCCGANGGGCAAGGTAGTCCTGCTTGGAAGTAGAGCTACTGAAACTCTCAGGTAAAAGGACAGAGCG
TTGAAAAATAGGCTTTTTCTGTATTTTTCACGTTGATTCTAGAGGTTGAAGTGTTTCAGCCTCTTTTTGTTTTTCC
GGCAGCTTTATCGGGTTAGAAACGCTTAGGAGGAATATGTTAGAACTATTTAAGGCTATCAACAATCTTGTTTG
GGGACCGCCCCCTCTTGTTACTATTGGTCGGAACGGGTGTCTATTTTACCCTACGGTTGGGAGTATTTACAGATTGG
CAAATTGCCGACGGCTTTTCTGCTGATTTTCTCCAGTGACCAGTCTGGTCAGGGAGATGTGTCCAGTTTTGCGGC
TCTGTGTACGGCTTTAGCAGCGACAGTTGGTACAGGAAATATCGTCGGAGTTGCGACAGCTATTACTACAGGTGG
TCCTGGGGCTCTTTTCTGGATGTGGGTGCGGCCTTTTTTGAATGGC

158. *Staphylococcus simulans* (SEQ ID NO. 158) SSIM

ATCCGGCTTTGAGTTTAAAGCTATTGATGCTTTAATTACGAACTTCCATCTGCCGAAGTCCACACTTGTATGTT
AGTTTCAGCATTCAGTTCAAACAATATATTTTAAATGCATACCAAACAGCTGTCGAAATGAAATATCGATTCTT
CAGCTTTGGTGATGCAATGTTAATTATTTAAGGGAGTCGTGAAAAAGTTATGCCCTGCAGTAACTTATGAACATAT
CAAAACATGTAAACAATCCGGTGCAAGGTTAGGAATCGTGCATACACCGCACGGTTCGTTTGAAACACCTATGTT

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TATGCCAGTAGGAACTCAAGCTACCGTTAAACTATGAGTCCTGAAGAACTAAGGGAAATTAATGCACAAATCAT
TTTAGGCAACACATACCATTTATGGTTGCAACCCGGCAATGACATTATTAAACGCGCGGGTGGTTTGCATAAATT
TATGATTTGGAATGGCCAC

159. *Enterococcus faecalis* (SEQ ID NO. 159) EFLS

GTAAAGGCACCGAAGGGGCAAGGCAGGTAACCTGCTCAAACCTCTCAGGTAAAAGGACAGAGCTAGGATAGACCGCT
TTTTGGCATTTATCTAAGCATTCAGAGTACATGTATCTTGCATGTACTCTTTCTTTTGGGGTTGAAAGATAGGA
GAAGGACATGTTAGAATTGCTTAAAGCGCTTGATGCTTTTGCTTGGGGGCCTCCCTCTTGATCTTATTGGTCGG
AACGGGTATCTATTTGACCATCCGACTGGGCCCTTTTGCAAGTTACTCGTCTCCCTAAGGCCTTTCAGTTGATCTT
TACCAAGGACAAGGGGCACGGCGATGTGTCGAGCTTTGCTGCTCTCTGTACGGCTCTAGCAGCCACAGTTGGTAC
GGGAAATATCATCGGGGTAGCGACAGCCATTAAGGTTGGAGGACCAGGGGCCCTCTTTTGGATGTGGATGGCGGC
CTTCTTTGGAATGGCCC

160. *Streptococcus pneumoniae* (SEQ ID NO. 160) SPNE

GTAAAGGCACCGAAGGGGCAAGGCAGGCAACTGCTCAAACCTCTCAGGTAAAAGGACAGAGCTAGGATAGACCGCT
TTTAGCATTTATCTAAGCATTCAGAGTACATGTATCTTGCATGTGCTCTTTCTTTTGGGGTTGAAACGATAGG
AGAAGGAAATGTTAGAATTGCTTAAATCAATCGATGCTTTTGCTTGGGGACCGCCCTCTTGATTTTATTGGTCG
GAACAGGGATTTACCTAACCATGCGGCTAGGACTCTTGCAAGTTTTCGCTCTGCCAAGGCCTTTCAGCTTATTT
TTATCCAGGATAAGGGACATGGTGATGTATCCAGTTTACAGCTCTGTGTACAGCCTTGGCATCAACTGTTGGAA
CAGGAAATATCATAGGAGTTGCGACGGCTATCAAGGTTGGTGGACCAGGAGCTCTATTTTGGATGTGGATGGCGG
TTTTCTTTGGAATGGCCC

161. *Enterococcus durans* (SEQ ID NO. 161) EDUR

NGNCCGAGGGGCAAGGTCAGNACAACCTGCTCAAACCTCTCAGGTAAAAGGACAGAGCTAGGATAGACCGCTTTT
GCATTTATCTAAGCATTCAGAGTACATGTATCTTGCATGTGCTCTTTCTTTTGGGGTTGAAACGATAGGAGAAG
GAAATGTTAGAATTGCTTAAATCAATCGATGCTTTTGCTTGGGGACCGCCCTCTTGATTTTATTGGTCGGAACA
GGGATTTACCTAACCATGCGGCTAGGACTCTTGCAAGTTTTCGCTCTGCCAAGGCCTTTCAGCTTATTTTATC
CAGGATAAGGGACATGGTGATGTATCCAGTTTACAGCTCTGTGTACAGCCTTGGCATCAACTGTTGGAACAGGA
AATATCATAGGAGTTGCGACGGCTATCAAGGTTGGTGGACCAGGAGCTCTATTTTGGATGTGGATGGCGGTTTTC
TTTGGAATGGCCC

162. *Bacillus anthracis* 1978 (SEQ ID NO. 162)

NGAGGAAAACGAGCACCGAAGGAGCAAATCCGCTACTATAGCGGATAATCTCTCAGGTAAAAGGACAGAGACAAG
CGAAAAGAAAATGCCGATTTGTATCGGTTTATTTTTCTATCCCTTGTTTCTCCAGAGACCATTTTCAATTTACTTGAA
GTGGTTTTTTATTTTTTCTAAAAAAGGAGAATAAAGATGGAGACAGTAAGTAAAGTATTAGAACAAATCAATCACT
ATGTGTGGGGATTACCAACGTTATTGTTACTCGTTGGTACTGGTATTATTCTCACAGTGCCTTTAAAAGGTTTAC
AGTTTAGTAAACTATTATACGCTCACAACTAGCTTTTAAAAAATCAGAAGATACATCTTCCTCTGGAGATATTA
GCCACTTCCAAGCGCTTATGACAGCTATGGCGGCAACGATTGGTATGGGAAATATAGCTGGTGTGCAACTGCTG
TGACGATCGGTGGACCTGGTGCAATCTTTTGGATGTGGATTACTGCTTTGTTTGAATGGCCAAAA

163. *Bacillus anthracis* Sterne (SEQ ID NO. 163)

TNCNCGCTTTAAATAGCGTAGNAGGCAAAACGAGCACCGAAGGAGCAAATCCGCTACTATAGCGGATAATCTCTC
AGGTAAAAGGACAGAGACAAGCGAAAGAAAATGCCGATTTGTATCGGTTTATTTTTCTATCCCTTGTTTCTCCAG
AGACCATTTCACTTGAAGTGGTTTTTATTTTTCTAAAAAAGGAGAATAAAGATGGAGACAGTAAGTAAAG
TATTAGAACAAATCAATCACTATGTGTGGGGATTACCAACGTTATTGTTACTCGTTGGTACTGGTATTATTCTCA
CAGTGCCTTTAAAAGGTTTACAGTTTAGTAACTATTATACGCTCACAACTAGCTTTTAAAAAATCAGAAGATA
CATCTTCCTCTGGAGATATTAGCCACTTCCAAGCGCTTATGACAGCTATGGCGGCAACGATTGGTATGGGAAATA
TAGCTGGTGTGCAACTGCTGTGACGATCGGTGGACCTGGTGCAATCTTTGGATGTGGATTACTGCTTTGTTTG
GAATGGCCCCAAAA

164. *Bacillus anthracis* Butare (SEQ ID NO. 164)

NNCNCNCGCTNTAAATAGCGTAGAGGCAAAACGAGCACCGAAGGAGCAAATCCGCTACTATAGCGGATAATCTCT
CAGGTAAAAGGACAGAGACAAGCGAAAGAAAATGCCGATTTGTATCGGTTTATTTTTCTATCCCTTGTTTCTCCA
GAGACCATTTCACTTGAAGTGGTTTTTATTTTTCTAAAAAAGGAGAATAAAGATGGAGACAGTAAGTAAA
GTATTAGAACAAATCAATCACTATGTGTGGGGATTACCAACGTTATTGTTACTCGTTGGTACTGGTATTATTCTC
ACAGTGCCTTTAAAAGGTTTACAGTTTAGTAACTATTATACGCTCACAACTAGCTTTTAAAAAATCAGAAGAT
ACATCTTCCTCTGGAGATATTAGCCACTTCCAAGCGCTTATGACAGCTATGGCGGCAACGATTGGTATGGGAAAT
ATAGCTGGTGTGCAACTGCTGTGACGATCGGTGGACCTGGTGCAATCTTTGGATGTGGATTACTGCTTTGTTT
GGAATGGCCCCAAAA

165. *Bacillus anthracis* 1655H85 (SEQ ID NO. 165)

TNTNCGCTTTNATAGCGTAGTAGGCAAAACGAGCACCGAAGGAGCAAATCCGCTACTATAGCGGATAATCTCTC
AGGTAAAAGGACAGAGACAAGCGAAAGAAAATGCCGATTTGTATCGGTTTATTTTTCTATCCCTTGTTTCTCCAG
AGACCATTTCACTTGAAGTGGTTTTTATTTTTCTAAAAAAGGAGAATAAAGATGGAGACAGTAAGTAAAG
TATTAGAACAAATCAATCACTATGTGTGGGGATTACCAACGTTATTGTTACTCGTTGGTACTGGTATTATTCTCA
CAGTGCCTTTAAAAGGTTTACAGTTTAGTAACTATTATACGCTCACAACTAGCTTTTAAAAAATCAGAAGATA
CATCTTCCTCTGGAGATATTAGCCACTTCCAAGCGCTTATGACAGCTATGGCGGCAACGATTGGTATGGGAAATA
TAGCTGGTGTGCAACTGCTGTGACGATCGGTGGACCTGGTGCAATCTTTGGATGTGGATTACTGCTTTGTTTG
GAATGGCCCCAAAA

166. *Bacillus anthracis* Coda-Cerva (SEQ ID NO. 166)

CTNTNCGCTTTAAATAGCGTAGAGGCAAAACGAGCACCGAAGGAGCAAATCCGCTACTATAGCGGATAATCTC
TCAGGTAAAAGGACAGAGACAAGCGAAAGAAAATGCCGATTTGTATCGGTTTATTTTTCTATCCCTTGTTTCTCC
AGAGACCATTTCACTTGAAGTGGTTTTTATTTTTCTAAAAAAGGAGAATAAAGATGGAGACAGTAAGTAA
AGTATTAGAACAAATCAATCACTATGTGTGGGGATTACCAACGTTATTGTTACTCGTTGGTACTGGTATTATTCT
CACAGTGCCTTTAAAAGGTTTACAGTTTAGTAACTATTATACGCTCACAACTAGCTTTTAAAAAATCAGAAGA
TACATCTTCCTCTGGAGATATTAGCCACTTCCAAGCGCTTATGACAGCTATGGCGGCAACGATTGGTATGGGAAA
TATAGCTGGTGTGCAACTGCTGTGACGATCGGTGGACCTGGTGCAATCTTTGGATGTGGATTACTGCTTTGTT
TGGAATGGCCCCAAAA

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167. *Bacillus anthracis* 2054H82 (SEQ ID NO. 167)

TNCNCGCTTTNAATAGCGTAGAGGCAAAACGAGCACCGAAGGAGCAAATCCGCTACTATAGCGGATAATCTCTCA
GGTAAAAGGACAGAGACAAGCGAAAGAAAATGCCGATTTGTATCGGTTTATTTTTCTATCCCTTGTTTCTCCAGA
GACCATTTTCACTTGAAGTGGTTTTTATTTTTCTAAAAAAGGAGAATAAAGATGGAGACAGTAAGTAAAGT
ATTAGAACAAATCAATCACTATGTGTGGGGATTACCAACGTTATTGTTACTCGTTGGTACTGGTATTATTCTCAC
AGTGC GTTTAAAAGGTTTACAGTTTAGTAACTATTATACGCTCACAACTAGCTTTTAAAAAATCAGAAGATAC
ATCTTCCTCTGGAGATATTAGCCACTTCCAAGCGCTTATGACAGCTATGGCGGCAACGATTGGTATGGGAAATAT
AGCTGGTGTGCAACTGCTGTGACGATCGGTGGACCTGGTGCAATCTTTGGATGTGGATTACTGCTTTGTTTGG
AATGGCCNAAAA

168. *Bacillus cereus* ATCC 10987 (SEQ ID NO. 168) BCER10987

TGCTTGCTAGAGCGCGGAGGAAAACGAGCACCGAAGGAGCAAATCCGCTACTTTAGCGGATAATCTCTCAGGTAA
AAGGACAGAGACAAGCGAAAGAAAAGCCGATTGTATCGGTTTATTTTTCTATCCCTTGTTTCTCCAGAGACCAT
TTCATTTACTTGAAGTGGTTTTTATTTTTCTAAAAAAGGAGAATAAAGATGGAGACAGTAAGTAAAGTATTAGA
ACAACTGAATCAATACGTGTGGGGATTACCAACTTTGTTGCTACTCGTTGGAACAGGTATCATTCTCACAGTGCG
TTTAAAAGGTTTACAGTTTAGTAACTATTATACGCTCACAACTAGCATTTAAAAAATCAGAAGATGCCTCTTC
TTCTGGAGATATTAGTCACTTCCAAGCACTTATGACAGCTATGGCCGCAACGATTGGTATGGGAAATATAGCCGG
TGTTGCAACAGCTGTTACAATTGGTGGTCCTGGTGCAATATTTTGGATGTGGATTACCGCTTTATTTGGAATGGC
CCAAAA

169. *Bacillus cereus* ATCC 14579 (SEQ ID NO. 169) BCER14579

TAGCAGTCGCGGCGGAAAAACGAGCACCGAAGGAGCAAATCCGCTACTTTAGCGGATAATCTCTCAGGTAAAAGG
ACAGAGACAAGCGAAAGAAAAGCCGATTGTATCGGTTTATTTTTCTATCCCTTGTTTCTCCAGAGACCATTTCA
TTTACTTGAAGTGGTTTTTATTTTTCTAAAAAAGGAGAATAAAGATGGAGACAGTAAGTAAAGTATTAGAACAA
CTAAATCAATACGTGTGGGGATTACCAACTTTGTTGCTACTCGTTGGAACAGGTATCATTCTCACAGTGCGTTTG
AAAGGTTTACAGTTTAGTAACTATTATACGCTCACAACTAGCGTTTAAAAAATCAGAAGATACTTCTTCTTCT
GGAGATATTAGTCACTTCCAAGCACTCATGACAGCTATGGCCGCAACGATTGGTATGGGTAATATAGCCGGTGTT
GCAACAGCGGTTACAATTGGTGGTCCTGGTGCAATATTTTGGATGTGGATTACCGCTTTATTTGGAATGGCCCCAA
AA

**170. *Bacillus thuringiensis* serovar *israelensis* BTHUISR
(SEQ ID NO. 170)**

TATAGCGCAGAGGAAAACGAGCACCGAAGGAGCAAATCCGCTACTATAGCGGATAATCTCTCAGGTAAAAGGACA
GAGACAAGCGAAAGAAAATGCCGATTTGTATCGGTTTATTTTTCTATCCCTTGTTTCTCCAGAGACCATTTCA
TACTTGAAGTGGTTTTTATTTTTCTAAAAAAGGAGAATACAGATGGAGACAGTAAGTAAAGTGTTAGAACAAA
TCAATCACTATGTGTGGGGACTACCAACGTTGTTGTTACTCGTTGGTACTGGTATCATTCTCACAGTGCGTTTAA
AAGGTTTACAGTTTAGTAACTATTATACGCTCACAACTAGCTTTTAAAAAATCAGAAGATACATCTTCTTCTG
GAGATATTAGCCACTTCCAAGCGCTTATGACAGCTATGGCGGCAACGATTGGTATGGGAAATATCGCTGGTGTG
CAACAGCTGTGACAATCGGTGGTCCCGGTGCAATCTTTTGGATGTGGATTACTGCTTTGTTTGAATGG

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171. *Bacillus mycoides* serovar MYC003 (SEQ ID NO. 171)**BMYC003**

GTGGAGGAAAGAGAGCACCGAAGGAGCAAATCCGCTAGCTAGTATAGCGGATAATCTCTCAGGTAAAAGGACAGA
GACAAGCGAAAGAAAATGCCGATTTGGATCGGTTTATTTTTCTATCACTTGTTTCTCCAGAGACCATTTCATTTT
GTGAAGTGGTTTTTTATTTTTTCTAAAAAGGAGAATAAAGATGGAGACAGTAAGTAAAGTACTAGAACAAATCAA
TCATTACGTATGGGGATTACCAACCTTGTTCCCTACTCGTTGGAAGTGAATCATTCTTACAGTGCGTCTAAAAGG
TTTACAGTTTAGTAACTATTATACGCTCACAACTAGCTTTTAAAAAATCAGAAGACACATCTTCTACTGGAGA
TATTAGTCATTTTCAAGCACTTATGACCGCTATGGCAGCAACAATTGGAATGGGAAATATAGCTGGTGTGCAAC
CGCTGTTACAATTGGTGGTCCCGGTGCAATATTTTGGATGTGGATTACCGCCCTGTTTGAATGGCCCCAAA

172. *Bacillus mycoides* serovar NRS306 (SEQ ID NO. 172)**BMYC306**

CGCTTCTATAGCGCGGAGGAAAACGAGCACCGAAGGAGCAAATCCGCTAATCTAGCGGATAATCTCTCAGGTAAA
AGGACAGAGACAAGCGAAAGAAAATGCCGATTTGTATCGGTTTATTTTTCTATCCCTTGTTTCTCCAGAGACCAT
TTCATTTCTTGAAGTGGTTTTTATTTTTTCTAAAAAGGAGAATACAGATGGAGACAGTAAGTAAAGTATTAGA
ACAAATTAATCAGTATGTGTGGGGTTGCCAACTTTATTGCTACTCGTTGGAAGTGGTATCATTCTCACAGTGCG
CTTAAAAGGTTTACAGTTTAGTAACTAATATACGCTCACAACTTGCTTTTAAAAAATCAGAGGATACATCATC
TTCTGGAGATATTAGTCACTTCCAAGCACTGATGACGGCTATGGCTGCAACGATTGGTATGGGAAATATAGCAGG
TGTCGCANCTGCTGTGACGATCGGTGGACCCGGTGCGATCTTCTGGATGTGGATTACCGCGTTGTTTGAATGGC
CCAAA

173. *Bacillus thuringiensis* serovar *Kurstaki***BTHUKUR****(SEQ ID NO. 173)**

GAGGAAACAGAGCACCGAAGGAGCAAATCCGCTTATATTAGCGGATAATCTCTCAGGTAAAAGGACAGAGACAAG
CGAAAGAAAACGCCGATTTGTATCGGTTTATTTTTCTATTCCCTTGTTTCTCCAGAGACCATTTCAATTTATGTGAA
GTGGTTTTTTATTTTTTCTAAAAGGAGAATAAAGATGGAGACAGTAAGTAAAGTATTAGAACAAATCAATCACTA
CGTATGGGGATTACCGACCTTATTCCCTTCTAATCGGAACTGGAATCATTCTCACAGTGCGCCTAAAAGGTTTACA
GTTTAGTAGACTATTATACGCTCACAACTAGCATTTGAAAAATCAGAAGACACATCTTCTTTGGGAGATATTAG
TCATTTCCAAGCACTCATGACAGCAATGGCCGCAACTATTGGGATGGGAAATATAGCCGGTGTGCAACAGCTGT
TACAATCGGTGGGCCAGGGGCAATATTTTGGATGTGGATCACTGCCTTGTTTGAATGGCCCCAAA

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174. *Enterococcus faecium* (SEQ ID NO. 174) FCM

GACGGAATTCTGGAGAGACCTTATTAGGCGCCGAAGGGGCAAGGCATACTGCTCAATCTCTCAGGCAAAAGGACA
GAAGGTAGAATACAAACACCATTAAGAACAGTCTTAGTCTTTTTTGTGTTTGCTGTTTTATCATTGCTTCAGAAG
TTGTCTCAAAGAAAGAGATAGCTTTTTTCTTTTGGCGTCTTCGATGACTTTTAGGAGAGAAAGATGATAGCACTC
GTTAAATTAATTGATAACCTTGTTTGGGGACCGCCCTCTTAATTTTATTGGTTGGGACGGGGATTTACCTTACC
AGTCATTTAGGATTAATTCAAATCTTAAACTACCAAGAGCCTTTAAACTCATTTTTTTCAGATGACGAAGGACAT
GGAGATATTTTCATCCTTTGCTGCTCTTGCAACTGCCCTTGCCGCTACTGTGCGAACTGGTAACATTGTTGGGGTT
GCCACTGCTATCAAGTCTGGTAGTCTGGAGCGCTCTTTTGGATGTGGGTTGCCGCTTTTTTTTGAATGGCAACA
AAATACGC

175. *Enterococcus casseliflavus* (SEQ ID NO. 175) ECAS

GNACCGGAATTCTGAGAGACCTTATTAGGGCGCCGAAGGGGCAAGGCATACTGCTCAATCTCTCAGGCNAAAGG
NCAGAAGGTAAAATACAAACACCATTAAGAACAGTCTTAGTCTTTTTTGTGTTTGCTGTTTTATCATTGCTTCAG
AAGTTGTCTCAAAGAAAGAGATAGCTTTTTTCTTTTGGCGTCTTCGATGACTTTTAGGAGAGAAAGATGATAGCA
CTCGTTAAATTAATTGATAACCTTGTTTGGGGACCGCCCTCTTAATTTTATTGGTTGGGACGGGGATTTACCTT
ACCAGTCATTTAGGATTAATTCAAATCTTAAACTACCAAGAGCCTTTAAACTCATTTTTTTCAGATGACGAAGGA
CATGGAGATATTTTCATCCTTTGCTGCTCTTGCAACTGCCCTTGCCGCTACTGTGCGAACTGGTAACATTGTTGGG
GTTGCCACTGCTATCAAGTCTGGTGGTCCTGGAGCGCTCTTTTGGATGTGGGTTGCCGCTTTTTTTTGAATGGCC
ACAAAATACGC

176. *Enterococcus flavescens* (SEQ ID NO. 176) EFLA

AGGCGCCGAAGGGGCAAGGCATACTGCTCAATCTCTCAGGCAAAAGGACAGAAGGTAAAATACAAACACCATTAA
GAACAGTCTTAGTCTTTTTTGTGTTTGCTGTTTTATCATTGCTTCAGAAGTTGTCTCAAAGAAAGAGATAGCTTT
TTCTTTTGGCGTCTTCGATGACTTTTAGGAGAGAAAGATGATAGCACTCGTTAAATTAATTGATAACCTTGTTT
GGGGACCGCCCTCTTAATTTTATTGGTTGGGACGGGGATTTACCTTACCAGTCATTTAGGATTAATTCAAATCT
TAAACTACCAAGAGCCTTTAAACTCATTTTTTTCAGATGACGAAGGACATGGAGATATTTTCATCCTTTGCTGCTC
TTGCAACTGCCCTTGCCGCTACTGTGCGAACTGGTAACATTGTTGGGGTTGCCACTGCTATCAAGTCTGGTGGTC
CTGGAGCGCTCTTTTGGATGTGGGTTGCCGCTTTTTTTTGGTATGGCCACAAAATACGC

177. *Enterococcus gallinarum* (SEQ ID NO. 177) EGAL

GAACGGAATTCTGGAGAGACCGTAAAGGCACCGAAGGGGCAAGGCAGGTAAGTCTCAAACTCTCAGGTAAAAGG
ACAGAGCTAGGATAGACCGCTTTTTTGGCATTATCTAAGCATTCAGAGTACATGTATCTTGCATGTACTCTTTC
TTTTGGGGTTGAAAGATAGGAGAAGGACATGTTAGAATTGCTTAAAGCGCTTGATGCTTTTGCTTGGGGGCCTCC
CCTCTTGATCTTATTGGTCGGAACGGGTATCTATTTGACCATCCGACTGGGCCTTTTGCAGGTTACTCGTCTCCC
TAAGGCCCTTCAGTTGATCTTTACCAAGGACAAGGGGCACGGCGATGTGTGAGCTTTGCTGCTCTCTGTACGGC
TCTAGCAGCCACAGTTGGTACGGGAAATATCATCGGGGTAGCGACAGCCATTAAGGTTGGAGGACCAGGGGCCCT
CTTTTGGATGTGGATGGCGGCCTTCTTTGGAATGGCAACTAAATACGC

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178. *Enterococcus raffinosus* (SEQ ID NO. 178) ERAF

GACGGAATTCTGGAGAGACCGTAAAGGCACCGAAGGGGCAAGGCAGGTAACCTGCTCAAACCTCTCAGGTAAAAGGA
CAGAGCTAGGATAGACCGCTTTTTGGCATTATCTAAGCATTCCAGAGTACATGTATCTTGCATGTACTCTTTCT
TTTGGGGTTGAAAGATAGGAGAAGGACATGTTAGAATTGCTTAAAGCGCTTGATGCTTTTGCTTGGGGGCCTCCC
CTCTTGATCTTATTGGTCGGAACGGGTATCTATTTGACCATCCGACTGGGCCTTTTGCAGGTTACTCGTCTCCCT
AAGGCCTTTCAGTTGATCTTTACCAAGGACAAGGGGCACGGCGATGTGTCGAGCTTTGCTGCTCTCTGTACGGCT
CTAGCAGCCACAGTTGGTACGGGAAATATCATCGGGGTAGCGACAGCCATTAAGGTTGGAGGACCAGGGGCCCTC
TTTTGGATGTGGATGGCGGCCTTCTTTGGAATGGCCACCAAATACGC

179. *Streptococcus mitis* (SEQ ID NO. 179) SMIT

ATNTTAAGGCACCCAAGGGCAAGGTCAGGCAACTGCTCAAACCTCTCAGGTAAAAGGACAGAGCTAGGATAGACCG
CTTTTATAGCATTTATCTAAGCATTCCAGAGTACATGTATCTTGCATGTGCTCTTTCTTTTGGGGTTGAAAAGATA
GGAGAAGGAAATGTTAGAATTGCTTAAATCAATTGATGCTTTTGCTTGGGGTCCACCCCTCTTGATTCTATTGGT
CGGGACAGGGATTTACCTAACTGCTCGTCTAGGCCTCTTGCAGGTTTTCGCTTTCCTAAGGCCTTTCAGCTTAT
TTTTACTAAGGACAAGGGGCATGGCGATGTATCCAGCTTTGCGGCCTTGTGTACAGCCCTAGCAGCGACAGTTGG
TACGGGAAATATTATCGGGGTGGCGACGGCTATCAAGGTCGGTGGCCCAGGAGCCCTCTTTTGATGTGGATGGC
CGCTTTCTTTGGAATGGCCCAAATACCGC

180. *Streptococcus canis* (SEQ ID NO. 180) SCAN

NTAGTNCTTTTAAATGACACTAGTGACCTTTCGTTAGTATGTTTTTAAGGACTGAGTATTGTAATACTAACATGA
AAGAACTAGACAGGCGCCGAAGGGCAAGGCTAGACACACAGCTAGCTCAAACCTCTCAGGCAAAAGGACAGAAGA
TAAGAATCGATTAAACAGGTAAGGTGTATTATCTTTGTCAGTCTTCTTATCACTTTTCAGGAGTTATCACTACGAT
AACTCCTTTTTTCTATTCTAACTGTCATCATAGGACGCTATGTTTTATTAGGAGACTTATTCGTATATGCTAAAC
TTTTTTACAATGCTAGATGATATGGTCTGGGGTGCCCCACTGCTTATTCTGTTGGTGGGAACAGGGATTTATTTA
ACTGTTTCGGCTTGGCTTACTCCAGGTTTTAAATTAACCTAAAGCCTTTAAATTAATTTTCGACAGATAAAGGT
CAAGGGGATATTTCTAGTTTTGCCGCTCTTGCTACTGCTCTTGCAGCAACAGTAGGTACTGGTAACATCGTTGGT
GTAGCAACAGCTATCAAAGCTGGTGGTCCTGGAGCCCTATTTTGATGTGGATTGCTGCTTTCTTTGGAATGG

Figure 7: Molecular marker IV (putative GTP-binding factor plus 160 nt downstream this ORF) sequences amplified from Gram-positive bacteria (SEQ ID NOs 181-193)

181. *Listeria monocytogenes* (SEQ ID NO. 181)

GTTAGAAAAAGGAAGTTCTATTGTAGCATCGCCAAAAATCCATCAAACCTTATTAGATAACTACCTGCCTTAAAG
AAAGCGCTCAACATAAAAAAAGTTGTTTTTCAGAAAATAAAAAATCGTGCCAAATCGGCTCAGCTATGCTATAATAG
GTAAGTTGATTTAAACGAGACGATAGCGACGGAGGAAAATAAATCTATTTTCTCTTTCTTTGGCTAATCTTCA
CGATAAATGTTTGGATTTTTAATTTAGGAGGAAACAAGATTGAATTTAAGAAATGATATTCGTAATGTAGCAATT
ATTGCCACGTTGACCATGGTAAACAACCTCTAGTAGACCAATTATTACGCCAGTCAGGCACATTCCGCGACAAT
GAAACAGTTGCAGAACGCGCAATGGACAACAATGATTTAGAAAGAGAACGCGGTATTACAATTTTAGCGAAAAAT
ACAGCGATTAAAGTATGAAGATACACGTGTAAACATCATGGATACACCTGGACACGCCGATTTCCGGTGGAGAAGTA
GAACGTATCATGAAAATGGTTGATGGTGTCTTTTAGTAGTGGACGCGTATGAAGGTACGATGCCTCAAACACGT
TTTGTACTAAAAAAGCACTAGAACAAAACCTAACTCCAATCGTAGTAGTAAACAAAATTGACCGTGACTTTTGCT
CGCCCAGAAGAAGTTGTTGATGAAGTATTAGAATTATTCATCGAACTAGGCGCAAACGACGATCAATTAGAATTC
CCAGTTGTTTATGCTTCTGCAATCAACGGAACCTCAAGCTATGATTCCGATCCAGCAGAACAAAAAGAAACAATG
AAACCACTTTTAGACACAATTATCGAACATATCCCGGCTCCAGTTGATAATAGCGACGAACCATTACAATTCCAA
GTATCATTACTTGATTATAATGACTATGTTGGTCGTATCGGTATTGGCCGCGTATTCCGTGGAACAATGCACGTG
GGACAAACAGTTGCTTTAATTAACTTGATGGCACAGTAAACAATTCCGTGTAACGAAAATGTTCCGGTTTCTTC
GGACTAAAACGTGACGAAATTAAGAAGCAAAAGCTGGTGATTTAGTAGCATTAGCAGGTATGGAAGACATCTTC
GTTGGTGAAACAGTAACACCATTTGACCACCAAGAAGCACTTCCGTTATTACGTATTGATGAGCCAAACCTTGCAA
ATGACTTTTCGTAACAAATAACAGTCCTTTTCGCTGGTCGTGAAGGTAAACACGTAACAAGCCGTAAAAATTGAAGAA
CGTTTACTTGCAGAGCTTCAAACGGACGTATCTTTACGCGTAGAGCCAACAGCTTCCCCTGACGCTTGGGTAGTT
TCTGGTCGTGGTGAGCTTCATTTATCCATTTTGATCGAAACAATGCGTCGCGAAGGTTATGAATTACAAGTTTCT
AAACCAGAAAGTAATCATCCGTGAAATTGATGGCGTGAAATGTGAACAGTAGAAGATGTTCAAATTGATACTCCA
GAAGAATTCATGGGTTCCGTTATTGAATCTATCAGCCAACGTAAAGGCGAAATGAAAAACATGATTAACGATGGC
AACGGACAAGTTCGTTTACAATTCATGGTTCCAGCTCGTGGCTTAATCGGTTATACAACCTGATTTCCCTTTCAATG
ACTCGTGGTTATGGTATTATCAACCACACA

182. *Listeria innocua* (SEQ ID NO. 182)

ATAAAAAAAGTCAATTTTCAGAAAATAAAAAATAGTGCTAAATCCGCTTAGCTATGCTATAATAGGTAAGTTGATTT
AAACGAGACGATAGCGACGGAGGAAAATAAATCTATTTTCTCTTTCTTTTGGCTAATCTTCACGATAAATGTTT
GGATTTTTAATTTAGGAGGAAACAAGATTGAATTTAAGAAACGATATTGTAATGTAGCAATTATTGCCACGTT
GACCATGGTAAAACTACACTAGTAGACCAATTACTACGCCAATCAGGTACTTTCCGCGACAATGAAACAGTTGCA
GAACGTGCAATGGACAACAATGATTTAGAAAGAGAACGCGGTATTACAATTTTAGCGAAAAATACAGCAATTAAG
TATGAAGATACACGCGTAAACATCATGGATACACCTGGACACGCCGATTTTGGTGGAGAAGTAGAACGTATCATG
AAAATGGTTGATGGTGTCTTTTAGTAGTGGACGCGTATGAAGGTACTATGCCTCAAACACGTTTTGTACTAAAA
AAAGCACTAGAACAAAACCTAACTCCAATCGTAGTAGTAAACAAAATTGACCGTGACTTTGCTCGCCAGAAGAA
GTTGTTGATGAAGTACTAGAATTATTCATCGAACTAGGTGCGAACGACGATCAATTAGAATTCAGTTGTTTAT
GCTTCTGCAATTAACGGAACTTCAAGCTTTGAATCCGACCCAGCAGAACAAAAAGAAACAATGAAACCACTTTTA
GACACTATTATTGAACATATTCAGCTCCAGTTGATAACAGCGACGAGCCATTACAATTCAGTTTCTTTACTT

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GATTATAATGACTATGTTGGTTCGTATTGGTATTGGCCGCGTTTTCCGTGGAACAATGCACGTAGGACAAACAGTT
GCCTTAATTAACTAGACGGCACAGTAAAAACAATTCCGTGTAACGAAAATGTTTCGGTTTCTTCGGACTAAAACGT
GACGAAATTAAAGAAGCAAAAGCGGGTGAAGTACTTAGTAGCACTTGCAGGAATGGAAGACATCTTCGTCGGTGAAACA
GTAACACCATTTGACCACCAAGAAGCACTTCCACTTTTACGTATTGATGAGCCAACCTTGCAAATGACTTTTGTA
ACAAATAACAGTCCTTTTCGAGGCCGTGAAGGTAAACACGTAACAAGCCGTAAAAATTGAAGAACGCTTACTTGCA
GAACTTCAAACGGATGTATCTTTACGCGTTGAACCAACAGCTTCTCCAGACGCATGGGTAGTATCTGGTCGTGGT
GAGCTTCACTTGTCTATCTTAATTGAAACGATGCGTCGTGAAGGTTATGAGTTACAAGTTTCTAAACCAGAAGTA
ATCATCCGTGAAATCGATGGCGTGAAATGTGAACCAGTAGAAGACGTTCAAATTGATACTCCAGAAGAATTCATG
GGTTCAGTTATTGAATCTATCAGCCAACGTAAAGGCGAAATGAAAAACATGATTAACGACGGCAATGGCCAAGTT
CGTTTACAATTCATGGTTCCAGCTCGTGGATTAATCGGTTATACAACCTGATTTCCCTTCAATGACACGTGGTTAT
GGTATTATCAACCATACATTTCGATAGCTACCAACCAATCCAAAAA

183. *Bacillus cereus* (SEQ ID NO. 183)

TTACTTTTCACAAAAGTAAGAATACAACATATATTTTCATTCTTGCTTTTATTTTAATTGCTATTGTATCCCCTTCG
CTCTTATAATAGAGAAGGATTAAAAAGACATTAGGAGTTGGACATGTTGAAAAACGACAAGATTTACGTAATAT
AGCAATTATTGCCACGTTGACCATGGTAAAACAACACTTGTGACCAAGTTATTACGTCAAGCGGGGACTTTCCG
TGCGAACGAACACGTTGAAGAACGCGCAATGGATTCAAATGATCTAGAAAGAGAACGCGGTATTACAATTTTAGC
GAAAAATACAGCGATTCACTATGAAGATAAAAGAATTAACATTTTAGATACACCTGGTCACGCTGACTTCGGTGG
AGAAGTAGAACGTATCATGAAATGGTTGATGGTGTCTTACTTGTGTTGATGCATATGAAGGTTGTATGCCACA
AACACGATTTGTTTTAAAGAAAGCTCTTGAGCAAACTTAACTCCAATCGTAGTTGTAAACAAAATTGACCGTGA
CTTCGCTCGTCCAGATGAAGTAGTTGATGAAGTAATCGACTTATTCATTGAGCTTGGTGCAAACGAAGATCAATT
AGAGTTCCCAGTTGTATTTGCATCAGCAATGAACGGAACAGCAAGCTTAGATTCAAATCCAGCAAATCAAGAAGA
GAATATGAAATCATTATTCGATACAATTATCGAACATATTCCAGCACCAATTGATAACAGCGAAGAGCCACTTCA
ATTCCAAGTAGCACTTCTTGATTACAACGACTACGTTGGACGTATTGGAGTTGGTCGCGTATTCCGCGGTACAAT
GAAGGTTGGACAACAAGTTGCTTTAATGAAAGTAGACGGAAGCGTGAAGCAATTCCGCGTAACGAAATTATTCGG
TTACATGGGATTAAAACGTCAAGAAATTGAAGAAGCAAAAGCAGGGGACTTAGTAGCCGTTTCTGGTATGGAAGA
CATTAACGTAGGTGAAACAGTATGTCCAGTTGAACATCAAGATGCGTTACCATTATTACGTATTGATGAGCCAAC
ACTACAAATGACGTTCCCTGTAAATAACAGCCCATTTGCAGGTCGTGAAGGTAAATACATTACATCTCGTAAAT
TGAAGAGCGTCTTCGTTACAATTAGAAACAGATGTAAGTTTACGTGTAGATAATACAGATTCTCCTGATGCGTG
GATCGTATCTGGACGTGGGGAACATTTATCTATCTTAATTGAAAACATGCGTCGTGAAGGTTATGAATTACA
AGTATCTAAGCCAGAAGTAATCATTAAGAAGTTGATGGCGTAAGATGTGAGCCTGTAGAGCGGTACAAATCGA
TGTAACCTGAAGAATACACTGGTTCTATTAT

184. *Bacillus anthracis* (SEQ ID NO. 184)

CTATATTTTCATTCTTGATTTTATTTTAATTGCTATTGTATCCCCTTCGCTCTTATAATAGAGAAGGATTAAAAA
GACATTAGGAGTTGGACATGTTGAAAAACGACAAGATTTACGTAATATAGCAATTATTGCCACGTTGACCATG
GTAAACAACACTTGTGACCAAGTTATTACGTCAAGCGGGGACTTTCCGTGCGAACGAACACGTTGAAGAACGCG
CAATGGATTCAAATGATCTAGAAAGAGAACGCGGTATTACAATTTTAGCGAAAAATACTGCGATTCACTATGAAG
ATAAAAGAATTAACATTTTAGATACACCAGGTCACGCTGACTTCGGTGGAGAAGTAGAACGTATTATGAAAATGG
TTGATGGTGTATTACTTGTGTTGATGCATATGAAGGTTGTATGCCACAAACACGATTTGTTTTAAAGAAAGCTC

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TTGAGCAAACTTAACTCCAATCGTAGTTGTAAATAAAATTGACCGTGACTTCGCTCGTCCTGATGAAGTAGTTG
ATGAAGTAATCGACTTATTCATCGAAGTTGGTGCAAACGAAGATCAATTAGAGTTCCCAGTTGTATTTGCATCAG
CAATGAACGGAACAGCAAGCTTAGATTCAAACCCAGCAAATCAAGAAGAGAATATGAAATCATTATTTGATACAA
TTATTGAACATATTCCTGCACCAATTGATAACAGCGAAGAGCCACTTCAATTCCAAGTAGCACTTCTTGATTACA
ACGACTATGTTGGACGTATCGGGGTTGGACGCGTATTCCGCGGTACAATGAAGGTTGGACAACAAGTTGCTTTAA
TGAAAGTAGACGGAAGTGTAACAATTCCGCGTAACGAACTATTTGGTTATATGGGATTAAAACGTCAAGAAA
TTGAAGAAGCAAAAGCTGGAGACTTAGTAGCTGTTTCTGGTATGGAAGACATTAACGTAGGTGAAACAGTATGTC
CAGTTGAACATCAAGATGCGTTACCATTATTACGTATTGATGAGCCAACACTACAAATGACATTCCTTGTAATA
ACAGCCCATTTGCAGGTCGTGAAGGTAAATACATTACATCTCGTAAAATTGAAGAGCGTCTTCGTTTACAATTAG
AAACAGATGTAAGTTTACGCGTAGATAATACAGAATCTCCTGATGCGTGGATCGTATCTGGACGTGGGGAACACTAC
ATTTATCTATCTTAATCGAAAACATGCGTCGTGAAGGTTATGAACTACAAGTATCTAAACCAGAAGTAATCATT
AAGAAGTTGATGGCGTAAGATGTGAGCCTGTAGAGCGTGTGCAAATTGATGTACCTGAAGAATACACTGGTTCTA
TTATGGAACTCTATGGGTGCACGTAAAGGTGAAATGTTAGATATGGTGAATAACGGAAACGGTCAAGTTCGCCTTA
CTTTCATGGTTCCAGCACGTGGTTTAATTGGTTACACAACAGAATTCCTAACATTAACCTCGTGGTTACGGTATTT
TAAACCATACATTGATTGCTACCAACCAGTACACGCTGGACAAGTTGGTGGACGTCGTCAAGGTGTTCTAGTTT
CACTTGAAACAGGAAAAGCATCACAAATACGGTATTATGCAAGTTGAAGACCGTGGTGTAATCTTCGTTGAACCAG
GTACAGAAGTATATGCTGGTATGA
TTGTTG

185. *Staphylococcus aureus* (SEQ ID NO. 185)

TCAATTATATGATATAATAAAAAAGTTGTAATTAAAAGTGGGATTTTACTTAAGAAAGAAGGAACTATTTATAT
GACTAATAAAAAGAGAAGATGTCCGCAATATAGCAATTATTGCTCACGTTGACCATGGTAAAACAACCTTAGTAGA
TGAGTTGTTAAACAATCTGGTATATTAGAGAAAATGAACATGTCGATGAACGTGCAATGGACTCTAACGATAT
CGAAAAGAGAGCGTGGAATTACGATTCTAGCCAAAAATACGGCTGTTGATTATAAAGGTACACGTATTAATATTTT
GGATACACCAGGACATGCAGACTTTGGTGGAGAAGTAGAACGTATTATGAAAATGGTTGATGGGGTTGTCTTAGT
AGTAGATGCGTATGAAGGTACAATGCCTCAAACACGTTTGTACTTAAAAAAGCGCTAGAACAAAACCTGAAACC
TGTTGTTGTTGTTAATAAAATTGATAAACCATCAGCACGTCCAGAGGGTGTGTTAGATGAAGTTTATAGATTTATT
TATTGAATTAGAAGCAAACGATGAACAATTAGAATCCCTGTTGTTTATGCTTCAGCAGTAAATGGAACAGCTAG
CTTAGATCCTGAAAACAAGATGATAATTTACAATCATTATATGAAACAATTATTGATTATGTACCAGCTCCAAT
TGATAACAGTGATGAGCCATTACAATTCCAAGTAGCATTGTTGGACTACAATGATTATGTTGGACGTATTGGTAT
TGGTCGTGTATTAGAGGTAAAATGCGTGTGCGGAGATAATGTATCACTAATTAAATTAGACGGTACAGTGAAAAA
CTTCCGTGTAACATAAAATCTTTGGTTACTTTGGATTAAAACGTTTAGAAATTGAAGAAGCACAAAGCTGGAGATTT
AATTGCTGTTTCAGGTATGGAAGACATTAATGTTGGTGAACTGTAACACCACATGACCATCAAGAAGCATTGCC
AGTTCTACGTATTGATGAGCCTACTCTTGAAATGACATTTAAAGTTAACAATTCTCCATTTGCTGGCCGTGAAGG
TGACTTTGTAACAGCACGTCAAATCAAGAAGCTTTAAATCAACAATTAGAAACAGATGTATCTTTGAAAGTTTC
TAACACAGATTCTCCAGATACATGGGTAGTTGCTGGTCGCGGTGAATTGCATTTATCAATCCTTATTGAAAATAT
GCGTCGTGAAGGTTATGAATTACAAGTTTCAAACCCACAAGTAATTATTAAAGAAATAGATGGTGTAATG

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186. *Staphylococcus epidermidis* (SEQ ID NO. 186)

ACCCACCTTTTACTTATCTTTTCAATAATATATGATATAATAAACAGTTGCAATTAAAAGTGGGAGTATACAC
AAGAAAGGAATTTATAAAATGACTAATTTAAGAGAAGATGTTTCGTAATATAGCGATTATTGCGCATGTCGACCAT
GGTAAACAACATTAGTAGACCAGTTGCTTAAACAATCAGGTATATTTTCGTGAAAACGAACATGTCGACGAGCGT
GCAATGGACTCTAATGATTTAGAAAGAGAACGTGGTATTACGATTCTTGCTAAGAATACAGCGATAGATTATAAA
GGAACGCGTATCAATATATTAGACACACCTGGCCACGCCGATTTTGGTGGTGAAGTTGAACGTATCATGAAAATG
GTTGACGGTGTCTACTAGTGGTTGACGCATATGAAGGTACAATGCCTCAAACCTCGTTTTGTTCTTAAAAAAGCT
TTAGAACAAAACCTTAAAACCGGTTGTAGTTGTGAATAAAATTGATAAACAGCTGCTAGACCTGAGGGAGTTGTA
GATGAAGTATTAGACTTATTCATTGAATTGGAAGCGAATGATGAGCAATTAGACTTCCCAGTTGTTTATGCTTCA
GCTGTGAATGGAACAGCAAGTTTAGACTCTGAAAAGCAAGACGAAAATATGCAATCCCTATACGAGACGATTATT
GACTATGTACCGGCACCAGTAGATAATTCAGATGAACCATTACAATTCCAAATTGCTTTACTAGATTATAATGAT
TATGTAGGTCGTATAGGCGTTGGACGTGTGTTTACAGAGTAAAATGCGTGTAGGTGATAATGTATCACTAATTAAA
TTAGATGGTACAGTTAAGAACCTTTCGTGTGACGAAAATATTTGGTTACTTTGGTCTTAAACGTGAAGAAAATTGAA
GAAGCACAAGCAGGAGACTTAATAGCTGTTTCAGGTATGGAAGATATTAACGTTGGTGAACAGTTACACCACAT
GATCATCGTGACCCATTACCGGTGTACGTATTGATGAACCAACCCTAGAAATGACTTTTAAAGTAAATAACTCT
CCGTTTGCTGGACGTGAAGGTGATTATGTAACAGCTCGACAAATTCAGAAAGATTAGATCAACAACCTTGAAACA
GATGTTTCTTTAAAAGTTACACCTACTGATCAACCAGATTTCATGGGTTGTTGCTGGTGTGTTGCTGGTGAACCTG
TCTATTCTTATTGAAAACATGAGACGTGAAGGCTTTGAATTACAGGTTTCTAAACCTCAAGTTATTTTAAGAGAA
ATCGATGGTGTGTTAAGTGAACCATTTGAGCGTGTACAATGTGAA

187. *Bacillus subtilis* (SEQ ID NO. 187)

GAAAAACGTGACGCTTTTAAAGAGGATGTGTGATATAATATGAAAGTTATCTAATTTTTTTTAGGAGATGAAAAAG
TGAAACTTCGAAATGATCTTCGCAACATCGCGATTATTGCCACGTTGACCATGGGAAAACGACTCTAGTCGATC
AGCTTTTACATCAGGCTGGTACGTTCGTCGCAACGAACAGGTTGCTGAACGCGCAATGGACTCTAATGATCTTG
AACGCGAACGCGGCATTACAATATTGGCGAAAAATACTGCGATTAACCTATAAAGATACACGTATCAATATTTTGG
ACACCCCTGGACATGCAGACTTTGGGGGAGAAGTAGAACGGATTATGAAAATGGTTGACGGCGTAGTGCTTGTCG
TTGACGCATATGAAGGCTGTATGCCTCAAACCTCGTTTTGTTCTGAAAAAAGCTCTTGAGCAAAACCTGAACCTG
TTGTTGTTGTAAACAAAATTGACCGTGACTTTGCTCGTCCAGAGGAAGTTATCGATGAAGTTCTGGATCTGTTCA
TTGAGCTTGATGCCAATGAAGAGCAGCTCGAGTTCCAGTGATATGCTTCCGCGATTAATGGAACAGCGAGTC
TTGATCCGAAACAACAGGATGAAAACATGGAAGCTTTATATGAAACCATTATTAAGCATGTTCCGGCACCTGTTG
ATAATGCAGAGGAGCCGCTTCAATTCGAAGTTGCCCTTCTTGACTACAACGACTATGTAGGCCGTATCGGAATCG
GACGCGTATTCCGCGGCACAATGAAAGTCGGACAGCAGGTTTCTCTTATGAAGCTTGACGGAACGGCAAAGTCAT
TCCGTGTTACAAAGATTTTTGGTTTCCAAGGCTTAAAGCGTGTGGAATTTGAAGAAGCAAAAGCGGGAGACCTCG
TTGCGGTTTCCGGGATGGAAGATATCAACGTTGGTGAACGGTATGTCTGTAGACCATCAAGATCCGCTTCCGG
TCCTTCGCATTGATGAGCCGACACTTCAAATGACATTTGTCTGAATAACAGTCCGTTTGCAGGCCGTGAAGGCA
AATATGTAACGGCCCGCAAAATCGAAGAGCGTCTTCAATCACAGCTTCAGACGGATGTGAGCTTGCGTGTTGAGC
CAACAGCTTCTCCTGATGCTTGGGTTGTTTTCAGGACGCGGTGAGCTGCACTTGTCAATTTTAATTGAAAATATGC
GTCGTGAGGGCTATGAGCTTCAAGTGTCAAACCTGAAGTTATTATCAAAGAAATCGACGGCGTACGCTGTGAGC
CTGTTGAACGTGTGCAAATTGATGTTTCTGAAGAGCATACTGGCT

188. *Streptococcus mutans* (SEQ ID NO. 188)

GGAATGGAAAAGTAAAAGAGAAGAATTAGTTCTTTTTTTGAGATAATGACAGGGATTAGTATGAGCTGTTGTCTTT
TGTTTTTGCAATACTGGTTGATTGAGGACTTATTTTATAAAATTTGGAGATACCAAGACTGCGACTTTGCTATCT
TGGTTTTTCTTTTATATTTTAAACATTTACATATCTCTCCTGAGTTTTTCCCTAATTTTTATGGTATAATAGAT
AAGTTGAAATAAATTAATGTAAATGTAAGAGGAATTATGACAAATTTTAGAGAAGATATTAGAAATGTTGCTAT
CATTGCCACGTTGACCATGGGAAAACAACCTTGTTGATGAGCTCTTAAAACAATCGCATACACTTGATGAGCA
TAAAAAATTAGAAGAACGTGCGATGGACTCTAATGATCTTGAAAAAGAGCGTGGGATTACTATTCTTGCAAAAAA
TACTGCTGTTGCCTACAATGGTGTACGTATTAACATTATGGACACACCAGGACATGCGGATTTTGGTGGAGAAGT
AGAGCGTATCATGAAAATGGTTGATGGGGTTGTTCTTGTTGTTGATGCTTATGAAGGTACCATGCCGCAAACACG
TTTTGTTTTGAAAAAGCTTTGGAACAAAACCTGGTTCCAATCGTGGTGGTGAATAAGATTGACAAGCCATCAGC
TCGTCGCCGAGAAAGTTGTTGATGAAGTTCTTGAACTTTTTCATTGAACCTTGAGCAGATGATGACCAGTTAGAGTT
TCCAGTCGTTTACGCTTCGGCGATTAATGGAACCTTCTTCATTATCAGATGAACCAGCGGATCAAGAACATACAAT
GGCACCCTTTTTGATACTATTATTGAGCATATTCCAGCACCGATCGATAATTCAGATCAGCCACTTCAATTTCA
AGTGTCTCTCCTTGATTATAACGACTTTGTTGGACGTATCGGTATTGGGCGAGTCTTCCGTGGTCTGTTAAAGT
CGGGGATCAAGTGACACTTTCTAACTTGATGGTACAACAAAGAATTTTCGTGTTACAAAACTTTTCGGTTTCTT
CGGTTTGAACGTCGTGAGATTAAGGAAGCTAAGGCTGGCGATTTGATTGCTGTTTCAGGTATGGAAGATATCTT
TGTTGGTGAACGATTACACCAACTGATGCTGTAGAACCCTTCCTATTCTTCACATTGATGAGCCAACCTCTGCA
AATGACCTTTTTAGCTAACAATTCCCCTTTTGAGGCGGTGAAGGTAAATTTGTAACCTCGCGTAAGGTAGAAGA
GCGTTTGTGGCAGAATTGCAAACAGATGTTTCCCTTCGTGTAGAAGCCACTGACTCACCAGATAAATGGACGGT
TTCAGGTCGTGGGAGTTACATCTGTCAATCCTTATTGAAACCATGCGCCGTGAAGGATATGAGCTGCAAGTATC
GCGTCCAGAAGTTATTATCAAAGAAATTGATGGCATCAAATGTGAGCCATTTGAACGCGTGCAAATTGACACACC
GGAAGAATACCAAGGTGCTGTTATCCAGTCCCTTTCAGAACGTAAAGGTGAAATGCTTGA

189. *Streptococcus pneumoniae* (SEQ ID NO. 189)

AAGCGGAGTGAAAACATTTACACTTGCTTGAGTTATGTTATTTATTTGAAATTATGGTATAATCGTTCAGTTAGA
AAATAAATTTTGAATATTATAGAGGAAATCATGACAAAATTAAGAGAAGATATCCGTAACATTGCGATTATCGCC
CACGTTGACCACGGTAAAACAACCTGGTTGACGAATTATTGAAACAATCAGAAACGCTTGATGCACGTACTGAA
TTGGCAGAGCGTGCTATGGACTCAAACGATATCGAAAAAGAGCGTGGAATCACCATCCTTGCTAAAAATACTGCC
GTTGCTTACAACGGAACCTCGTATCAACATTATGGACACACCAGGACACGCGGACTTCGGTGGAGAAGTTGAGCGT
ATCATGAAAATGGTTGACGGTGTGTCTTGCTGCTAGATGCCTATGAAGGAACCATGCCACAAACTCGTTTCGTA
TTGAAAAAGCCTTGGAACAAGACCTTGTCCTAATCGTGGTTGTTAACAAAATCGATAAGCCATCAGCTCGTCCA
GCAGAAGTAGTGGATGAAGTCTTGAACCTTTTCATCGAGCTTGGTGCAGATGACGACCAGCTTGATTTCCAGTG
GTTTATGCTTCAGCGATCAACGGAACCTTCTTCATTGTGAGATGATCCAGCTGACCAAGAAGCGACTATGGCACCA
ATCTTTGACACGATTATCGACCATATCCAGCTCCAGTAGATAACTCAGATGAGCCTTTGCAGTTCCAAGTGTC
CTTTTGGACTACAATGACTTCGTTGGACGTATCGGTATCGGTGCTTCCGTGGTACAGTTAAGGTTGGGGAC
CAAGTTACCCTTTCTAACTTGACGGTACAACCTAAAACTTCGTGTTACAAAACCTCTTCGGTTTCTTTGGTTTG
GAACGTCGTGAAATCCAAGAAGCCAAAGCGGGTGAAGTTGATTGCCGTTTCAGGTATGGAAGACATCTTTGTCGGT
GAAACCATCACTCCGACAGATGCAGTAGAAGCTTTCCTAATCCTACACATCGATGAGCCAACCTTTCAAATGACT
TTCTTGGTCAACAACCTCACCATTGCTGGTAAAGAAGGTAAATGGGTAACTTCTCGTAAGGTGGAAGAAGCGTTG

CAGGCAGAATTGCAAACAGACGTTTCCCTTCGTGTTGACCCAACTGATTCACCAGATAAATGGACTGTTTCAGGA
CGTGGAGAATTGCACTTGTCAATCCTTATCGAAACAATGCGTCGTGAGGGCTATGAACT

190. *Streptococcus agalactiae* (SEQ ID NO. 190)

AGAAATGAATTAAATTGAAAAAGTAGAAAATAAATGGCATAAATAATGAAATGATGAAAAGTTTTCTTATCACA
AATAGGCAGTTAATATGAAAACATTTACACTTGTGTAAATTCTGTTTTTTAAGAAAAATTGTGTTATAATTTCATA
AGTTAACAGAATTACATTATAAAATAGAGGAAAACATGACAAATTTAAGAACAGATATCCGTAACGTTGCGATCA
TTGCCACGTTGACCACGGTAAAACAACCTCTCGTTGATGAATTATTAAAACAATCACATACTCTTGATGAGCGTA
AAGAGCTTGAAGAACGTGCAATGGATTCAAATGATATCGAAAAAGAACGTGGTATCACCATTCTTGCAAAAAATA
CAGCCGTAGCATACAACGATGTTTCGTATCAATATTATGGACACACCTGGTCACGCGGACTTTGGTGGTGAAGTTG
AGCGTATTATGAAAATGGTTGATGGTGTGTTTTAGTCGTTGATGCCTACGAAGGAACAATGCCACAAACACGTT
TTGTTTTGAAGAAAGCTCTTGAACAAAACCTTAATTCCAATCGTTGTTGTAAATAAAATTGATAAGCCGTCAGCTC
GTCCATCAGAGGTTGTTGATGAAGTTCTTGAACATTTATTGAGCTCGGTGCTGATGATGATCAACTAGATTTCC
CTGTTGTTTATGCTTCAGCTATCAATGGAACATCTTCAATGTCAGATGATCCTTCAGATCAAGAAAAACAATGG
CACCGATTTTGTACTATCATTGATCACATTCCAGCCCCAGTTGACAACCTCGGAAGAACCACTTCAATTTCCAAG
TTTCTCTTCTTGATTACAATGATTTTGTAGGACGTATTGGTATTGGACGTGTTTTCCGCGGGACTGTCAAAGTTG
GAGATCAAGTTACTCTTTCAAACCTTGATGGTACAACCTAAAACTTCCGCGTAACAAAACCTTTTTGGTTTCTTTG
GACTTGAACGTAAAGAAATCCAAGAGGCTAAAGCGGGTGATTTAATCGCTGTTTCTGGTATGGAAGATATCTTCG
TTGGTGAGACAGTAACTCCGACAGATGCTATTGAACCACTACCAGTTTTACGTATTGACGAGCCAACACTTCAAA
TGACTTTCTTGGTGAATAATTCACCATTTCAGGTCGCGAAGGTAAATGGATTACGTCACGTAAGGTTGAAGAAC
GTCTTTTAGCAGAATTACAAACAGACGTTTCTTTACGTGTTGACCCAACAGATTCGCCAGATAAATGGACGGTTT
CAGGGCGTGGAGAATTACATTTATCTATCCTTATTGAAACAATGCGTCGTGAGGGATATGAACTTCAAGTATCAC
GTCCAGAAGTTATCATCAAAGAAATTGATGGTGTTCATGCGAGCCGTTTGAGCGTGTTCAAATTGATACTCCAG
AAGAATATCAGGGTGCTATTATCCAAAGTTTGTGAGAGCGTAAAGGTGATATGCTTGATATGCAGATGGTTGGTA
ATGGTCAAACGCGTTTGATTTTCTTGATTCTGCACGTGGTTTGATTGGTTATTCAACAGAGTTTCTTTCAATGA
CACGTGGATATGGTATCATGAATCATACTTTTGACCAGTATCTACCGTTGTTCAAGGAGAAATTGGTGGTCGTC
ATCGTGGTGCTTGGTTTCTATTGAAAATGGTAAAGCAACTACATATTCAATTATGCGTATTGAAGAACGTGGGA
CTATCTTTGTAAATCCAGGTATAGAAGTTTATGAAGGAATGATTGTTGGTGAGAATTCTCGTGATAATGACCTCG
GAGTCAATATTACAACCTGCTAAACAATGACAAATGTCCGTTTCAGCAACTAAAGATCAAA

191. *Streptococcus pyogenes* (SEQ ID NO. 191)

GTCTTAAAAGACGGTATTGATTATTGGGATGGCAAAGTTAAACAAACAACCTAGTTAAGAGTAACGTGGAGTTAA
GGGAATAAAGGCAGTCACTGTCTCAAAAACCTTAATTCCTTTTTTTGCTGTATCCAGACTTGCTGAAAGTCTGA
AAATATTTACAATTGATTAAAACAGTTTTTTTAAACATTTTGTGTTATACTTATCTAGTTAAATATATTTACT
TAGAGGAACAAATGACTAACTTAAGAAACGATATCCGTAACGTAGCGATTATTGCCACGTTGACCACGGAAAAA
CAACACTTGTAGATGAATTATTAAAACAATCCCATACTCTTGATGAGCGTAAAGAGCTTCAAGAGCGTGCCATGG
ATCCAATGACCTTGAAAAAGAACGTGGGATTACAATCCTTGCGAAAAATACGGCAGTAGCCTATAACGATGTTT
GTATTAACATCATGGATACCCAGGACACGCGGACTTCGGTGGTGAAGTTGAACGTATCATGAAAATGGTTGACG
GGGTTGTTCTTGTGTGGATGCCTACGAAGGAACAATGCCCCAGACGCGTTTCGTATTGAAAAAGCACTTGAGC
AAAACCTTATCCCGATCGTTGTGGTGAACAAGATTGACAAACCTTCAGCTCGTCCAGCAGAAGTTGTAGATGAAG

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TGCTTGAATTATTCATCGAACTTGGTGCCGATGATGAGCAATTGGAATCCCAGTTGTTTACGCATCAGCTATTA
ATGGAACATCATCATTATCAGATGACCCTGCTGACCAAGAGCATACTATGGCACCGATCTTTGATACGATTATTG
ATCATATTCCAGCGCCAGTTGATAATTCAGATGAGCCTTTGCAATCCAAGTGTCACTTTTGGACTACAACGATT
TCGTAGGTCGTATCGGTATCGGTGCTGTTTTCCGTGGTACTGTTAAAGTGGGTGACCAAGTAACCTTTCAAAC
TTGATGGTACCACTAAAACTTCCGTGTTACAAAAGTGTGGTTTCTTCGGTTTGGAAACGTCGTGAAATTCAAG
AAGCTAAAGCAGGTGACTTGATTGCTGTTTCAGGTATGGAAGATATCTTTGTTGGAGAAACCATTACACCAACTG
ACTGTGTGGAAGCTCTGCCAATTCTTCGTATTGATGAGCCAACACTTCAGATGACTTTCTTGGTCAATAACTCTC
CTTTTGACGGTCGTGAAGGTAAATGGATCACGTACGTAAGGTTGAAGAAGCTCTTTTAGCAGAATTGCAAACAG
ACGTGTCACTTCGTGTTGACCAACAGATTGCCAGATAAATGGACGGTTTCAGGGCGTGGAGAATTGCATTTAT
CTATCCTCATTGAAACCATGCGCCGTGAAGGCTATGAACTTCAAGTATCACGTCCAGAAGTTATCATCAAAGAAA
TTGATGGTGTCAAATGTGAACCGTTTGAGCGTGTCAAATTGATACACCAGAAGAATATCAGGGTGCAATCATCC

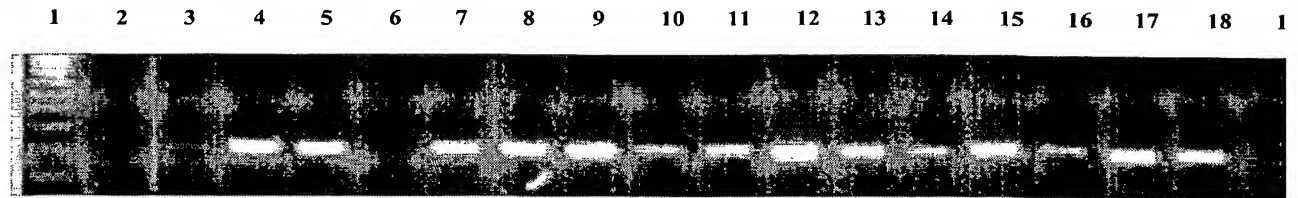
192. *Enterococcus faecalis* (SEQ ID NO. 192)

CATCACGCAACGGAAATCGGACAAGCAAGCATGGGCGTGCCTATTAGCGGTTGTGCAGGTTTGGAATTATTGCT
ATGTTAAAAGGCAACCATCATGGCTATTTATCTAATCTAAGTCCTTGGGATTATGCAGCAGGCTTAGTACTTTTG
GAAGAATTTGGGTTTAAATACTCTGGTATTACAGGAAAACCATTAACTTTTGCGGGTCGTGAATACTTTATTGCA
GCAACTCCTGAAACCTATGATGAAGTATTTACCCGATATTTAAATGAATCGGAATAATCAAAGAAGAGCGTTGCT
GAAAGGTAAGGCTCTTCCTCTTTTAAAAGAGAAAAATTTGTAAAAAATGTCCTTGTTTTTCAGAAAAAGCCGAAT
AATTTCTAAACTTTTCATTATTTTTGTCAGGCGAAAGCCTTTTTTTAATGAAAAAGTTTGTCTATAATAAGCAGTC
GGCTTTTATGGACTTAAGTAACATAAGCGTATATAGATAAGGAGCAATTAAATTGAAATACAGAGATGATATTG
TAACGTGGCAATTATCGCCACGTTGACCATGGTAAAACAACCTTAGTAGATGAACTTTTAAAACAATCTGACAC
TTTAGATGGACACACACAATTACAAGAACGTGCAATGGATTCCAATGCACCTTGAAAGTGAACGTGGAATTACTAT
CTTAGCAAAAAATACAGCCGTAGATTATAACGGTACACGTATCAACATTCTAGATACACCAGGACACGCGGACTT
CGGTGGTGAAGTAGAACGTATCATGAAATGGTAGACGGTGTGTTTTAGTTGTGCGATGCGTATGAAGGAACAAT
GCCTCAAACACGTTTCGTATTGAAAAAGCATTAGAACAAAAAGTAACACCAATCGTGGTTGTTAACAAAATTGA
CAAACCTTCTGCTCGTCCTGAACACGTAGTAGATGAAGTTTTAGAGTTATTCATCGAATTAGGTGCAGACGACGA
TCAATTAGATTTCCAGTTGTTTATGCTTCTGCTTTAAACGGAACCTCAAGTGAATCAGATGATCCAGCAGATCA
AGAGCCAACAATGGCCCCAATTTTTGATAAAATTATTGAACATGTGCCAGCTCCAGTTGACAATTCAGACGAACC
ACTTCAATCCAAGTCTCATTACTAGACTACAACGATTACGTTGGACGTATTGGGATTGGCCGTGTGTTCCGTGG
CACAATGAAAGTCGGCGACCAAGTTGCGTTGATGAAATTAGATGGCAGCGTGAAAAATTTCCGTGTAACGAAAAT
TTTAGGTTTCTTTGGCTTACAACGTGTGGAATTGATGAAGCAAAAGCGGGCGATTTAATTGCCGTTTCTGGAAT
GGAAGACATTTTCGTGGGGAAACAGTTGTAGATGTTACAATCAAGAAGCATTACCAATTCTACACATTGATGA
GCCAACCTTACAAATGACTTTCTTAGTTAACAATTCTCCATTTGCGGGACGTGAAGGAAAATACATCACCGCTCG
TAAATCGAAGAACGTTTAAATGGCTGAGTTACAAACAGACGTATCTTTACGTGTTGATCCAATTGGCCCAGATTC
TTGGACTGTATCAGGTCGTGGCGAATTGCATTTATCAATTTAATTGAAAACATGCGTCGTGAAGGCTATGAATT
ACAAGTTTCTCGTCCAGAAGTTATTGAACGTGAAATTGATGGAGTTAAATGTGAACCATTTGAACGTGTTCAAAT
TGACACACCTGAAGA

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193. *Lactococcus lactis* (SEQ ID NO. 193)

CGAAAAAGCAAGTTAAATATGTTGTAAATAATGGTGTTACATTAGATAAATACTAGTGGTGGGCCTAATTTGGCTG
CACCTGTGACGGTGGATAGTCAGGTAATTTGGAACGATAAAGGTACGATTATGGGTGTAAGGACCTATACAGCAG
ATTTAAGCCAAGCAGAAGTAGTTAAAAAAGTGGGTAATTTGAATGCAATGTCCTTTGGAGAATTTTGGGGTACAA
AAGTTTTTGTGCCAGCCAAAATCAGACAAATTCAGATAAGACTTATTCTGTTACGTTTAAACTGAATATAAATT
GGATAGTATCTAATGGCTATGCTTCGCTAACAAAAGTAACAGGTGGCTATGGTTCTTGCAATTGACCATGTTTATG
TTGCTAATTCTAGTGTTACTACTGCAACGAATGGTCAGATTAAAGGTTCAAGTGGTTATACTCAACAAGTTGATG
ACAAATCAGAAGGGAATAGTTTATCGTGGTCAATTACGCGAACTATAAACCTGTAAAAGTTCCAGCAAGTGGGG
CAAATGTAGGAGCTACGTATTTTGCCACACTTAAACGGGGAAATAGTACATGGAAATTCAAAACAACAAATAGAG
CTTATTAAGTGGGAGGAAGTGAATGAATATAAAAGGCATAAAAATTTGGCAAGTATTTCTTGCAATTCATCATTT
GGATAGGAACCATGTTTCTTCCGTCAACGGTAAATCAGGCTAAATTGAATACGAATTTTGACTATAAAAAAAGTC
GAGAAAATTTCTTTTATTTTCTTTTTCATCAAGTCCCTTTTTATAGTTTCATTTTGGGATTGGTGTGCTTATAT
CACTTTTTCTCATTTATAGGAAAATAAATTTTAGTGTCTATTTTCTTTTGCTAGTCTTATTTTTTACATTAGTT
TCTTAGTTATAGCTTTTCCGTCTATGATTATTTTAAATCATAGTTTATCTGGGAATACTTTTGGGGCTGAACTTT
CTATCTTTCTAACCTTTTATGGAGCTGGATATATTATTGCTGTTCTATTTGGTTTAGTTGCTTTTCTTTTACTCT
TTCTCTACAGTTTAAGAATAAAAGAATGTTAACAACATAATCATTTTTACTGATTTTATTAATTATAAAAAAATA
AAGAACTCCTTAGAAATTTTCTTTGGGGTTTTTCATTTTGGAAGTAAAAAATCTTTGTTAGGCTTGTAACGTG
TGCATTTACAGCTTTTAGAAAAGTGTGCTATAATGGGTAGATATATACGAAAGTAAGGTATGATAAAATTGACT
AAATTACGCGAAGATATTAGAAACGTCGCTGTTATTGCCCACGTTGACCATGGTAAAACTACATTGGTTGACGAA
CTCTTAAACAATCTCAAACGTTGGATGCTCGTAAAGAATTAGCTGAACGTGCGATGGACTCAAATGCACTTGAG
CAAGAACGTGGGATTACTATCCTTGCCAAAAATACAGCAGTTGAATATAACGGAACTCGTATCAACATCTTGAC
ACACCAGGTCACGCGGACTTCGGTGGAGAAGTTGAACGTATTATGAAAATGGTTGATGGGGTTGTCCCTCGTTGTC
GATGCTTATGAAGGAACAATGCCTCAAACACGTTTTGTTTTGAAA

Figure 8. Amplification of molecular marker V (carB) in Gram-negative bacteria

1. DNA Ladder (123 bp)
2. *Pseudomonas aeruginosa*
3. *Pseudomonas pseudoalcaligenes*
4. *Stenotrophomonas maltophilia*
5. *Citrobacter freundii*
6. *Serratia liquefaciens*
7. *Providencia stuartii*
8. *Klebsiella pneumoniae*
9. *Klebsiella oxytoca*
10. *Pseudomonas syringae*
11. *Pseudomonas putida*
12. *Enterobacter aerogenes*
13. *Pseudomonas diminuta*
14. *Proteus mirabilis*
15. *Burkholderia cepacia*
16. *Burkholderia pickettii*
17. *Proteus vulgaris*
18. *Serratia marcescens*
19. Negative control

Figure 9. Molecular marker V (carB) sequences amplified from different Gram-negative bacteria (SEQ ID NOs 194-232, 238-239, 242-254) and from various Gram-positive bacteria (SEQ ID NOs 233-237, 240-241, 255)

194. *Neisseria meningitidis* groupe B (SEQ ID NO. 194) NMENB

TTTNNGGCGGNTGTTACCTACATCGAGCCGATTATGTGGCAGACGGTGGAGAAGATTATCGCCAAAGAGCGGCCCG
GATGCGATTCTGCCCACGATGGGCGGCCAGACCGCGCTGAACTGTGCGCTGGATTTGGCGCGCAACGGCGTGCTG
GCGAAATACAACGTGCGAGTTAATCGGCGCGACAGAAGACGCGATTGACAAGGCGGAAGACCGTGGCCGCTTTAAA
GAAGCGATGGAAAAAATCGGTTTGTCTTGCCCGAAATCTTTTGTCTGCCACACGATGAACGAAGCCTTGGCGGCG
CAAGAACAGGTCGGCTTCCCGACGCTGATTCGTCCGTCTTTCACGATGGGCGGTTTCGGGCGGCGGCATTGCCTAC
AATAAAGACGAGTTTTTGGCGATTGCGAACGCGGTTTCGATGCGTCGCCCACGCACGAGCTGCTGATTGAGCAG
TCCGTCCTCGGCTGGAAA

195. *Neisseria meningitidis* groupe C (SEQ ID NO. 195) NMENC

GTTACCTACATCGAGCCAATTATGTGGCAGACGGTGGAGAAGATTATCGCCAAGGAGCGTCTGATGCGATTCTG
CCCACGATGGGCGGTCAGACCGCGCTGAACTGTGCGCTGGATTTGGCGCGCAACGGCGTGCTGGCGAAATACAAT
GTGAGCTGATCGGCGCGACGGAAGACGCGATTGACAAGGCGGAAGACCGCGGTCGTTTTAAAGAAGCGATGGAA
AAAATCGGCCTCTCCTGCCCCGAAATCTTTTGTCTGCCACACGATGAACGAAGCTTTGGCAGCGCAAGAACAGGTC
GGCTTCCCTACCCTGATTTCGTCCGTCTTTCACGATGGGCGGTTTCGGGCGGCGGCATTGCCTACAATAAAGATGAG
TTTTTGGCGATTGCGAACGCGGTTTCGATGCGTCGCCTACGCACGAGCTGCTGATTGAGCAGTCTGTTCCCTCGG
CTGGAAAGA

196. *Enterobacter cloacae* (SEQ ID NO. 196) ECLO

GCAACCTACATCGAGCCAATTCACTGGGAAGTGGTACGTAAAATCATCGAGAAAGAGCGTCCGGATGCGGTTCTG
CCGACCATGGGTGGCCAGACTGCGCTGAACTGTGCGCTGGAGCTGGAGCGTCAGGGCGTGCTGGAAGAGTTCGGC
GTGACCATGATTGGTGCGACCGCCGACGCGATTGATAAAGCAGAAGACCGTCGTCGCTTCGACGTGGCGATGAAA
AAAATCGGCCTCGACACCGCGCGTTCCGGTATCGCTCACAACATGGAAGAGGCGCTGGCCGTTGCGGCTGAAGTG
GGTTATCCGTGCATCATCCGTCCTTCCTTACCATGGGCGGCACCGGCGGCGGTATCGCCTACAACCGCGAAGAG
TTTGAAGAGATTTGCGAGCGCGGCCTGGATCTCTCCCAACCAAAGAGCTGCTGATTGATGAATCGCTGATTGGC
TGGAAGA

197. *Klebsiella pneumoniae* (SEQ ID NO. 197) KPNE

CTACATCGAGCCGATTCACTGGGAAGTGGTGCCTAAAATCATCGAAAAAGAGCGCCCGGATGCGGTGCTGCCGAC
CATGGGCGGCCAGACGGCGCTGAACTGCGCGCTCGAGCTGGAGCGTCAGGGGGTCTGGCTGAATTCGGCGTGAC
CATGATTGGTGCCACCGCCGATGCGATTGATAAAGCCGAAGACCGTCGCCGTTTCGATATCGCAATGAAAAAAT
CGGCCTCGACACCGCGCGCTCTGGTATCGCCACACGATGGAAGAGGCGCTGGCGGTTGCCGCCGACGTTGGTTT
CCCGTGCATCATCCGTCCGTCCTTACCATGGGCGGCACCGGCGGCGGTATCGCCTATAACCGCGAAGAGTTCTGA

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AGAAATCTGCGAACGCGGCCTGGATCTCTCTCCGACCAACGAACTGCTGATCGATGAATCGCTGATCGGCTGGAA
AGA

198. *Shigella sonnei* (SEQ ID NO. 198)

SSON

GCGACCTACATCGAGCCGATTCACTGGGAAGTAGTACGCAAGATTATTGAAAAAGAGCGCCCGGACGCGGTGCTG
CCAACGATGGGCGGTGAGACGGCGCTGAACTGCGCGCTGGAGCTGGAGCGTCAGGGCGTGTTGGAAGAGTTCGGC
GTGACTATGATTGGTGCGACCGCCGATGCGATTGATAAAGCAGAAGACCGCCGTCGTTTCGACGTAGCGATGAAG
AAAATTGGTCTGGAAACCGCGCGTTCCGGTATCGCACACACGATGGAAGAAGCGCTGGCGGTTGCCGCTGACGTG
GGCTTCCCGTGCAATTATTCGCCCATCCTTTACCATGGGCGGTAGCGGCGGCGGTATCGCTTATAACCGCGAAGAG
TTTGAAGAAATTTGCGCCCGCGGTCTGGATCTCTCCCAACCAAGAGCTGCTGATTGATGAGTCGCTGATCGGC
TGGAAGA

199. *Escherichia coli* K12 (SEQ ID NO. 199)

ECOK12

GCAACCTACATCGAGCCGATTCACTGGGAAGTTGTACGCAAGATTATTGAAAAAGAGCGCCCGGACGCGGTGCTG
CCAACGATGGGCGGTGAGACGGCGCTGAACTGCGCGCTGGAGCTGGAACGTCAGGGCGTGTTGGAAGAGTTCGGT
GTCACCATGATTGGTGCCACTGCCGATGCGATTGATAAAGCAGAAGACCGCCGTCGTTTCGACGTAGCGATGAAG
AAAATTGGTCTGGAAACCGCGCGTTCCGGTATCGCACACACGATGGAAGAAGCGCTGGCGGTTGCCGCTGACGTG
GGCTTCCCGTGCAATTATTCGCCCATCCTTTACCATGGGCGGTAGCGGCGGCGGTATCGCTTATAACCGTGAAGAG
TTTGAAGAAATTTGCGCCCGCGGTCTGGATCTCTCTCCGACCAAGAGTTGCTGATTGATGAGTCGCTGATCGGC
TGGAAGA

200. *Pseudomonas aeruginosa* (SEQ ID NO. 200)

PAER

CTACATCGAGCCGATCAAGTGGGCCACCGTGGCCAAGATCATCGAGAAGGAACGCCCCGACGCGCTGCTGCCGAC
CATGGGCGGCCAGACCGCGCTGAACTGCGCCCTGGACCTGGAGCGCCACGGCGTGCTGGAGAAGTTCGGCGTGGA
GATGATCGGCGCCAATGCCGATACCATCGACAAGGCCGAGGACCGCTCGCGCTTCGACAAGGCGATGAAGGATAT
CGGCCTGGCCTGTCCGCGCTCGGGCATCGCCACAGCATGGAGGAGGCCTACGGCGTGCTCGAGCAGGTCCGGCTT
CCCCTGCATCATCCGTCCGTCCCTTACCATGGGCGGCACCGGCGGCGGTATCGCCTACAACCGTGAAGAGTTCGA
AGAGATCTGCGCCCGTGGCCTCGACCTGTCGCCGACCAACGAGCTGTTGATCGACGAGTCGCTGATCGGCTGGAA
AGA

201. *Escherichia coli* O157 :H7 (SEQ ID NO. 201)

ECO157

GCGACCTACATCGAGCCGATTCACTGGGAAGTGGTACGTAAGATTATTGAAAAAGAGCGCCCGGACGCGGTGCTG
CCAACCATGGGCGGTGAGACGGCGCTGAACTGCGCGCTGGAGCTGGAACGTCAGGGCGTGTTGGAAGAGTTCGGC
GTCACCATGATTGGTGCCACTGCCGATGCGATTGATAAAGCAGAAGACCGCCGTCGTTTCGACGTAGCGATGAAG
AAAATTGGTCTGGAAACCGCGCGTTCCGGTATCGCACATACGATGGAAGAAGCGCTGGCGGTTGCCGCTGACGTG
GGCTTCCCGTGCAATTATTCGCCCATCCTTTACCATGGGCGGTAGCGGCGGCGGTATCGCTTATAACCGCGAAGAG
TTTGAAGAAATTTGCGCCCGCGGTCTGGATCTCTCTCCGACCAAGAGTTGCTGATTGATGAGTCGCTGATCGGC
TGGAAGA

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202. *Salmonella typhimurium* (SEQ ID NO. 202) STPM

CCTACATCGAGCCGATTCACTGGGAAGTGGTGCGCAAAATCATTGAAAAAGAGCGTCCGGATGCGGTGCTGCCGA
CCATGGGCGGCCAGACCGCGCTGAACTGCGCGCTGGAGCTGGAGCGGCAGGGCGTGCTGGAAGAGTTCGGCGTCA
CCATGATTGGTGCGACCGCCGACGCCATTGATAAAGCCGAAGACCGTCGTCGCTTCGATATCGCGATGAAGAAAA
TTGGTCTCGACACCGCGCGTTCCGGTATCGCGCACACTATGGAAGAAGCGCTGGCGGTTGCCGCTGACGTGGGCT
TCCCGTGTCATCATCCGGCCTAGCTTTACCATGGGCGGCACCGGCGGCGGTATCGCTTACAACCGTGAAGAGTTCG
AAGAAATCTGCGAACGCGGTCTGGACCTCTCGCCAACCAACGAGCTGCTGATTGATGAATCGCTGATCGGCTGGA
AAGA

203. *Salmonella enterica hadar* (SEQ ID NO. 203) SHAD

TGATGCNCCTACATCGAGCCGATTCACTGGGAAGTGGTACGCAAAATCATCGAAAAAGAGCGTCCGGATGCGGTG
CTGCCGACCATGGGCGGCCAGACGGCGCTGAACTGCGCGCTGGAGCTGGAGCGGCAGGGCGTGCTGGAAGAGTTC
GGCGTCACCATGATTGGCGCCACCGCCGACGCCATTGATAAAGCCGAAGACCGTCGTCGCTTCGATATCGCGATG
AAGAAAATTGGTCTCGACACCGCGCGTTCCGGTATCGCGCACACTATGGAAGAAGCGCTGGCGGTTGCCGCTGAC
GTGGGCTTCCCGTGTCATCATCCGTCCGTCTTTACCATGGGCGGCACCGGCGGCGGTATCGCTTACAACCGTGAA
GAGTTCGAAGAAATCTGCGAACGCGGTCTGGACCTCTCGCCAACCAACGAGCTGCTGATTGATGAATCGCTGATC
GGCTGGAAAGA

204. *Salmonella enteritidis* (SEQ ID NO. 204) SENT

GGCTGATGCCCTACATCGAGCCGATTCACTGGGAAGTGGTACGCAAAATCATCGAAAAAGAGCGTCCGGATGCG
GTGCTGCCGACCATGGGCGGCCAGACGGCGCTGAACTGCGCGCTGGAGCTGGAGCGGCAGGGCGTGCTGGAAGAG
TTCGGCGTCACCATGATTGGCGCCACCGCCGACGCCATTGATAAAGCCGAAGACCGTCGTCGCTTCGATATCGCG
ATGAAGAAAATTGGTCTCGACACCGCGCGTTCCGGTATCGCGCACACTATGGAAGAAGCGCTGGCGGTTGCCGCT
GACGTGGGCTTCCCGTGTCATCATCCGTCCGTCTTTACCATGGGCGGCACCGGCGGCGGTATCGCTTACAACCGT
GAAGAGTTCGAAGAAATCTGCGAACGCGGTCTGGACCTCTCGCCAACCAACGAGCTGCTGATTGATGAATCGCTG
ATCGGCTGGAAAGA

205. *Salmonella enterica Brandenburg* (SEQ ID NO. 205) SBRA

TACATCGAGCCGATTCACTGGGAAGTGGTGCGCAAAATCATTGAAAAAGAGCGTCCGGATGCGGTGCTGCCGACC
ATGGGCGGCCAGACGGCGCTGAACTGCGCGCTGGAGCTGGAGCGGCAGGGCGTGCTCGAAGAGTTCGGCGTCACC
ATGATTGGCGCCACCGCCGACGCCATTGATAAAGCCGAAGACCGTCGTCGCTTCGATATCGCGATGAAGAAAATT
GGTCTCGACACCGCGCGTTCCGGTATCGCGCACACTATGGAAGAAGCGCTGGCGGTTGCCGCTGATGTGGGCTTC
CCGTGTCATCATCCGTCCGTCTTTACCATGGGCGGCACCGGTGGCGGTATCGCTTACAACCGTGAAGAGTTCGAA
GAAATCTGCGAACGCGGTCTGGACCTCTCGCCAACCAACGAGCTGCTGATTGATGAATCGCTGATCGGCTGGAAA
GA

206. *Salmonella enterica derby* (SEQ ID NO. 206) SDER

CTACATCGAGCCGATTCACTGGGAAGTGGTGCGCAAAATCATCGAAAAAGAGCGTCCGGATGCGGTGCTGCCGAC
CATGGGCGGCCAGACCGCGCTGAACTGCGCGCTGGAGCTGGAGCGGCAGGGCGTGCTCGAAGAGTTCGGCGTCAC
CATGATTGGCGCCACCGCCGACGCCATTGATAAAGCCGAAGACCGTCGTCGCTTCGATATCGCGATGAAGAAAAT

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CGGTCTCGACACCGCGCGTTCCGGTATCGCGCACACTATGGAAGAAGCGCTGGCGGTTGCCGCTGACGTGGGCTT
CCCGTGCATCATCCGTCCGTCTTTACCATGGGCGGCACCGGCGGCGGTATCGCTTACAACCGTGAAGAGTTCGA
AGAAATCTGCGAACGCGGTCTGGACCTCTCGCCAACCAACGAGCTGCTGATTGATGAATCGCTGATCGGCTGGAA
AGA

207. *Salmonella enterica virschow* (SEQ ID NO. 207) SVIR

CTACATCGAGCCGATTCACTGGGAAGTGGTGCGCAAAATCATTGAAAAAGAGCGTCCGGATGCAGTGCTGCCGAC
CATGGGCGGCCAGACGCGCTGAACTGTGCGCTGGAGCTGGAGCGGCAGGGCGTGCTGGAAGAGTTCCGGCGTCAC
CATGATTGGCGCCACCGCCGACGCCATTGATAAAGCCGAAGACCGTCGTCGCTTCGATATCGCGATGAAGAAAAT
TGGTCTCGACACCGCGCGTTCCGGTATCGCGCACACTATGGAAGAAGCGCTGGCGGTTGCCGCTGACGTGGGCTT
CCCGTGCATCATCCGTCCGTCTTTACCATGGGCGGCACCGGCGGCGGTATCGCTTACAACCGTGAAGAGTTCGA
AGAAATCTGCGAACGCGGTCTGGACCTCTCGCCAACCAACGAGCTGCTGATTGATGAATCGCTGATCGGCTGGAA
AGA

208. *Salmonella paratyphi B* (SEQ ID NO. 208) SPTB

CTACATCGAGCCGATTCACTGGGAAGTGGTGCGCAAAATCATTGAAAAAGAGCGTCCGGATGCAGTGCTGCCGAC
CATGGGCGGCCAGACCGCGCTGAACTGCGCGCTGGAGCTGGAGCGGCAGGGCGTGCTCGAAGAGTTCCGGCGTCAC
CATGATTGGCGCCACCGCCGACGCCATTGATAAAGCCGAAGACCGTCGTCGCTTCGATATCGCGATGAAGAAAAT
TGGTCTCGACACCGCGCGTTCCGGTATCGCGCACACTATGGAAGAAGCGCTGGCGGTTGCCGCTGACGTGGGCTT
CCCGTGCATCATCCGGCTAGCTTTACCATGGGCGGCACCGGCGGCGGTATCGCTTACAACCGTGAAGAGTTCGA
AGAAATCTGCGAACGCGGTCTGGACCTCTCGCCAACCAACGAGCTGCTGATTGATGAATCGCTGATCGGCTGGAA
AGA

209. *Proteus vulgaris* (SEQ ID NO. 209) PVUL

CGACAGTCATGACCGACCCTGAAATGGCGGATGCCACCTACATCGAGCCTATTCATTGGCAAGTCGTCAGAAAAA
TTATTGAAAAAGAGCGCCCTGATGCGATTTTGCCAACAATGGGGGGGCAAACGGCATTAAATTGCGCATTAGAAT
TAGAACGTCAAGGTGTGTTAGCTGAATTCGGTGTGACCATGATTGGTGCTACGGCTGATGCTATCGATAAAGCAG
AAGATAGACAACGCTTTGATAAAGCAATGAAAAAAATCGGCTTAGGCACAGCTCGCTCAGGTATTGCTCATAATC
TAGAAGAAGCTTTTGCCGTCGCTGAAGATGTGCGATTCCCTTGCATCATTCGTCCTTCATTTACTATGGGCGGCA
CGGGGGGCGGTATCGCTTATAACCGTGAAGAAATTTGAAGAAATTTGTACTCGTGGATTAGATTTATCACCGACTA
ACGAGTTATTGATTGATGAATCACTTATTGGTTGGAAAGAGTACGAGATGGAA

210. *Enterobacter aerogenes* (SEQ ID NO. 210) EAER

CGACACTCATGACCGACCCGGAAATGGCCGATGCGACCTATATCGAGCCGATTCACTGGGAAGTGGTGCCTAAAA
TTATCGAAAAAGAGCGTCCGGACGCGGTGCTGCCGACCATGGGCGGCCAGACCGCGCTGAACTGCGCGCTGGAGC
TGGAGCGTCAGGGCGTGCTGGCAGAGTTCGGCGTGACCATGATTGGTGCGACCGCCGATGCGATCGATAAAGCGG
AAGACCGCCGTCGCTTCGACGTGGCGATGAAGAAAATCGGTCTCGACACCGCGCGTTCGGGCATTGCGCACACCA
TGGAAGAAGCGCTGGCGGTGGCCGCTGAAGTTGGCTTCCCATGCATCATCCGTCCGTCTTTACTATGGGCGGCA
CCGGCGGCGGTATCGCCTATAACCGCGAAGAGTTCGAAGAAATCTGCGAACGCGGCCTGGATCTCTCTCCGACCA
ACGAACTGCTGATTGATGAATCGCTGATCGGCTGGAAGGAATACGAAATGGAA

211. *Burkholderia cepacia* (SEQ ID NO. 211) BCEP

CGACAGTCATGACCGATCCGGACCGCGACATCACAGCGACAGTGATGCGTGAACGAACTAGGCTAGTGAAATTTA
TCCGGCGCCGGATACGCGACCCGGACGATGCCGAGGACATCCTGCAGGATGTGTTTCACGAGTTCGTACAAGCGT
ATCGACTTCCAGCGCCCATTTGAACAGGTGAGCGCGTGGCTTTTCCGTGCCGCGCGCAACCGAATCGTCGACCGTT
TTCGCAAGAAGAAGGAGCAGCCGCTGGCCGACCTGTCGGAGGTCGACGATGACGCGAACAGCGAGTATCGCCTCG
ACCTCGCGCTACCGGCGCATGATGCCGGCCCCGAAGCACTCTACGCTCGCACGCTCGTGCTCAAGGCCTTGCAGG
ATGCGCTCGACGAGTTGCCGACGAATCAGCGTGACGTCTTTATCGCACACGAGCTGGAGGGTCAGTCATAAATGT
CGA

212. *Burkholderia mallei* (SEQ ID NO. 212)

GGCGTTGCGTGAGGAGGGCTACAAGGTCATCCTCGTCAACAGCAACCCGGCGACGATCATGACCGATCCGAACAC
GGCGGACGTCACGTACATCGAGCCGATCACGTGGGAAGTCGTCGAGCGCATCATCGCGAAGGAGCGCCCCGACGC
GATCCTGCCGACGATGGGCGGCCAGACCGCGCTGAACTGCGCGCTCGACCTGTTCCACCACGGCGTGCTCGAGAA
GTACGGCGTCGAGCTGATCGGCGCGTCGCCGGAGGCGATCGACAAGGCCGAAGACCGCCAGAAGTTCAAGGACGC
GATGACGAAGATCGGCCTCGGCTCGGCGAAGTCCGGCATCGCGCACTCGATGGAAGAGGCGCTGAAGGTGCACGC
GGACATCGCGGCGGCGACGGGCGGCAGCGGCTACCCGGTCGTGATCCGCCCGTCGTTACGCTCGGCGGCTCGGG
CGGCGGCATCGCGTACAACCGCGAGGAGTTCGAGGAGATCTGCAAGCGCGGCCTCGATCTGTGCGCGACGCGCGA
GCTGCTGATCGAGGAATCGCTGCTCGGCTGGAAGGAGTACGAGATGGAGGTCGTGCGCGATCGCGCCGACAACTG
CATCATCGTCTGCTCG

213. *Burkholderia pseudomallei* (SEQ ID NO. 213)

GGCGTTGCGTGAGGAGGGCTACAAGGTCATCCTCGTCAACAGCAACCCGGCGACGATCATGACCGATCCGAACAC
GGCGGACGTCACGTACATCGAGCCGATCACGTGGGAAGTCGTCGAGCGCATCATCGCGAAGGAGCGCCCCGACGC
GATCCTGCCGACGATGGGCGGCCAAACCGCGCTGAACTGCGCGCTCGACCTGTTCCACCACGGCGTGCTCGAGAA
GTACGGCGTCGAGCTGATCGGCGCGTCGCCGGAGGCGATCGACAAGGCCGAAGACCGCCAGAAGTTCAAGGACGC
GATGACGAAGATCGGCCTCGGCTCGGCGAAGTCCGGCATCGCGCACTCGATGGAAGAGGCGCTGAAGGTGCACGC
GGACATCGCGGCGGCGACGGGCGGCAGCGGCTACCCGGTCGTGATCCGCCCGTCGTTACGCTCGGCGGCTCGGG
CGGCGGCATCGCGTACAACCGCGAGGAGTTCGAGGAGATCTGCAAGCGCGGCCTCGATCTGTGCGCGACGCGCGA
GCTGCTGATCGAGGAATCGCTGCTCGGCTGGAAGGAGTACGAGATGGAGGTCGTGCGCGATCGCGCCGACAACTG
CATCATCGTCTGCTCG

214. *Legionella pneumophila* (SEQ ID NO. 214)

CGACACTTATGACTGATCCTGAGCTTGCTGATGCCACCTATATAGAGCCTGTTCAATGGAAGAAGTGGCTCGTA
TTATCGAAATAGAGAGGCCAGATGCTCTTTTACCGACGATGGGAGGACAAACAGCCTTAAACTGCGCCTTGGACT
TGTAAGAGAAGGGGTATTAGCCAAGTACTCTGTTGAAATGATAGGAGCGACGCGTGAAGCCATAGACAGGGCGG
AAGATAGAGAAAAATTTGCCAGCTGATGATTAATAATCGGATTGGATATGCCAAGGTCGACGATTGCTCATAGCC
TGGAAGAAGCAATTCAAGTACAAGCCCGTTTAGGCTTTCCTGCCATCATCAGGCCTTCATTTACCATGGGTGGTA
GTGGAGGCGGTATTGCCTATAATCGTGAAGAATTTGAAGAAATTTGCATTAGAGGATTGGAGTTGTGCGCAACTC
ACGAGCTTTTGATTGATGAATCGGTTCTGGGTTGGAAAGAATATGAAATGGA

215. *Citrobacter freundii* (SEQ ID NO. 215)

CGACACTTATGACTGATCCGGAAATGGCCGATGCCACCTACATCGAGCCGATTCACTGGGAAGTGGTACGCAAAA
TCATTGAGAAAGAGCGCCCGGATGCGGTGCTGCCAACCATGGGCGGTGAGACGGCGCTGAACTGTGCGCTGGAGC
TGGAACGCCAGGGCGTACTGGCTGAATTCGGCGTGACCATGATTGGCGCAACGGCGGATGCCATTGATAAAGCGG
AAGACCGTCGTCGCTTTGATATCGCGATGAAGAAAATTGGTCTCGACACCGCGCGCTCTGGCATCGCTCACACCA
TGGAAGAAGCGCTGGCGGTTGCTGCTGACGTGGGCTTCCCGTGCATCATCCGACCGAGCTTCACCATGGGCGGCA
CCGGCGGCGGTATCGCTTATAACCGTGAAGAGTTCGAAGAGATTTGTGAACGCGGTCTGGACCTTTCCCCAACCA
ACGAGCTGCTGATTGATGAATCGCTGATTGGCTGGAAAGAGTACGAAATGGA

216. *Acinetobacter baumanii* (SEQ ID NO. 216) ABAU

TCCATTTCTACTCTTTCCAGCCAATTAAAGATTCCCTCGATCAATAATTGGTGAGTAGGAGAGAGGTGCAAACCA
CGTTCACAAATCTCTAGGAATTCTTCGCGGTTATATGCAATACCACCGCCTGAACCACCCATAGTGAATGACGGA
CGGATAATTACTGGGAAACCAAAGCGAGATTGAATTTCCAATGCTTCTTCCATTGTTTCAGCAATGGCAGCTTTT
GGACATTCCAAGCCGATTTTGCGCATTGCTTCATCAAACAATTTACGGTCTTCAGCTTTTTCAATTGCTTCTTTT
GTTGCACCAATAAGTTCTACGCCGTATTTTTCTAATACACCATTTTCATCAAGTGCAAGTGCGCAGTTAAGAGCA
GTTTGTCCACCCATAGTAGGGAGTACTGCATCTGGGCGCTCTTTTTCAATGATTTGAGCAACAGTTTGCCAAGTA
ATTGGCTCAATATAAGTTGCATCAGCCATTGAAGGGTCAGTCATAAGTGTCTGA

217. *Serratia marcescens* (SEQ ID NO. 217) SMAR

CGACAGTTATGACCGACCCGGAGATGGCCGACGCGACCTATATTGAGCCGATCCACTGGGAAGTGGTGCGCAAGA
TCATCGAAAAAGAGCGCCCGGATGCGGTGCTGCCGACCATGGGCGGCCAGACGGCGCTGAACTGCGCGCTGGAGC
TGAGAGCGCCAGGGCGTGTGGCCGAGTTCGGCGTTACCATGATCGGCGCCACCGCCGATGCGATTGACAAGGCCG
AAGACCGTCGCCGCTTCGATGTGGCGATGAAGAAAATCGGTCTGGATACCGCGCGTTCGGGCATCGCGCACACCA
TGGAAGAAGCGCTGGCGGTAGCCGCTGACGTGGGCTTCCCGTGCATCATCCGCCCTTCTTTTACCATGGGCGGCA
CCGGCGGCGGCATCGCCTACAACCGCGAAGAGTTCGAAGAGATCTGCGAACGCGGTCTGGACCTGTGCGCGACCA
ACGAGCTGCTGATCGATGAATCGCTGATCGGTTGGAAAGAATACGAGATGGAA

218. *Pseudomonas putida* (SEQ ID NO. 218) PPUT

CGACACTCATGACCGACCCCGGATTTGAGTGACCACCATGCCAAAACGTACAGACATCAAAGCATCCTGATTCT
CGGTGCCGCGCCGATCGTGATCGGCCAGGCCTGTGAATTGCACTACTCCGGCGCCAGGCCTGCAAGGCCCTGCG
CGAGGAAGGTTTCCGCGTCATCCTGGTGAATCCAACCCAGCCACCATCATGACCGACCCGGCCATGGCCGACGC
CACCTACATCGAGCCGATCAAGTGGCAGTCGGTGGCCAAGATCATCGAGAAAGAGCGCCCGACGCCGTTTTGCC
GACCATGGGTGGCCAGACCGCCCTGAACTGCGCCCTGGACCTGGAGCGCCACGGCGTTCTGGAGAAGTTTGGCGT
AGAGATGATCGGTGCCAACGCCGATACCATCGACAAGGCTGAAGACCGCTCGCGCTTCGACAAGGCCATGAAAGA
CATCGGCCTGGAATGCCGCGCTCGGGTATCGCCACAGCATGGAAGAGGCCAATGCGGTCTCGAAAAGCTCGG
CTTCCCGTGCATCATTCGCCCGTCTTCACCATGGGGTGGCACCGGCGGTGGTATCGCTTACAACCGTGAAGAAT
TCGAAGAAAT

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219. *Morganella morganii* (SEQ ID NO. 219) MMOR

CGAAAAAGAGCGCCCGGATGCCGTTCTGCCGACCATGGGCGGACAAACCGCGCTGAACTGTGCGCTGGATCTGGA
ACGTCACGGCGTGCTGGCAGAGTTCGGCGTCGAAATGATTGGCGCGACAGCAGATGCGATTGATAAAGCCGAAGA
TCGCCGCCGTTTCGATATCGCGATGAAAAAATCGGTCTGGATACAGCGCGTTCCGGTATCGCACACACCATGGA
AGAAGCGTTTGCGGTCGCCGATGATGTCGGTTTCCCGTGCATTATCCGCCCGTCATTACCATGGGCGGCACCGG
CGGCGGTATTGCGTATAACCGTGAAGAATTGAGGAAATCTGTACCCGCGGCCTGGATCTCTCCCTGACCAACGA
ACTGCTGATTGATGAATCACTGATTGGCTGGAAAGAGTACGAAATGGAAAGGGCGAATTCCAGCACACTGGCGGC
CGTTACTAGTGGATCA

220. *Klebsiella oxytoca* (SEQ ID NO. 220) KOXY

CGACAGTTATGACTGACCCGGAAATGGCCGATGCCACCTACATCGAGCCGATTCACTGGGAAGTGGTGCGCAAGA
TCATTGAGAAAGAGCGTCCGGATGCGGTTCTGCCGACCATGGGCGGCCAGACGGCGCTGAACTGCGCGCTGGAGC
TGGAGCGTCAGGGCGTGCTGGCCGAGTTCGGCGTGACCATGATTGGCGCGACCGCCGACGCGATTGATAAAGCCG
AAGACCGCCGCCGTTTCGACGTGGCGATGAAGAAAATCGGTCTCGATACCGCGCGTTCCGGTATCGCGCATACCA
TGGAAGAAGCGCTGGCGGTTGCCGCTGAAGTTGGCTTCCCGTGCATCATCCGTCCGTCTTTACGATGGGCGGCA
CCGGCGGCGGTATCGCCTACAACCGCGAAGAGTTGGAAGAGATCTGCGAACGCGGTCTGGATCTCTCGCCGACCA
ACGAGCTGCTGATTGATGAATCGCTGATCGGCTGGAAAGAATACGAAATGGAA

221. *Moraxella catarrhalis* (SEQ ID NO. 221) MCAT

CCACATTATGACTGACCCGTCCATGGCTGATGCCACTTATATTGAACCGATTACCTGGCAGACGGTAGAGCAAAT
CATTGCCAAAGAGCGTCCTGATGCCATTTTGCCAACCATGGGTGGACAAACGGCACTTAACCTGTGCGCTTGACCT
TGACAAACATGGCGTGCTTGCCAAATATGGCTGTGAGCTGATTGGGGCGACCAAAGAAGCCATTGAAAAAGCCGA
AGACCGTGAACCTGTTTGATAAAGCCATGAAAAAATCGGTCTGGAATGCCCCAAAGCAGAAATTGCACAGAGCAT
GGATGATGCTTTTGCCATTCAAGCTAAGGTTGGTTTTCCGTGCATTATCCGCCCATCATTCACCATGGGGGGTTC
TGGGGGTGGCATTGCTTATAACCGTGAGGAGTTTATTGAGATTTGTGAGCGTGGGTTTGAATTATCACCCACCCA
CCAGCTGCTCATTGATGAGAGTTTAATCGGNTGGAAAGAGTANGAAATGGAA

222. *Brucella melitensis* biovar 1 (SEQ ID NO. 222) BMEL1

TCTTCGATCAGAACTTCGGTCGTCGGCGAAGCGTCGAGGCCGCGTTTCGATAATCTCGAAGAATTCTTGACGGTTA
TAGGCAATGCCGCCGCCGGTGCCGCCGAGCGTGAAGGAGGGCGGATGATCGCGGCAGGCCAACCACGTCGAGC
GCCTGTGCTGCCTTTGCAAGCGCATGGCTCATATAGCGCTGCTTGCGCTCCACTTCGCCGAGCTGCCATTCCGGTT
TCAAGCTTGTCGAGCGCCTTGTCAGTTCGTCGCCGAGAATTGCGCCTTCACCTCCGCGCGCTTGACCTCGTGG
CGCTTGCGGTCTCATCCTTGATTTCAGTCGCATTGGCGAACATCGAGCCCGGCGTGTGAGGCCGATCTTCTTC
ATGGCTTCGCGGAAGAGCGCGCGGTCTTCGGCCTTGTCGATAGCTTCGGCCTTGGCGCCGATCATCTCGACGTTA
TAACGTTCAAGCACGCCCATGCGGCGCAAGGAAAGCGCGGTGTTGAGCGCGGTCTGTCCGCCCATCGTCGGCAGG
ATCGCGTCCGGGCGCTCCTTGCGGATGATCTTGGCGACGACTTCGGGCGTGATCGGCTCGATATAGGTTGCATCC
GCCAGATCGGGATCAGTATAAAAT

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223. *Brucella melitensis* biovar 2 (SEQ ID NO. 223) BMEL2

TTCTTCGATCAGAACTTCGGTCGTCGGCGAAGCGTCGAGGCCGCGTTCGATAATCTCGAAGAATTCCTGACGGTT
ATAGGCAATGCCGCCGCCGGTGCCGCCGAGCGTGAAGGAGGGGCGGATGATCGCGGGCAGGCCAACACGTCGAG
CGCCTGTGCTGCCTTTGCAAGCGCATGGCTCATATAGCGCTGCTTGCGCTCCACTTCGCCGAGCTGCCATTTCGGT
TTCAAGCTTGTGAGCGCCTTGTCAGTTCGTCGCCGAGAATTGCGCCTTCACCTCCGCGCGCTTGACCTCGTG
GCGCTTGCGGTCCTCATCCTTGATTTAGTCGCATTGGCGAACATCGAGCCCGGCGTGTCGAGGCCGATCTTCTT
CATGGCTTCGCGGAAGAGCGCGCGGTCTTCGGCCTTGTCGATAGCTTCGGCCTTGCGCCGATCATCTCGACGTT
ATAACGTTCAAGCACGCCCATGCGGCGCAAGGAAAGCGCGGTGTTGAGCGCGGTCTGTCCGCCCATCGTCGGCAG
GATCGCGTCCGGGCGCTCCTTGGCGATGATCTTGGCGACGACTTCGGGCGTGATCGGCTCGATATAGGTTGCATC
CGCCAGATCGGGATCAGT

224. *Brucella abortus* biovar 1 (SEQ ID NO. 224) BAB01

TCTTCGATCAGTAACTTCGGTCGTCGGCGAAGCGTCGAGGCCGCGTTCGATAATCTCGAAGAATTCCTGACGGTT
ATAGGCAATGCCGCCGCCGGTGCCGCCGAGCGTGAAGGAGGGGCGGATGATCGCGGGCAGGCCAACACGTCGAG
CGCCTGTGCTGCCTTTGCAAGCGCATGGCTCATATAGCGCTGCTTGCGCTCCACTTCGCCGAGCTGCCATTTCGGT
TTCAAGCTTGTGAGCGCCTTGTCAGTTCGTCGCCGAGAATTGCGCCTTCACCTCCGCGCGCTTGACCTCTTG
GCGCTTGCGGTCCTCATCCTTGATTTAGTCGCATTGGCGAACATCGAGCCCGGCGTGTCGAGGCCGATCTTCTT
CATGGCTTCGCGGAAGAGCGCGCGGTCTTCGGCCTTGTCGATAGCTTCGGCCTTGCGCCGATCATCTCGACGTT
ATAACGTTCAAGCACGCCCATGCGGCGCAAGGAAAGCGCGGTGTTGAGCGCGGTCTGTCCGCCCATCGTCGGCAG
GATCGCGTCCGGGCGCTCCTTGGCGATGATCTTGGCGACGACTTCGGGCGTGATCGGCTCGATATAGGTTGCATC
CGCCAGATCGGGATCAG

225. *Brucella abortus* biovar 2 (SEQ ID NO. 225) BAB02

CGCCTCTTCGATCAGTAACTTCGGTCGTCCGGCGAAGCGTCGAGGCCGCGTTCGATAATCTCGAAGAATTCCTGA
CGGTTATAGGCAATGCCGCCGCCGGTGCCGCCGAGCGTGAAGGAGGGGCGGATGATCGCGGGCAGGCCAACACG
TCGAGCGCCTGTGCTGCCTTTGCAAGCGCATGGCTCATATAGCGCTGCTTGCGCTCCACTTCGCCGAGCTGCCAT
TCGGTTTCAAGCTTGTGAGCGCCTTGTCAGTTCGTCGCCGAGAATTGCGCCTTCACCTCCGCGCGCTTGACC
TCTTGGCGCTTGCGGTCTCATCCTTGATTTAGTCGCATTGGCGAACATCGAGCCCGGCGTGTCGAGGCCGATC
TTCTTCATGGCTTCGCGGAAGAGCGCGCGGTCTTCGGCCTTGTCGATAGCTTCGGCCTTGCGCGCGATCATCTCG
ACGTTATAACGTTCAAGCACGCCCATGCGGCGCAAGGAAAGCGCGGTGTTGAGCGCGGTCTGTCCGCCCATCGTC
GGCAGGATCGCGTCCGGGCGCTCCTTGGCGATGATCTTGGCGACGACTTCGGGCGTGATCGGCTCGATATAGGTT
GCATCCGCCAGATCGGGATCAGTATAAATTAGT

226. *Brucella suis* biovar 1 (SEQ ID NO. 226) BSUI1

TTAGANCGCCTCTTCGATCAGAACTTCGGTCGTCGGCGAAGCGTCGAGGCCGCGTTCGATAATCTCGAAGAATTC
CTGACGGTTATAGGCAATGCCGCCGCCGGTGCCGCCGAGCGTGAAGGAGGGGCGGATGATCGCGGGCAGGCCAAC
CACGTCGAGCGCCTGCGCTGCCTTTGCAAGCGCATGGCTCATATAGCGCTGCTTGCGCTCCACTTCGCCGAGCTG
CCATTTCGGTTTCAAGCTTGTGAGCGCCTTGTCAGTTCGTCGCCGAGAATTGCGCCTTCACCTCCGCGCGCTT
GGCCTCGTGGCGCTTGCGGTCTCATCCTTGATTTAGTCGCATTGGCGAGCATCGAGCCCGGCGTGTCGAGGCC
GATCTTCTTCATGGCTTCGCGGAAGAGCGCGCGGTCTTCGGCCTTGTCGATAGCTTCGGCCTTGCGCGCGATCAT

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CTCGACGTTATAACGTTCAAGCACGCCCATGCGGCGCAAGGAAAGCGCGGTGTTGAGCGCGGTCTGTCCGCCCAT
CGTCGGCAGGATCGCGTCCGGGCGCTCCTTGCGGATGATCTTGGCGACGACTTCCGGCGTGATCGGCTCGATATA
GGTTGCATCCGCCAGATCGGGATCAGTATAAA

227. *Brucella suis* biovar 3 (SEQ ID NO. 227) BSUI3

CCCGCATTCTTCGATCAGTAACTTCGGTCGTCGGCGAAGCGTCGAGGCCGCGTTCGATAATCTCGAAGAATTCCT
GACGGTTATAGGCAATGCCGCCGCCGGTGCCGCCGAGCGTGAAGGAGGGGCGGATGATCGCGGGCAGGCCAACCA
CGTCGAGCGCCTGCGCTGCCTTTGCAAGCGCATGGCTCATATAGCGCTGCTTGCGCTCCACTTCGCCGAGCTGCC
ATTCGGTTTCAAGCTTGTCGAGCGCCTTGTCAGTTTCGTCGCCGAGAATTGCGCCTTCACCTCCGCGCGCTTGG
CCTCGTGGCGCTTGCGGTCTCATCCTTGATTTAGTCGCATTGGCGAGCATCGAGCCCCGGCGTGTGAGGCCGA
TCTTCTTCATGGCTTCGCGGAAGAGCGCGCGGTCTTCGGCCTTGTCGATAGCTTCGGCCTTGCGCGCCGATCATCT
CGACGTTATAACGTTCAAGCACGCCCATGCGGCGCAAGGAAAGCGCGGTGTTGAGCGCGGTCTGTCCGCCCATCG
TCGGCAGGATCGCGTCCGGGCGCTCCTTGCGGATGATCTTGGCGACGACTTCCGGCGTGATCGGCTCGATATAGG
TTGCATCCGCCAGATCGGGATCAGTATAAAATTAGT

228. *Brucella canis* (SEQ ID NO. 228) BCAN

TTCTTCGATAGAACTTCGGTCGTCGGCGAAGCGTCGAGGCCGCGTTCGATAATCTCGAAGAATTCCTGACGGTTA
TAGGCAATGCCGCCGCCGGTGCCGCCGAGCGTGAAGGAGGGGCGGATGATCGCGGGCAGGCCAACACGTCGAGC
GCCTGCGCTGCCTTTGCAAGCGCATGGCTCATATAGCGCTGCTTGCGCTCCACTTCGCCGAGCTGCCATTTCGGTT
TCAAGCTTGTCGAGCGCCTTGTCAGTTTCGTCGCCGAGAATTGCGCCTTCACCTCCGCGCGCTTGCCCTCGTGG
CGCTTGCGGTCTCATCCTTGATTTAGTCGCATTGGCGAGCATCGAGCCCCGGCGTGTGAGGCCGATCTTCTTC
ATGGCTTCGCGGAAGAGCGCGCGGTCTTCGGCCTTGTCGATAGCTTCGGCCTTGCGCGCCGATCATCTCGACGTTA
TAACGTTCAAGCACGCCCATGCGGCGCAAGGAAAGCGCGGTGTTGAGCGCGGTCTGTCCGCCCATCGTCGGCAGG
ATCGCGTCCGGGCGCTCCTTGCGGATGATCTTGGCGACGACTTCCGGCGTGATCGGCTCGATATAGGTTGCATCC
GCCAGATCGGGATCAGTATAAAAA

229. *Brucella ovis* 69/290 (SEQ ID NO. 229) BOVI

ACCGCTTCTTCGATCAGTAACTTCGGTCGTCGGCGAAGCGTCGAGGCCGCGTTCGATAATCTCGAAGAATTCCTG
ACGGTTATAGGCAATGCCGCCGCCGGTGCCGCCGAGCGTGAAGGAGGGGCGGATGATCGCGGGCAGGCCAACAC
GTCGAGCGCCTGCGCTGCCTTTGCAAGCGCATGGCTCATATAGCGCTGCTTGCGCTCCACTTCGCCGAGCTGCCA
TTCGGTTTCAAGCTTGTCGAGCGCCTTGTCAGTTTCGTCGCCGAGAATTGCGCCTTCACCTCCGCGCGCTTGGC
CTCGTGGCGCTTGCGGTCTCATCCTTGATTTAGTCGCATTGGCGAGCATCGAGCCCCGGCGTGTGAGGCCGAT
CTTCTTCATGGCTTCGCGGAAGAGCGCGCGGTCTTCGGCCTTGTCGATAGCTTCGGCCTTGCGCGCCGATCATCTC
GACGTTATAACGTTCAAGCACGCCCATGCGGCGCAAGGAAAGCGCGGTGTTGAGCGCGGTCTGTCCGCCCATCGT
CGGCAGGATCGCGTCCGGGCGCTCCTTGCGGATGATCTTGGCGACGACTTCCGGCGTGATCGGCTCGATATAGGT
TGCATCCGCCAGATCGGGATCAGTATAAAATT

230. *Francisella tularensis* strain 4/j7 (SEQ ID NO. 230)

CCNACTATTATGACTGATCCANCAACCGCAGATAAAATCTTTATCGAGCCAATTACGGTTGAGAGTGTTGGTAAA
ATTATCGCTAGAGAAAGACCAGATGCAATCTTACCTACAGTAGGTGGACAAACTGCGCTTAAGTGTGCTTTAGCA

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TTAGACAAAGCTGGTATTTTAGAAAAATATAATGTCGAAATGCTTGGTGCAAAAGCTGACTCTATTGATAAGGCA
GAAAAATAGAGAAAGATTTAACAAAGCCATGGCAAAAATTGGCTTAGAGGTTCTTAGAAATGTTGTAGTGCAATCG
ATGGAGCAAGCTTATAAAGCTCTAGAAGATATCGGACTACCGGCTATTATCAGACCATCATTTACACTTGGTGGT
AGCGGTGGTGGTATCGCTTATACAAAAGAAGAGTTTGAAAAAATTGTCAAAAATGGTCTAAGCCTATCACCAACA
AATGAAGTACTAATAGAGAGGCACCCTAANAT

231. *Francisella tularensis* strain sva/t7 (SEQ ID NO.231)

ACGAANTAGACTGATCCAACAACCGCAGATAAAATCTTTATCGAGCCAATTACGGTTGAGAGTGTTGGTAAATTT
ATCGCTAGAGAAAGACCAGATGCAATCTTACCTACAGTAGGTGGACAACTGCGCTTAAGTGTGCTTTAGCATT
GACAAAGCTGGTATTTTAGAAAAATATAATGTCGAAATGCTTGGTGCAAAAGCTGACTCTATTGATAAGGCAGAA
AATAGAGAAAAATTTAACAAAGCCATGGCAAAAATTGGCTTAGAGGTTCTTAGAAATGTTGTAGTGCAATCGATG
GAGCAAGCTTATAAAGCTCTAGAAGATATCGGACTACCGGCTATTATCAGACCATCATTTACACTTGGTGGTAGC
GGTGGTGGTATCGCTTATACAAAAGAAGAGTTTGAAAAAATTGTCAAAAATGGTCTAAGCCTATCACCAACAAAT
GAAGTACTAATAGATGAGNCANCTNAANC

232. *Acinetobacter calcoaceticus* (SEQ ID NO. 232) ACAL

CGACAGTTATGACTGATCCTTCAATGGCTGATGCAACTTATATTGAGCCGATTACTTGGCAAACAGTTGCACAGA
TTATTGAAAAAGAACGTCCAGATGCAGTATTGCCAACTATGGGTGGTCAAAGTGCATTGAACTGTGCCCTCGCAC
TTGATGAGCACGGCGTTCTTGCTAAATATAATGTTGAATTAATTGGTGCAAGCAAAGAAGCGATTGAGAAAGCCG
AAGATCGTAACTCTTCGATATCGCTATGCGCAAAATTGGCTTGAATGTCCAAAAGCTGCCATTGCTGAAACAA
TGGAAGAAGCTTTAACAAATCCAGTCGCGCTTTGGTTTTCTGTAAATTATTCGTCCATCATTTACAATGGGTGGTT
CGGGCGGTGGCATTGCATATAACCGCGAAGAATTCCTTGAAATTTGTGAACGTGGTTTTGACCTCTCTCCTACTC
ACCAGTTATTGATCGATGAATCTTTAATTGGCTGGAAAGAATACGAGATGGAA

233. *Mycobacterium tuberculosis* (SEQ ID NO. 233)

GGTGCTGCGCGCCGAGGGCTTGCAAGTCAAGCTGTAATCCGGCCACCATCATGACCGACCCGGAGTT
CGCCGACCACACCTACGTAGAGCCCATACCCCGGCGTTTCGTGGAGCGGGTTATCGCCCAACAGGCCGAGCGGGG
CAACAAGATCGACGCCCTGCTGGCGACCCTGGGTGGGCAGACCGCGCTGAACACCGCGGTTCGCGCTGTACGAGAG
CGGGGTGCTGGAAAAGTACGGCGTGGAATCATCGGCGCCGATTTTCGACGCCATCCAGCGCGGCGAGGACCGGCA
GCGGTTCAAGGACATCGTCGCCAAGGCCGGTGGCGAATCCGCCCGGAGCCGAGTGTGTTTCACCATGGCCGAAGT
GCGTGAGACGGTCGCCGAGCTCGGCCTGCCGGTGGTGGTGCGGCCGAGCTTCACCATGGGCGGGCTGGGTTCGGG
GATAGCGTACTCCACCGACGAGGTCGACCGGATGGCCGGCGCCGGGCTGGCGGCCTCGCCACGCGCAACGTGCT
CATCGAGGAATCGATTTACGGCTGGAAGGAATTCGAACTCGAGCTGATGCGCGACGGCCACGACAATGTGGTGGT
GGTGTGCTCGATCGAAA

234. *Mycobacterium bovis* subspecies *bovis* (SEQ ID NO. 234)

GGTGCTGCGCGCCGAGGGCTTGCAAGTCAAGCTGTAATCCGGCCACCATCATGACCGACCCGGAGTT
CGCCGACCACACCTACGTAGAGCCCATACCCCGGCGTTTCGTGGAGCGGGTTATCGCCCAACAGGCCGAGCGGGG
CAACAAGATCGACGCCCTGCTGGCGACCCTGGGTGGGCAGACCGCGCTGAACACCGCGGTTCGCGCTGTACGAGAG
CGGGGTGCTGGAAAAGTACGGCGTGGAATCATCGGCGCCGATTTTCGACGCCATCCAGCGCGGCGAGGACCGGCA

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GCGGTTCAAGGACATCGTCGCCAAGGCCGGTGGCGAATCCGCCCGGAGCCGAGTGTGTTTCACCATGGCCGAAGT
GCGTGAGACGGTCGCCGAGCTCGGCCTGCCGGTGGTGGTGCGGCCGAGCTTCACCATGGGCGGGCTGGGTTTCGGG
GATAGCGTACTCCACCGACGAGGTGACCGGATGGCCGGCGCCGGGCTGGCGGCCTCGCCCAGCGCCAACGTGCT
CATCGAGGAATCGATTTACGGCTGGAAGGAATTCGAACTCGAGCTGATGCGCGACGGCCACGACAACGTGGTGGT
GGTGTGCTCGATCGAAA

235. *Mycobacterium avium subspecies paratuberculosis*
(SEQ ID NO. 235)

GGTGCTCAAGGCCGAGGGCCTGCAGGTGAGCCTGGTCAACTCCAACCCGGCCACCATCATGACCGATCCGGAGTA
CGCCGACCACACCTACGTGAGCCCATCACGCCGGCCTTCGTGCAACGGGTGATCGCGCAGCAGGCCGAGCGGGG
CAACAAGATCGACGCGCTGCTGGCCACCCTGGGCGGGCAGACCGCGCTGAACACCGCCGTCGCGCTGTACGAGAA
CGGGGCGCTGGACCGCTACGGGGTGGAACTGATCGGCGCCGACTTCGACGCCATCCAGCGCGGCGAGGACCGGCA
GCGGTTCAAGGACATCGTCGCCAAGGTGCGCGGTGAATCCGCCCGCAGCCGAGTGTGTTTCACCATGGACGAGGT
GCGCGAGACCGTCGCCGAACCTGGGCCTGCCGGTGGTGGTGCGGCCGAGCTTCACCATGGGCGGCCTGGGCTCGGG
GATGGCGCGCTCCGTGAGGAGGTGACCGGATGGCCGGCGCCGGGCTGGCCGAAAGCCCCAGCGCCAACGTGCT
GATCGAGGAATCCATCTACGGCTGGAAGGAATTCGAACTCGAGCTGATGCGCGACGGCAACGACAACGTGCTCGT
GGTGTGCTCGATCGA

236. *Mycobacterium leprae* (SEQ ID NO. 236)

CAAGTGAGTCTGGTCAACTCTAACCCGGCCACCATCATGACCGATCCGGAGTTCGCCGACCACACCTATGTCGAG
CCGATTACGCCGGCCTTCGTGGAGCGGGTGATTGTTTCAGCAGGCCGAGCGTGGCAACAGGATTGACGCTTTGCTA
GCCACCTTAGGTGGGCGAGACCGCGCTCAACACAGCGGTAGCGCTGTACGAAAACGGAGTGTTGGAGCGCTATGGC
GTCGAGCTCATCGGTGCTGATTTTCGAGGCTATCCAGCGTGGTGAGGACCGGCAGCGATTCAAAGATCTCGTCGCT
AAGGTTGGTGGTGAATCCGCTCGCAGTAAAGTGTGTTTCACCATGGATGAGGTGCGTGAAACAGTCGAGGATCTT
GGCCTTCGGTGGTGGTGCGGCCAAGTTTCACGATGGGCGGATTGGGTTCCGGGCATGGCTCACTCCGACGAGGAG
GTTGGCCGATGGCCGGCGCCGGGCTGGTAGCTTCACCTAGTGCCAACGTGCTGATCGAGGAATCGGTCTATGGT
TGGAAGGAATTCGAACTCGAGCTAATGCGCGATGGACACGACAGCGTCGTGGTGGTGTGCTCGATCGAGAACGTT

237. *Nocardia farcinica* (SEQ ID NO. 237)

GGTGCTCAAGTCCGAGGGCCTGCGCGTGTGCTGGTGAACCTCGAACCCGGCCACGATCATGACCGATCCCGAGTT
CGCCGACGCCACCTACGTGAGCCGATACCCCCGAATTCGTGAGAAAGGTCATCGCCAAGGAGCGCCCCGACGC
GATCCTGGCGACCTCGGCGGGCAGACCGCGCTCAACACCGCGGTGCGCGTGCACGAGCGCGGCGTGCTGGAGAA
GTACGGCGTCGAACTGATCGGCGCCGACTTCGACGCCATCCAGCGCGGTGAGGACCGGCAGAAGTTCAAGGACAT
CGTCGCCAAGGTCGGCGGTGAGAGCGCCGCTCGCGGGTCTGCTTCACCATGGACGAGGTCCGCGAGACCGTCGC
CGAACTGGGCTTCCCGGTGCTCGTGCGGCCCTCGTTACCATGGGCGGGCTCGGCTCGGGCATGGCCTACAACGA
CGAGGACCTGGACCGGATCGCCGGTGGCGGCCTGGCCGCCTCGCCGACCGCCAACGTCTGATCGAGGAGTCCAT
CCTCGGCTGGAAGGAATACGAGCTCGAGCTCATGCGCGACGGCCGCGACAACGTGTTGGTGGTCTGCTCCATCGA
GAACGTGACCCGATGGG

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238. *Streptomyces coelicolor* (SEQ ID NO. 238)

CCGGCGACGATCATGACCGACCCGGAGATCGCCGACGCCACCTACGTCGAGCCGATCACCCCGAGTTCGTCGAG
AAGATCATCGCCAAGGAGCGCCCCGACGCCCTCCTGCCCACGCTCGGCGGCCAGACGGCCCTGAACACCGCGATC
TCCCTGCACGGCAACGGCGTCCTGGAGAAGTACGGCGTCGAACTGATCGGCGCCAATGTGGAGGCCATCAACAAG
GGCGAGGACCGCGACCTGTTCAAGGAGGTCGTCGAGGAGGTCCGCAAGAAGATCGGCCACGGCGAGTCCGCCCGG
TCCTACATCTGCCACTCCATGGACGACGTCCTCAAGGGCGTCGACGCGCTCGGCGGCTACCCCGTCGTCGTCCGC
CCCTCCTTCACCATGGGCGGCGCCGGCTCCGGCTTCGCCCACGACGAGGACGAAC'TGCGCCGGATCGCCGGACAG
GGCCTCACCTCTCGCCGACCACCGAGGTGCTCCTGGAGGAGTCCATCCTCGGCTGGAAGGAGTACGAGCTGGAG

239. *Streptomyces avermitilis* (SEQ ID NO. 239)

ATCCTGCGCGCCGAGGGCCTCAGGGTCATCCTGGTCAACTCCAACCCGGCGACGATCATGACCGACCCGGAGATC
GCCGACGCCACCTACGTCGAGCCGATCACCCCGGAGTTCGTCGAGAAGATCATCGCCAAGGAGCGGCCGGACGCG
CTGCTGCCCACCCTCGGTGGTCAGACGGCCCTGAACACCGCCATCTCCATGCACGAGCAGGGTGTGCTGGAGAAG
TACGGTGTGAGCTGATCGGCGCCAACGTCGAGGCGATCAACAAGGGCGAGGACCGCGACCTGTTCAAGGGCGTCT
GTCGAGGCCGTCCGCGCGAAGATCGGGCACGGCGAATCCGCCCCGCTCGGTTCATCTGCCACTCCATGGACGACGTG
CTCGAGGGCGTCGAGACCCTCGGCGGTTACCCCGTCGTCGTCCGTCCCTCCTTCACCATGGGCGGCGCCGGCTCC
GGCTTCGCGCACGACGAGGAGGAGCTGCGCCGCATCGCGGGTCAGGGCCTGACGCTCTCCCCGACCACCGAGGTG
CTCCTGGAGGAGTCCATCCTCGGCTGGAAGGAGTACGAGCTGGAGCTGATGCGCGACAAGAACGACAACGTCGTG
GTCGTCTGCTCCATCGAG

240. *Corynebacterium efficiens* (SEQ ID NO. 240)

TGCTCAAGGAGGAGGGCCTGCGCGTCACCCTCATCAACTCCAACCCGGCCACCATCATGACCGACCCCGAGATGG
CGGACCACACCTACGTCGAGCCGATCGAGCCCGAGTACATCGAGAAGATCTTCCAGAAGGAGATCGAACAGGGCC
ACCCGATCGACACCGTCCTGGCAACCCTCGGCGGACAAACCGCCCTTAACGCTGCCATCCAGCTGGACCGCCTCG
GCATCCTGGAGAAGTACAACGTCGAGCTCATCGGTGCCGACATCGACGCCATCGAGCGTGGTGAGGACCGCCAGA
AATTCAAGGACATCGTCGCCACCATCGGTGGTGAATCAGCACGCTCCGCGCTTGCCACAACATGGATGAGGTCT
ACGCCACCGTCGAGGAGCTCGGTCTCCCGGTGTCGTGCGCCCCCTCCTTCACCATGGGTGGTCTGGGTTCGGTCT
TGGCCTACACCATGGAGGACCTCGACCGCATCGCCGGCGGTGGCCTCGCCGCTCCCCGGAGGCCAATGTCCTGA
TCGAGGAGTCCATCCTCGGCTGGAAGGAATACGAGCTGGAGCTCATGCGCGACGGCGATGACAATGTGGTGGTCA
TCTGCTCCATCGAGAACGTCGATGC

241. *Corynebacterium glutamicum* (SEQ ID NO. 241)

CTGAAGGAAGAGGGACTGCGCGTCACCCTCATCAACTCCAACCCAGCAACGATCATGACCGACCCAGAAATGGCT
GACCACACCTACGTGGAGCCAATCGAGCCGGAATACATCGACAAGATTTTCGCTAAGGAAATCGAGCAGGGCCAC
CCAATCGACGCCGTCTGGCAACCCTTGGTGGCCAGACTGCACTTAACGCAGCTATCCAGCTGGATCGCCTCGGC
ATCCTGGAAAAGTACGGCGTTGAACTCATCGGTGCAGACATCGATGCCATTGAGCGCGGCGAAGATCGCCAGAAG
TTCAAGGATATTGTCACCACCATCGGTGGCGAATCCGCGCGTTCGCGCGTCTGCCACAACATGGAAGAAGTCCAC
GAGACTGTGCGAGAACTCGGCCTTCCAGTAGTCGTGCGTCCATCCTTCACTATGGGTGGCCTGGGCTCCGGTCTT
GCATACAACACCGAAGACCTTGAGCGCATCGCTGGTGGCGGACTTGCTGCATCTCCTGAAGCAAACGTCTTGATC

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GAAGAATCCATCCTTGGTTGGAAGGAATTCGAGCTCGAGCTCATGCGGATACCGCAGACAACGTTGTGGTTATC
TGCTCCATTGAAAACGTGACGCACTGGGCGTGAC

242. *Bordetella parapertussis* (SEQ ID NO. 242)

CCCGCCACCATCATGACCGACCCCGAAACGGCGGACGTACCTATATCGAGCCCATCACGTGGCAAGCGGTCGAG
AAGATCATCGAGCGCGAGAAGCCCGATGCGCTGCTGCCACCATGGGTGGCCAGACCGCGCTGAACTGCGCGCTC
GACCTGGCCCCACCACGGCGTGCTGAAAAAGCACAACGTGAGCTGATCGGCGCCAACGAGCAGCCATCGAGAAG
GCCGAAGACCGCCAGAAGTTCAAGCAGGCCATGACCGACATCGGCCTGGAATCGGCCAAGTCGGGCGTGCCCCAC
TCGATGGACGAGGCCTGGGAAGTGCAGCGCCGCATCGCGGCCGACATCGGCACGGCGGGCTTTCCCGTCGTCATC
CGCCCCAGCTTACGCTGGGCGGCTCGGGCGGCGGCATCGCCTATAACGCCGAGGAATTCGAGGTCATCTGCCGC
CGCGGCCTGGAAGCCTCGCCGACCAAGGAGCTGCTGATCGAGGAGTCGCTGCTCGGCTGGAAAGAGTTCGAGATG

243. *Bordetella bronchiseptica* (SEQ ID NO. 243)

GCGCTCAAGGCCGAGGGTTACCGGACCATCCTGGTCAACAGCAACCCGCCACCATCATGACCGACCCCGAAACG
GCGGACGTACCTATATCGAGCCCATCACGTGGCAAGCGGTCGAGAAGATCATCGAGCGCGAGAAGCCCGATGCG
CTGCTGCCACCATGGGCGGCCAGACCGCGCTGAACTGCGCGCTCGACCTGGCCCCACCACGGCGTGCTGAAAAAG
CACAACGTGAGCTGATCGGCGCCAACGAGCAGCCATCGAGAAGGCCGAAGACCGCCAGAAGTTCAAGCAGGCC
ATGACCGACATCGGCCTGGAATCGGCCAAGTCGGGCGTGCCCCACTCGATGGACGAGGCCTGGGAAGTGCAGCGC
CGCATCGCGGCCGACATCGGCACGGCGGGCTTTCCCGTCGTCATCCGCCCCAGCTTACGCTGGGCGGCTCGGGC
GGCGGCATCGCCTATAACGCCGAGGAATTCGAGGTCATCTGCCGCCGCGGGCTGGAAGCCTCGCCGACCAAGGAG
CTGCTGATCGAGGAGTCGCTGCTCGGCTGGAAAGAGTTCGAGATGGAAGTGGTGCGGACAAGGCGGACAACCTGC
ATCATCGTCTGCTCGAT

244. *Bordetella pertussis* (SEQ ID NO. 244)

GCGCTCAAGGCCGAGGGTTACCGGACCATCCTGGTCAACAGCAACCCGCCACCATCATGACCGACCCCGAAACG
GCGGACGTACCTATATCGAGCCCATCACGTGGCAAGCGGTCGAGAAGATCATCGAGCGCGAGAAGCCCGATGCG
CTGCTGCCACCATGGGTGGCCAGACCGCGCTGAACTGCGCGCTCGACCTGGCCCCACCACGGCGTGCTGAAAAAG
CACAACGTGAGCTGATCGGCGCCAACGAGCAGCCATCGAGAAGGCCGAAGACCGCCAGAAGTTCAAGCAGGCC
ATGACCGACATCGGCCTGGAATCGGCCAAGTCGGGCGTGCCCCACTCGATGGACGAGGCCTGGGAAGTGCAGCGC
CGCATCGCGGCCGACATCGGCACGGCGGGCTTTCCCGTCGTCATCCGCCCCAGCTTACGCTGGGCGGCTCGGGC
GGCGGCATCGCCTATAACGCCGAGGAATTCGAAGTCATCTGCCGCCGCGGGCTGGAAGCCTCGCCGACCAAGGAG
CTGCTGATCGAGGAGTCGCTGCTCGGCTGGAAAGAGTTCGAGATGGAAGTGGTGCGGACAAGGCGGACAACCTGC
ATCATCGTCTGCTCGAT

245. *Burkholderia mallei* (SEQ ID NO. 245)

GGCGTTGCGTGAGGAGGGCTACAAGGTCATCTCGTCAACAGCAACCCGGCGACGATCATGACCGATCCGAACAC
GGCGGACGTACGTACATCGAGCCGATCACGTGGGAAGTCGTCGAGCGCATCATCGCGAAGGAGCGCCCCGACGC
GATCTGCCGACGATGGGCGGCCAGACCGCGCTGAACTGCGCGCTCGACCTGTTCCACCAGGCGTGCTCGAGAA
GTACGGCGTCGAGCTGATCGGCGGTCGCCGAGGCGATCGACAAGGCCGAAGACCGCCAGAAGTTCAAGGACGC
GATGACGAAGATCGGCCTCGGCTCGGCGAAGTCCGGCATCGCGCACTCGATGGAAGAGGCGCTGAAGGTGCACGC

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GGACATCGCGGCGGCGACGGGCGGCAGCGGCTACCCGGTCTGTGATCCGCCCGTCTGTTACGCTCGGCGGCTCGGG
CGGCGGCATCGCGTACAACCGCGAGGAGTTCGAGGAGATCTGCAAGCGCGGCCTCGATCTGTGCGCCGACGCGCGA
GCTGCTGATCGAGGAATCGCTGCTCGGCTGGAAGGAGTACGAGATGGAGGTCGTGCGCGATCGCGCCGACAACTG
CATCATCGTCTGCTCG

246. *Burkholderia pseudomallei* (SEQ ID NO. 246)

GGCGTTGCGTGAGGAGGGCTACAAGGTCATCCTCGTCAACAGCAACCCGGCGACGATCATGACCGATCCGAACAC
GGCGGACGTCACGTACATCGAGCCGATCACGTGGGAAGTCGTGAGCGCATCATCGGAAGGAGCGCCCCGACGC
GATCCTGCCGACGATGGGCGGCCAAACCGCGCTGAACTGCGCGCTCGACCTGTTCCACCACGGCGTGCTCGAGAA
GTACGGCGTCGAGCTGATCGGCGCGTCGCCGGAGGCGATCGACAAGGCCGAAGACCGCCAGAAGTTC AAGGACGC
GATGACGAAGATCGGCCTCGGCTCGGCGAAGTCCGGCATCGCGCACTCGATGGAAGAGGCGCTGAAGGTGCACGC
GGACATCGCGGCGGCGACGGGCGGCAGCGGCTACCCGGTCTGTGATCCGCCCGTCTGTTACGCTCGGCGGCTCGGG
CGGCGGCATCGCGTACAACCGCGAGGAGTTCGAGGAGATCTGCAAGCGCGGCCTCGATCTGTGCGCCGACGCGCGA
GCTGCTGATCGAGGAATCGCTGCTCGGCTGGAAGGAGTACGAGATGGAGGTCGTGCGCGATCGCGCCGACAACTG
CATCATCGTCTGCTCG

247. *Pseudomonas putida* (SEQ ID NO. 247)

GCCTGTAAAGCCCTGCGCGAGGAAGGTTTCCGCGTCATCCTGGTGAACTCCAACCCAGCCACCATCATGACCGAC
CCGGCCATGGCTGACGCCACCTACATCGAGCCGATCAAGTGGCAATCGGTGGCCAAGATCATCGAGAAAGAGCGC
CCGGACGCCGTCCTGCCGACCATGGGTGGCCAGACCGCCCTGAACTGCGCCCTGGACCTGGAGCGCCACGGCGTT
CTGGAGAAGTTCGGCGTGAGATGATCGGTGCCAACGCTGACACCATCGACAAGGCCGAAGACCGTTTCGCGCTTC
GACAAGGCCATGAAGGACATCGGCCTGGAGTGCCCGCGCTCCGGTATCGCCCACAGCATGGAAGAGGCCAATGCG
GTCTCTGAGAAGCTCGGCTTCCCGTGTCATCATTCGCCCGTCGTTACCATGGGCGGCACCGGCGGCGGTATCGCT
TACAACCGTGAAGAGTTCGAAGAAATCTGCACCCGTGGTCTGGACCTGTGCGCCGACCAAAGAGCTGCTGATCGAC
GAATCGCTGATCGGCTGGAAGGAATACGAGATGGAGGTGGTCCGCGACAAGAAGGACAACCTGCATCATCGTCTGC
TCGATCGAGAACTTCGACCCGATGG

248. *Yersinia pseudotuberculosis* (SEQ ID NO. 248)

ATGCCAAAACGTACAGATATAAAAAGCATCCTGATTCTGGGCGCAGGCCCGATTGTTATCGGCCAGGCTTGTGAG
TTTGACTACTCCGGTGCCCAAGCGTGTAAGCACTGCGCGAAGAGGGTTACCGTGTCATTTTGGTGAACTCCAAT
CCGGCGACTATCATGACTGACCCGGAATGGCCGATGCAACTTATATCGAGCCAATTCAATTGGGAAGTGGTGCGT
AAGATTATCGAAAAAGAGCGTCCAGATGCTGTTTTGCCTACGATGGGTGGCCAAACTGCACTGAACTGTGCATTG
GAACTGGAGCGTCAGGGTGTTCTGGCAGAATTTGGCGTCACCATGATTGGTGCGACCGCCGATGCCATCGATAAA
GCCGAAGACCGCGTCGCTTTGATATCGCGATGAAGAAGATTGGTCTGGATACGGCCCGCTCAGGTATTGCGCAT
AACATGGAAGAAGCACTGGCTGTTGCCGCTGATGTGGGCTTCCCGTGCAATTATCCGCCCATCCTTTACGATGGGG
GGCACTGGTGGCGGTATCGCTTATAACCGTGAAGAGTTCGAAGAGATCTGCGAGCGCGGTCTGGATTTGTCACCA
ACCAAAGAGTTGTTGATTGACGAATCGCTGATTGGCTGGAAAGAGTACGAGATGGAAGTTGTCCGTGATAAAAAC
GACAACTGCATCATCGTTTGCTCCATTGAAAACCTCGATGCGATGGGGATTACACCCGGCGACTCTATCACTGTCT
GCACCGGCTCAGACCCTGACCGATAAAGAATACCAAATCATGCGTAATGCCTCGATGGCGGTACTGCGTGAAATC
GGGGTAGAAACCGGGGGCTCTAACGTACAGTTCTCCGTCAACCCAAAAAATGGTCTGTTTGATTGTTCATTGAGATG

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AACCCGCGTGTTTCTCGCTCTTCAGCACTGGCCTCTAAAGCAACCGGTTTCCCGATTGCCAAGATTGCCGCCAAA
CTGGCGGTTCGGTTACACACTGGATGAGTTGATGAATGACATCACCGGTGGCCGTA CTCTGCGTCCTTTGAGCCT
TCTATCGACTATGTTGTTACCAAGATCCACGCTTTAACTTTGAAAAATTTGCGGGTGCCAACGACCGTTTGACC
ACGCAAATGAAGTCTGTGGGTGAAGTCATGGCCATTGGCCGCACGCAGCAAGAATCACTGCAAAAAGCACTGCGC
GGGCTGGAAGTGGGCGCGACCGGTTTTGACCCGAAAGTGAGCCTGGATGATCCCGAAGCACTGACTAAAATTCGT
CGTGAATTGAAAGAAGCGGGTGCAAGCTATCTGGTATATCGCTGATGCTTTCCGTGCGGGCATGTGCGTTGAT
GGTGTGTTCAATCTGACCAATGTTGATCGCTGGTTCCTGGTGCAGATTGAAGAGCTGGTTTCGTCTGGAAGAGAGC
GTGGCAGAACTCGGTATCAACGGCTTGACTGCTGAATTTATGCGTCACTTGAAACGTAAAGGTTTCGCCGATGCT
CGTTTGGCTAAATTGGTCGGTGCAAGCAAGTGAAGTCCGTAACTGCGTTACAAATATGGTTTACACCCGGTT
TATAAGCGTGTTGATACCTGCGCGGCAGAGTCTCGACGGATACGGCTTACATGTACTCCACCTACGAGGAAGAG
TGCGAATCTAACCAACCAGCGATCGTCCGAAAGTGATGGTGTGGGTGGCGGCCCGAACCGTATCGGACAAGGT
ATTGAGTTCGACTATTGCTGCGTACACGCTTCATTGGCACTGCGTGAAGACGGTTACGAAACCATCATGGTGAAC
TGTAACCTGAGACGGTTTCAACCGATTATGACACCTCTGATCGTCTCTACTTCGAGTCAGTCACGCTGGAAGAT
GTGTTGGAATTTGTCCGTATTGAGAAACCACAGGGCGTTATCGTGCAGTACGGTGGTCAGACACCGCTGAAATTA
GCCCCGAGTTGGAAGCGGTGGCGTCCCCATTATTGGGACCAGTCCGGATGCCATTGACCGTGCCGAAGACCGT
GAGCGTTTCCAGCAGGCGGTAAATCGTCTGGGCTGAAACAGCCAGCGAATGCCACCGTAGCGACTATCGAGCAG
GCGGTGGA AAAAGCCACTGGTCTGGGCTATCCACTGGTGTGACGCCCTTCTTATGTTTTGGGTGGCCGCGCGATG
GAAATTGTTTATGACGAGATTGACCTGCGCCGTTACTTCCAGAATGCCGTGAGTGTATCGAATGATGCGCCGGTA
TTGCTTGACCGCTTCTTTGATGATGCCGTGCAAGTGGATGTGATGCCATTTGTGATGGTGAACGCGTGTGATC
GGCGGCATTATGGAACATATAGAGCAAGCCGGGGTCACTCTGGTGACTCAGCCTGTTTATTGCTGCTTACACC
CTGAGCAAAGAAATTCAGGATGTGATGCGCCAACAAGTGGAAAACTGGCCTTTGAACTCTGTGTCCGCGGCCCTG
ATGAATGTGCAGTTTTCGGTGAAAAACAACGAAGTTTACCTGATTGAGGTTAACCACGGGCGGCCCGTACTGTA
CCTTTCGTGTCCAAAGCGACCGGTATGCCACTGGCAAAAATTGCCGCTCGTGTGATGGTTCGGCCAATCGCTGGCT
GAGCAGGGCATGCTGGAAGAAATTTCCGCTTACTACTCAGTCAAGGAAGTGGTACTGCCGTTTAAATAAATTC
CCCGGTGTTGACCAATTTTAGGGCCAGAAATGCGCTCTACCGGTGAAGTCATGGGGGTTGGCCGTACCTTCGCT
GAGGCGTTCTCTAAAGCGATGTTGGGCAGTCAATCTGGCATGAAAAAGAGTGGCCGTGCGCTATTATCCGTCCGT
GAGGGGGATAAGCACCGGGTGGTAGACTTGGCGGCGAAGCTGCTAAAACAAGGCTTTGAACTGGATGCAACCCAC
GGAACGGCGGTGCTGCTGGGCGAGGCGGGGATAAACCCACGTTTGGTTAACAAGGTGCATGAAGGCCGTCCGCAT
ATTACAGGACCGTATTAAGAATGGCGAGTACACCTATATCGTGAATACCACAGCTGGGCGTCAGGCGATTGAAGAT
TCTAAGCTGATCCGTGCGAGTGCTTTGCAATATAAAGTGCATTACGATACGACCTTGAACGGTGGTTTTGCTACG
GCGATGGCGTTAAATGCGGATCCAACCGATCAAGTGATTTCCGTGCAAGAGATGCATGCCAAGATTAAGAATATG
AAAGCGTAA

249. *Yersinia pestis* (SEQ ID NO. 249)

ATGCCAAAACGTACAGATATAAAAAGCATCCTGATTCTGGGCGCAGGCCCGATTGTTATCGGCCAGGCTTGTGAG
TTTGA CTACTCCGGTGCCCAAGCGTGTAAGCACTGCGCGAAGAGGGTTACCGTGTCA TTTTGGTGA ACTCCAAT
CTGGCGACTATCATGACTGACCCGGAATGGCCGATGCAACTTATATCGAGCCAATTCATTGGGAAGTGGTGCCT
AAGATTATCGAAAAAGAGCGTCCAGATGCTGTTTTGCC TACGATGGGTGGCCAACTGCACTGAACTGTGCATTG
GAACTGGAGCGTCAGGGTGTCTGGCAGAAATTTGGCGTCACCATGATTGGTGC GACCGCCGATGCCATCGATAAA
GCCGAAGACCGCCGTGCTTTGATATCGCGATGAAGAAGATTGGTCTGGATACGGCCCGCTCAGGTATTGCGCAT

AACATGGAAGAAGCACTGGCTGTTGCCGCTGATGTGGGCTTCCCGTGCATTATCCGCCCATCCTTTACGATGGGG
GGCACTGGTGGCGGTATCGCTTATAACCGTGAAGAGTTTGAAGAGATCTGCGAGCGCGGTCTGGATTTGTCTCCA
ACCAAAGAGTTGTTGATTGACGAATCGCTGATTGGCTGGAAGAGTACGAGATGGAAGTTGTCCGTGATAAAAAC
GACAACTGCATCATCGTTTGCTCCATTGAAAACCTTCGATGCGATGGGGATTACACCGGCGACTCTATCACTGTC
GCACCGGCTCAGACCCTGACCGATAAAGAATACCAAATCATGCGTAATGCCTCGATGGCGGTACTGCGTGAAATC
GGGGTAGAAACCGGGGGCTCTAACGTACAGTTCTCCGTCAACCCAAAAAATGGTCGTTTGATTGTCATTGAGATG
AACCCGCGTGTCTCTCGCTCTTCAGCACTGGCCTCTAAAGCAACCGGTTTCCCGATTGCCAAGATTGCCGCCAAA
CTGGCGGTGCGTTACACACTGGATGAGTTGATGAATGACATCACCGGTGGCCGTACTCCTGCGTCCTTTGAGCCT
TCTATCGACTATGTTGTTACCAAGATCCCACGCTTTAACTTTGAAAAATTTGCGGGTGCCAACGACCGTTTGACC
ACGCAAATGAAGTCTGTGGGTGAAGTCATGGCCATTGGCCGCACGCAGCAAGAATCACTGCAAAAAGCACTGCGC
GGGCTGGAAGTGGGCGCGACCGGTTTTGACCCGAAAGTGAGCCTGGATGATCCCGAAGCACTGACTAAAATTCGT
CGTGAACTGAAAGAAGCGGGTGCAAGACGTATCTGGTATATCGCTGATGCTTTCCGTGCGGGCATGTGCGTTGAT
GGTGTGTTCAATCTGACCAATGTTGATCGCTGGTTCCTGGTGAGATTGAAGAGCTGGTTTCGTCTGGAAGAGAGC
GTGGCAGAACTCGGTATCAACGGCTTGACTGCTGAATTTATGCGTCACCTGAAACGTAAAGGTTTTCGCCGATGCT
CGTTTGCTTAAATTGGTCGGTGCAAGCAGAAAGTGAAGTCCGTAACTGCGTTACAAATATGGTTTACACCCGGTT
TATAAGCGTGTGATACCTGCGCGGCAGAGTTCTCGACGGATACGGCTTACATGTACTCCACCTACGAGGAAGAG
TGCGAATCTAACCCAACAGCGATCGTCCGAAAGTGATGGTGCTGGGTGGCGGCCCGAACCGTATCGGACAAGGT
ATTGAGTTCGACTATTGCTGCGTACACGCTTCATTGGCACTGCGTGAAGACGGTTACGAAACCATCATGGTGAAC
TGTAACCTGAGACGGTTTCAACCGATTATGACACCTCTGATCGTCTCTACTTCGAGTCAGTCACGCTGGAAGAT
GTGTTGGAATCGTCCGTATTGAGAAACCACAGGGCGTTATCGTGAGTACGGTGGTCAGACACCGCTGAAATTA
GCCCCGAGTTGGAAGCGGCTGGCGTCCCCATTATTGGGACCAGTCCGGATGCCATTGACCGTGCCGAAGACCGT
GAGCGTTTCCAGCAGGCGGTAAATCGTCTGGGCCTGAAACAGCCAGCGAATGCCACCGTAGCGACTATCGAGCAG
GCGGTGGAAAAAGCCACTGGTCTGGGCTATCCACTGGTTCGTACGCCCTTCTTATGTGTTGGGTGGCCGCGCATG
GAAATCGTTTATGACGAGATTGACCTGCGCCGTTACTTCCAGAATGCCGTCAGTGTATCGAATGATGCGCCGGTA
TTGCTTGACCGCTTCCTTGATGATGCCGTGCAAGTGATGTCGATGCCATTTGTGATGGTGAACGCGTGTGATC
GGCGGCATTATGGAACATATAGAGCAAGCCGGGGTTCCTCTGGTGACTCAGCCTGTTTATTGCTGCTTACACC
CTGAGCAAAGAAATTCAGGATGTGATGCGCCAACAAGTGGAAGAACTGGCCTTTGAACTCTGTGTCCGCGGCCCTG
ATGAATGTGCAGTTTGCAGTGAAGCAACGAAGTTTACCTGATTGAGGTTAACCACGGGCGGCCCGTACTGTA
CCTTTCGTGTCCAAAGCGACCGGTATGCCACTGGCAAAAATTGCCGCTCGTGTGATGGTTGGCCAATCGCTGGCT
GAGCAGGGCATGTTGGAAGAAATTATTCCGCCCTTACTACTCAGTCAAAGAAGTGGTACTGCCGTTTAAATAAATTC
CCCGGTGTTGACCAATTTTAGGGCCAGAAATGCGCTCTACCGGTGAAGTCATGGGGGTTGGCCGTACCTTCGCT
GAGGCGTTCTCTAAAGCGATGTTGGGCAGTCAATCTGGCATGAAAAAGAGTGGCCGTGCGCTATTATCCGTCCGT
GAGGGGGATAAGCACCGGGTGGTAGACTTGCGGGCGAAGCTGCTAAAACAAGGCTTTGAACTGGATGCAACCCAC
GGAACGGCGGTGCTGCTGGGCGAGGCGGGGATAAACCACGTTTTGGTTAACAAGGTGCATGAAGGCCGTCCGCAT
ATTCAGGACCGTATTAAGAATGGCGAGTACACCTATATCGTGAATACCACAGCTGGGCGTCAGGCGATTGAAGAT
TCTAAGCTGATCCGTGCGAGTGCTTTGCAATATAAAGTGCAATTACGATACGACCTTGAACGGTGGTTTTGCTACG
GCGATGGCGTTAAATGCGGATCCAACCGATCAAGTGATTTCCGGTGCAAGAGATGCATGCCAAGATTAAGAATATG
AAAGCGTAA

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250. *Vibrio cholerae* (SEQ ID NO. 250)

ATGCCAAAACGTACTGACATTCAAAGCATCCTTATCCTTGGTGCGGGTCCAATTGTTATCGGTCAGGCTTGTGAG
TTTGACTACTCAGGCGCGCAAGCGTGTAAGCCCTGCGCGAAGAGGGTTACCGCGTTATTCTGGTTAACTCAAAC
CCAGCGACCATCATGACTGACCCAGAAATGGCCGATGCGACTTACATCGAGCCTATCCACTGGGAAGTGGTGCGT
AAGATCATCGAAAAAGAGCGCCCAGATGCGATTTTGCCACCATGGGCGGCCAGACTGCGCTGAACTGTGCGCTG
GCACTCGAAAAACATGGCGTATTGGCTGAGTTTGGCGTTGAGATGATCGGCGCAACCGCCGATGCGATTGATAAA
GCGGAAGACCGCTCACGCTTTGATAAAGCGATGAAATCAATCGGCCTAGAGTGTCTCGCGCTGATACCGCAAAA
AGCATGGAAGAAGCGTACAAAGTCCTCGATATGGTTGGCTTCCCATGTATCATCCGTCTTCTTTACCATGGGC
GGCAGCGGTGGTGGTATCGCTTACAACCGTGAAGAGTTTGAAGAAATCTGTACTCGCGGTCTGGATCTTTCACCG
ACCAATGAACTGCTGATCGATGAATCACTGATTGGTTGGAAAGAGTACGAGATGGAAGTGGTGCGTGATAAGAAC
GATAACTGCATCATCGTCTGTGCGATTGAAAACCTCGACCCAATGGGCATCCACACGGGTGACTCGATCACTGTC
GCTCCAGCGCAAACGCTAACTGACAAAGAATACCAAATCATGCGTAACGCCTCTTTGGCGGTACTGCGTGAAATC
GGCGTAGAAACCGGCGGTTCAAACGTTCACTTTGGTATCAACCCGAAAGATGGCCGCATGGTGATCATCGAGATG
AATCCACGTGTATCGCGCTCTTCTGCGTTGGCTTCAAAGCCACCGGTTTCCCAATTGCGAAAGTGGCGGCCAAA
CTGGCAGTGGGTTTCACTCTGGATGAGTTGATGAACGACATCACAGGCGGCGCAACACCAGCCTCGTTTCGAACCG
ACCATCGACTACGTGGTCACTAAGATCCCTCGTTTCAACTTCGAAAAATTCGCCGGTGCCAATGACCGTCTGACT
ACACAAATGAAGTCAGTAGGTGAGGTGATGGCGATTGGTCGTAACCAACAAGAATCACTGCAAAAAGCACTGCGC
GGCTTGGAAGTGGGTGCGGCTGGTCTGGATGAGAAAGTGGATCTGGACGCGCCAGACGCTCTGACCAAAATTCGT
TATGAGCTGAAAGAAGCAGGCGCAGAGCGTATTTGGTACATCGCGGATGCATTCCGTGCCGGTATGTCAGTGGAT
GGGGTATTTAACCTGACCAACATCGATCGCTGGTTCCCTAGTGCAAATTGAAGAACTGGTGAAGCTGGAAGCCGAA
GTGAAAGCCGGTGGCTTTGCGGGCTTGAACCAAGACGTAAGTGCCTAAGATGAAGCGCAAAGGCTTCTCTGATGCG
CGTTTGTCAAACCTGCTCGGCGTGAGCGAAAACGAAATCCGTGCTCTGCGTGACCAATACAACATCCACCCAGTT
TACAAGCGTGTGGATACCTGCGCGGCAGAAATTTAAGTCAGATACGGCTTACATGTACTCCACGTATGATGAAGAG
TGTGAAGCCAATCCGACTGACAAAGACAAGATCATGGTGCTGGGCGGTGGTCCAAACCGTATCGGTCAAGGTATC
GAGTTTGACTACTGCTGTGTACACGCCGCGCTTGCACTGCGTGAAAGATGGTTACGAAACCATCATGGTTAACTGT
AACCCAGAAACCGTATCAACCGATTACGACACCTCAGATCGCCTCTACTTTGAGCCTGTAACCTCTAGAGGATGTG
CTGGCTATCGTGCGTGTGAGAAGCCAAAAGGCGTGATCGTGCACTACGGCGGTCAAACACCACTGAAACTGGCG
CGAGCGCTGGAAGCGGCTGGCGTACCTGTGATTGGTACCAGCCCAGATGCGATTGACCGCGCTGAAGACCGTGAA
CGTTTCCAACAAGCGGTACAGCGTTTAGGCCTCAAACAGCCAGACAACGCAACCGTAACCGCTATCGAGCAAGCG
ATTGAGAAGTCGCGTGAAATCGGTTTCCCACTCGTAGTTCGCCCCCTCTTATGTTCTGGGTGGCCGTGCGATGGAG
ATTGTGTACGATGAGCAAGATCTGCGTCTTACTTCAACGAAGCGGTGAGCGTGTGCAATGAATCACCAGTTCTG
CTGGATCGCTTCCCTTGATGATGCAACCGAAGTGGACGTGGATGCGATTGTGACGGTGAGCGCGTGGTGATTGGC
GGCATCATGGAGCACATTGAACAAGCGGGTGTTCACTCAGGTGACTCAGCCTGTTCTCTGCCGGCTTACACCTTG
AGCCAAGAAATCCAAGACAAGATGCGTGAGCAAGTTGAGAAGTTGGCATTTGAACTCGGTGTTCTGTGGCCTGATG
AACATTCACTTTGCACTCAAAGACAACGAAGTTTACCTGATTGAAGTAAACCCACGTGCTGCGCGTACTGTGCCG
TTTGTCTTCTAAAGCAACCGGTGCTCCGCTGGCGAAAATCGCGGCGCGCGTGATGGTTGGACAACTCTGGAGCAA
CAAGGCTTCACCAAAGAGATCATTCACCTTACTACTCAGTTAAAGAAGTGGTTCTGCCGTTCAACAAGTTCCCG
GGGGTTGACCCACTGCTTGGCCCTGAAATGCGCTCAACCGGTGAAGTGATGGGTGTGGGTGCCACGTTTGTGAA
GCCTATGCTAAAGCAGAGTTGGGCTGTGGCTCGGTTTACCCTGAAGGTGGTCTGCGCTACTTTCCGTGCGTGAA
GGTGACAAACAGCGTGTAGTGGATCTGGCTTCTAAGCTAGTGAACTGGGTACCAGTTGGATGCGACTCACGGT

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ACTGCAGTGATTCTGGGCGAAGCGGGCATCAACCCACGTCTGGTTAACAAAGTGCATGAAGGTCGTCCACACATT
CTGGATCGCATCAAAAACACGAGTACACCTACATTGTGAACACGGCTTCTGGCCGCCAAGCAATTGAAGACTCA
AAAGTACTGCGCCGTGGTGCATTGGCTCACAAAGTGAACCTACACCACCACACTGAACGCCGCCTTCGCAACTTGT
ATGTCACACACGGCGGATGCCAAAGCATCCGTCACCTCAGTACAAGAGCTGCATGCGCGTGTAAAAGCGAACC
AAAGCTTAA

251. *Vibrio vulnificus* (SEQ ID NO. 251)

ATGCCAAAACGTACTGACATTCAAAGCATTCCTTATCCTAGGTGCTGGTCCAATTGTTATCGGTCAGGCTTGTGAG
TTTGACTIONTCAAGGCGCACAAAGCATGTAAAGCGCTACGTGAAGAAGGTTACCGAGTTATCCTAGTAACTCGAAC
CCAGCGACCATCATGACAGACCCAGATATGGCGGATGCGACCTACATCGAGCCAATTCAATGGGAAGTGGTACGC
AAGATTATCGAAAAAGAGCGTCCAGATGCGGTTCTACCAACCATGGGTGGTCAGACGGCTCTAAACTGTGCGCTT
GCGCTTGAAAAGCACGGCGTGCTAGCGGAATTTGGCGTAGAAATGATCGGTGCAACTGCTGATGCCATCGATAAA
GCGGAAGACCGTTTCGCGTTTTGACAAAGCGATGAAATCTATCGGCCTAGAGTGTCTCTGTGCTGATACGGCGAAG
ACCATGGAAGAAGCGTACAAAGTGTCTGATATGGTTGGCTTCCCATGTATCATCGCCCCGTCAATCACCATGGGT
GGTACGGGGGGGGTATCGCGTACAACAAAGAAGAGTTCGAAGAAATCTGTGCGCGTGGTCTTGACCTGTGCGCA
ACCAATGAAGTGTCTATCGATGAATCTTTGATCGGTTGGAAGAGTACGAAATGGAAGTGGTTCGCGACAAAGCG
GACAACTGTATCATCGTATGTTCAATCGAAAACCTTCGACCCAATGGGCATCCACACCGGTGACTCTATCACCCTG
GCACCGGCTCAAACGCTGACAGATAAAGAATACCAACTGATGCGTAATGCGTCGCTAGCGGTACTTCGTGAAATC
GGTGTAGAGACAGGTGGTTCAAACGTGCAGTTTGGTATCAACCCGAAAGATGGCCGTATGGTTATCATCGAGATG
AACCACGTTGATCGCGCTCTTCTGCTCTAGCGTCAAAAGCGACAGGTTTCCCTATTGCGAAGATTGCAGCGAAA
CTAGCCGTTGGCTTCACGCTTGATGAGCTACAAAATGACATCACTGGTGGTGGCAGCGCCAGCATCATTTGAACCG
ACCATCGACTACGTAGTACTAAGATTCCCTCGTTTCAACTTCGAGAAATTTGCCGGTGCTAACGACCGTTTGACG
ACGCAAATGAAGTCAAGTGGTGAAGTGTGATGGCCATTGGCCGTAACCAACAAGAATCACTGCACAAAGCGCTGCGC
GGTCTAGAAGTGGGCGCGACTGGTTTTGATGAGATGGTTGATCTTGATTCACCAGATGCACTGACCAAAATTCGC
CACGAGCTGAAAGAAGCGGGCGCTGAGCGTATTTGGTACATTGCCGATGCATTCGCTGCGGGTATGTGAGTTGAT
GGTGTGTTTTAACCTAATAACATCGATCGCTGGTTTCTGGTTCAAATCGAAGAGATTGTGAAGCTGGAAGAGCAA
GTGAAAGCGGGTGGTTTTGCTGGTTTAACTCAAGATGTGCTTCGTCAAATGAAGCGTAAAGGTTTTCTCCGACGCT
CGCCTATCAAACTACTCGGCGTGGCTGAAAGTGAATCCGTCGTCTACGTGACCAATTCGACATCCACCTGT
TACAAGCGTGTGATACCTGTGCGGCAGAAATCTCATCGGATACGGCTTACATGTACTCATCTTATGATGATGAG
TGTGAAGCGAACCACCGATAAAGAAAAGATCATGGTTCTGGGCGGTGGTCCAAACCGTATCGGTCAAGGTATT
GAGTTTGACTACTGCTGTGTACACGCTTCGCTAGCGCTACGTGAAGATGGTTACGAGACCATCATGGTGAAGTGT
AACCAGAAACCGTATCAACCGACTACGACACTTCAGACCGTCTCTACTTTGAACCGTTACTCTAGAAGATGTG
TTGGCGATTGCTCGTGTGAAAAGCCAAAAGGCGTGATCGTGCAGTACGGTGGTCAAACCTCACTGAAACTGGCG
CGTGCGCTAGAAGCGGCGGGTGTACCAATTATCGGTACTAGCCCTGATGCCATCGACCGTGCGGAAGACCGTGAG
CGTTTCCAACAAGCGGTTGACCGCTTAGGCCTGTACAGCCAGAGAACGCAACCGTAACCACCATGGAGCAAGCG
GTTGAGAAGTCGCGTGAATTTGGCTTCCCATTTGGTCGTTTCGTCCATCTTACGTACTGGGTGGCCGCGCTATGGAA
ATCGTTTTATGACGAGCAAGACCTACGCCGCTACTTCAACGAAGCGGTTAGCGTGTGCAACGAATCACCAGTTCTA
CTGGATCGCTTCCCTAGACGATGCAATTGAAGTCGATATCGACGCTATCTGTGACGGTGAGCGCGTGGTGATTGGC
GGTATCATGGAGCACATCGAGCAAGCGGGTGTTCCTCAGGTGACTCAGCATGTTCACTGCCTGCTTACACGTTA
AGCCAAGAAATCCAAGACAAGATGCGTGAGCAAGTTGAAAAGCTGGCATTTGAGTTGGGCGTTCTGTGGCCTAATG

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AACACGCAGTTT GCCGTAAAAGACAACGAAGTGACCTCATCGAAGTGAACCCCTCGTGCTGCACGTACCGTTCCA
TTCGTATCGAAAGCGACCGGTGCACCACTTGCGAAAATCGCAGCACGTGTTATGGCTGGTCAGTCTCTGGAATCG
CAAGGTTTCACCAAAGAGATTATTCCTCCTTACTACTCGGTAAAAGAAGTGGTTCTGCCATTTAACAAGTTCCTT
GGCGTTGACCCACTATTGGGCCCTGAAATGCGCTCAACGGGTGAAGTGATGGGTGTAGGTGCAACTTTTGCTGAA
GCGTATGCGAAAGCAGAACTGGGTGTGGCAATGTGTATCCTGAAGGTGGTCGTGCGCTGCTTTCGGTACGCGAA
GGCGACAAGCAACGTGTGGTTGACCTAGCGTCTAAATTACTGAAACTAGGGTACAAGCTGGATGCGACACACGGT
ACGGCAGTGATCTTAGGTGAAGCGGGCATCAACCCACGTCTAGTAAACAAAGTGCACGAAGGTCGTCTCACATT
CTTGACCGCATCAAGAACAACGAATACACCTACATCGTGAACACGGCGGCTGGTCGTCAAGCGATTGAAGATTGCG
AAAGTTCTACGCCGTGGCGCACTTGCGAAAAAGTGAACACACCACGACACTTAACGCGGCATTTGCGACCTGT
ATGTCTCATACGGCGGACGCGAAAGCAAGCGTGACGTGGTACAGGAAGTGCACGCGCAAGTGCAAGCGAGTTTG
AAAGCGTAA

252. *Vibrio parahaemolyticus* (SEQ ID NO. 252)

ATGCCAAAACGTACTGACATTCAAAGTATTCTAATTCTTGGTGCTGGTCCGATTGTTATCGGTCAGGCATGTGAG
TTTGACTACTCTGGCGCACAAGCGTGTAAGCTCTTCGTGAAGAAGGCTACCGAGTTATTCTAGTTAACTCTAAC
CCAGCAACCATCATGACAGACCCTGAAATGGCAGATGCAACTTACATCGAGCCGATTCAATGGGAAGTTGTTGCGC
AAGATCATTGAGAAAGAACGCCAGATGCAGTATTGCCAACAATGGGTGGTCAGACGGCGCTTAACTGTGCGCTA
GATCTAGAGAAGCACGGCGTTCTTGCTGAATTCGGCGTAGAGATGATTGGCGCAACGGCTGACGCGATTGATAAA
GCAGAAGACCGTTCTCGCTTCGATAAAGCAATGAAGTCTATCGGCCTTGAGTGTCTCGTGCTGATACCGCGAAG
ACGATGGAAGAAGCTTACAAAGTTTTAGACATGGTTGGCTTCCCTTGATCATCCGTCCATCGTTCACCATGGGT
GGTACGGGTGGCGGTATCGCGTACAACAAAGAAGAGTTTGAAGAAATCTGTCTCGTGGTCTGGATCTTTCTCCG
ACTAACGAACTTCTTATCGATGAATCGCTAATCGGTTGGAAAGAGTACGAAATGGAAGTAGTTCGCGACAAAGCG
GACAACTGTATCATCGTATGTTCAATCGAAAACCTTCGACCCAATGGGCATCCACACCGGTGACTCAATCACGGTT
GCTCCAGCGCAAACTCTGACTGACAAAGAATACCAGCTAATGCGTAATGCATCGCTAGCGGTTCTGCGTGAAATC
GGTGTGAGACAGGTGGTTCAAACGTACAGTTTGGTATCAACCCGAAAGATGGCCGTATGGTTATCATCGAGATG
AACCACGTGTATCTCGCTCTTCTGCTCTGGCATCAAAGCAACAGGTTTCCCAATCGCTAAGATTGCGGCGAA
CTGGCTGTTGGCTTTACTCTAGACGAGCTGCAAACGACATTACAGGTGGTGCAACTCCGGCATCATTCGAACCT
ACTATCGACTACGTAGTGACCAAGATTCCTCGTTTTAACTTCGAGAAATTTGCTGGCGCTAACGATCGACTGACG
ACTCAGATGAAGTCAGTTGGTGAGGTAATGGCGATTGGTCGTAACCAACAAGAATCTCTTACAAAGCATTACGT
GGCCTAGAGGTTGGCGCGACTGGCTTTGATGAGATGGTTGACCTAGATGCACCTGACGCATTAACCTAAGATTCGT
CACGAACTAAAAGAAGCTGGCGCAGAGCGTATCTGGTATATCGCAGATGCATTCCGTGCGGGCATGTCTAGTGGAT
GGCGTGTTTAACTGACGAACATTGATCGCTGGTTCCTAGTTCAAATTGAAGAGCTAGTTAACTAGAAAGAGCAA
GTGAAAGCCGGTGGCTTTGCTGGTCTAACAGAAGAAGTTCTACGCCAGATGAAACGTAAAGGTTTCTCTGATGCT
CGCCTATCTAACTGTTAGGTGTGGCGGAAAGCGAAATCCGTGCTCTACGTGACAGTTTGACATCCACCCTGTC
TACAAGCGAGTGATACGTGTGCGGCTGAGTTCTCTTCTGATACGGCTTACATGTACTCATCTTACGATGAAGAG
TGTGAAGCAAACCCAACAGATAAAGACAAGATCATGGTACTGGGCGGTGGTCCAAACCGTATCGGTCAAGGTATC
GAATTCGACTACTGTTGTGTACATGCATCACTAGCGCTTCGTGAAGATGGCTACGAAACCATTATGGTGAAGTGT
AACCAGAAACAGTATCGACAGACTACGATACATCTGACCGTCTTTACTTCGAACCAGTAACTCTTGAAGATGTG
TTGTCTATCGCCGCGTTGAAAAGCCAAAAGGTGTGATTGTTCAATACGGTGGTCAAACGCCACTTAACTGGCT
CGCGCACTAGAAGCTGCAGGCGTGCCAATCATCGGTACAAGCCCGGATGCGATTGACCGCGCAGAAGACCGTGAG

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CGTTTCCAGGCTGCAGTTGAGCGTTTAGGTCTTCTACAACCACAAAACGCAACAGTAACGGCGATGGAGCAAGCG
GTTGAGAAATCTCGTGAAATCGGCTTCCCACTCGTTGTTTCGTCCATCTTACGTTTTGGGTGGTCGTGCGATGGAA
ATCGTCTACGATGAACAAGACTTGCGTCGTTACTTCAACGAAGCAGTAAGCGTATCGAATGAATCTCCAGTTCTA
CTAGACCGATTCTTAGATGATGCAACAGAAGTGGATATCGACGCTATCTGTGACGGTGAGCGCGTGGTTATCGGC
GGCATCATGGAGCACATTGAGCAAGCGGGCGTTCACTCTGGTGACTCTGCATGTTTCGCTTCCTGCTTATACACTA
AGCCAAGAAATCCAAGACAAGATGCGTGAGCAAGTTGAGAAGCTGGCGTTTGAACCTTGGTGTACGTGGCCTGATG
AACACGCAGTTTGCTGTAAAAGACAACGAAGTTTACCTAATTGAAGTAAACCCCTCGTGCTGCGCGTACGGTACCA
TTCGTATCGAAAGCGACAGGCGCACCCTAGCGAAAATCGCGGCACGTGTAATGGCGGGTCAATCTCTGGAATCA
CAAGGTTTCACTAAAGAGATTATTCCTCCTTACTACTCAGTCAAAGAAGTCGTTCTACCTTTCAATAAGTTCCCT
GGCGTTGACCCTCTATTAGGTCTGAAATGCGCTCAACAGGTGAAGTGATGGGTGTTGGTGCTACGTTTGCAGAA
GCTTACGCAAAAGCAGAGCTTGGCTGTGGCAGTGTGTACCCTGAAGGTGGTCGTGCGCTACTTTCTGTTTCGTGAA
GGTGATAAGCAGCGTGTTGTTGACCTTGCCTAAGCTAGTAAAATTGGGTACCAATTGGATGCGACTCACGGT
ACTGCTGTAATCCTTGGTGAAGCGGGTATTAACCCTCGCCTGGTAAACAAAGTACATGAAGGTCGTCCACACATT
CTTGACCGCATCAAGAACAACGAATACACCTACATTGTGAACACGGCTGCAGGTCGTCAAGCTATTGAAGATTGCG
AAAGTTCTACGCCGCGGTGCTCTAGCAGAAAAAGTGAAGTACACAACAACGCTAAACGCTGCGTTTGCAACGTGT
ATGTCTCACACTGCTGATGCAAAAGCGTCAGTAACTTCTGTTTCAGGAGCTACACGCTAAAGTAAAAGCGAGTCTG
GAAGCGTAA

253. *Vibrio fischeri* (SEQ ID NO. 253)

ATGCCAAAACGTACTGATATTAAAGCGTTCTAATTCTAGGTGCCGGTCCAATTGTAATCGGCCAAGCATGTGAA
TTTGACTACTCTGGTGCACAAGCATGTAAAGCACTTCGTGAAGAAGGCTACCGTGTTATTCTTGTGAAGTCTAAC
CCAGCAACAATCATGACTGACCCAGACATGGCTGATGCAACGTACATTGAACCAATTCATTGGGAAGTGGTTCGT
AACATCATCGAAAAAGAGCGTCCAGATGCGGTATTACCAACAATGGGTGGTCAAACAGCATTAAACTGTGCGCTT
GATTTAGAAAAGCACGGTGTCTTGCTGAATTCGGTGTGAGATGATTGGTGCAACAGCTGATGCAATTGATAAG
GCGGAAGACCGTTCTCGTTTTGATAAAGCGATGAAGTCTATTGGACTTGAGTGTCACGTGCTGATACAGCAAAA
ACCATGGAAGAAGCTTACGGCGTTCTAGATATGGTTGGTTTTCCCATGTATTATTTCGTCCATCATTTACGATGGGT
GGTACGGGCGGTGGTATCGCATAACAACAAGAAGAGTTCGAAGAAATTTGTCGTCGCGGTTTAGACCTTTCGCCA
ACTAACGAGCTTCTAATCGATGAATCATTAATCGGTGGAAAGAGTACGAGATGGAAGTGGTTCGTGATAAGAAC
GATAACTGTATCATCGTATGTGCAATTGAAAACCTTTGATGCGATGGGTATTCACACTGGTGACTCAATCACGGTT
GCGCCAGCACAAAACGCTAACGGATAAAGAATACCAACTAATGCGTAATGCATCTCTAGCTGTACTGCGTGAGATT
GGTGTGTAACGGGTGGCTCAAACGTACAGTTTGGTATTAACCCGAAAGATGGTCGTATGGTTATCATCGAAATG
AACCACGAGTATCTCGTTCATCTGCACCTTGCTTCTAAAGCAACAGGTTTCCCTATTGCAAAAATTGCAGCGAAA
TTGGCTATTGGCTTTACGCTTGACGAGCTAATGAATGACATTACAGGTGGGGCAACGCCTGCGTCATTTGAACCA
ACAATCGATTACGTTGTTACTAAGATCCCTCGTTTTAACTTCGAAAAATTTCGAGGGGCTAACGATCGCCTAACA
ACACAGATGAAATCAGTTGGTGAAGTGATGGCTATCGGCCGTAACCAACAAGAATCTCTACAAAAAGCACTTCGT
GGCCTAGAAGTAGGTGCGACTGGTTTTGATGAGATGGTTGATTTAGATGCTCCTGATGCATTAACAAAAATTCGT
CATGAACTGAAAGATGCTGGTGCTGAGCGTATTTGGTACATCGCTGATGCGTTCGCTGCGGGTATGTCTGTTGAT
GGTGTGTTAATCTAACGAATGTTGATCGTTGGTTCCTAGTTCAAATTGAAGATTTAGTAAAAGAAGAAGCGG
GTTAAAGCGGGTGGTTTTGCTAATTTAACCGCAGATGCACTTCGTAACTTAAGCGTAAAGGTTTTGCTGATGCG
CGTCTTTCTAAACTATTGGGCGTTGGTGAGAGTGAAATTCGTGCGCTGCGTGACCAGCATGATATTCACCCTGTA

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TACAAGCGTGTAGATACGTGTGCTGCTGAGTTCTCATCAGATACGGCTTACATGTACTCATCTTATGATGAAGAG
TGTGAAGCAAATCCAACAGACAAAGATAAGATCATGATCTTAGGTGGCGGTCCAAACCGTATCGGTCAAGGTATT
GAGTTTGATTACTGTTGTGTACACGCATCATTAGCACTACGAGAAGATGGCTACGAAACTATCATGGTTAACTGT
AACCCTGAGACTGTTTCTACGGATTACGATACGTCTGACCGTCTATACTTCGAACCAGTTACTCTAGAAGATGTA
CTAGCAATTGCTCGTGTGAGAAACCAAAAGGCGTGATAGTTCAGTACGGTGGTCAAACCTCCACTTAAACTGGCT
CGCGCTCTTGAAGCAGCTGGTGTTCGAATCATAGGTACAAGCCCTGATGCTATCGACCGTGCAGAAGACCGTGAG
CGTTTCCAAGTTGCTGTGCGACCGTTTGGAGCTTCTTCAACCAGAAAATGCAACGGTTACTACAATGGAGCAGGCG
ATTGATAAATCAAAAGAAAATCGGCTTCCCACTCGTAGTACGTCTTCTTATGTTCTTGCTGGTCGTGCGATGGAA
ATCGTATATGACGAGCAAGACTTACGTCGTTACTTCAATGAAGCAGTAAGCGTATCAAATGAATCTCCAGTACTT
CTTGATAGCTTCCCTTGATGATGCTGTAGAAGTGGATGTTGATGCGATTTGTGACGGTGAGCAAGTGGTTATCGGC
GGTATCATGGAGCACATCGAGCAAGCGGGTGTTCCTCTGGTGACTCAGCATGTTCTCTTCTGCTTATACATTA
AGCGAAGAAAATCCAAGATGTAATGCGTGATCAAGTACGTAAGCTGGCATTTCGAGCTAGGTGTTCTGCTGGCTTAATG
AATACACAGTTTGGCTGTTAAAGATAACAAAGTATACCTAATCGAAGTTAACCACGTGCTGCTCGTACGGTTCCA
TTCGTATCGAAAGCAACTGGTGCACCATTAGCTAAGATTGCAGCGCGTGTAATGGCGGGTCAATCTCTAGAGTCT
CAAGGCTTTACTAAAGAGATCATCCCACCATACTACTCAGTTAAAGAAGTGGTATTACCGTTCAACAAATTCCTT
GGTGTGACCCACTGTTAGGCCCGAGAAATGCGCTCAACGGGTGAAGTTATGGGTGTTGGTACAACGTTTGCTGAA
GCATTTGCTAAAGCTGAACTTGGCTGTAGCAAGAATACCCAGAAGGTGGTTCGTGCATTACTTTCTGTTCTGTA
GGTGATAAGAAACGTGTTGTAGATTTAGCAAAACATCTTGTTAAATTGGGTTACCAACTGGATGCAACTCACGGT
ACAGCAGTTATTCTTGGCGAAGCGGGTATTAACCCACGTCTAGTAAACAAGGTACATGAAGGCCGTCCTCATATT
CTTGACCGTATCAAGAATGGTGAGTACACCTACATCGTTAATACTGCAGCAGGTTCGTCAAGCGATTGAAGATTCT
AAAGTATTACGTCTGTTGGTGCCTAGCTGAGAAAGTAACTACACAACAACGCTAAATGCAGCATTTGCTAGTTGT
TTAGCTCATGAAGCGGATGACCGTAAAACGGTTAACTCTGTTCAAGAGCTACACGCTAAAGTGGCAGCTAAATAC
GCTTAA

254. *Campylobacter jejuni* (SEQ ID NO. 254)

ATGCCAAAACGAACAGATATTAAAAGCATTTTACTTATAGGAAGTGGTCCTATTGTGATAGGACAAGCTTGTGAA
TTTGATTATTCTGGAACCTCAAGCCGCAAAGACTTTAAAAGAATTAGGATATCGTGTAGTATTAATCAACTCAAAT
CCTGCAACCATCATGACAGATCCCGAATTTGCAGATGCGACTTATATAGAACCATAACAAAAGAAAGTATTTTA
AGTATTATTAAAAAAGAAAAAATTGATGCAATTTTGCCAACTATGGGTGGACAAGTAGCGTTAAATGTTGCTATG
GAAGTTTATGAAAGCGGACTTTTAGGAGATGTGAAATTTTAGGCGCAAATCCTGAGGCGATTAAAAAAGGCGAA
GATCGTCAGGTTTTTAAAGAATGTATGAAAAAATTGGCATGGATTTGCCAAAATCGATGTATGCGTATAATTAT
GACGAAGCTTTAAAAGCCGTAGATGAAATCGACTTTCCTTTGATGATCCGTGCTTCTTATACTTTAGGGGGTGCT
GGAAAGTGGTGTGGTTTACAATATGGACGAATTTAAAGAAGTTACCAATACTGCTTTAGCTTTATCACCTATTCAT
GAAATTTTGATTGAAGAAAGTTTGTAGGTTGGAAAGAATATGAAATGGAAGTTATACGCGATAGAGCGGATAAT
TGTATCATAGTTTGTAGCATAGAAAATATCGATCCTATGGGAGTTTCATACAGGAGATAGTATTACAATAGCTCCA
GCATTAACCTTTGACAGATAAAGAATATCAAGTTATGCGTAATGCTTCTTTTGCTATTTTGCCTGAAATTGGTGTA
GATACAGGCGGAAGTAATGTGCAATTTGCTATCAACCCAAAAAATGGAAGAATGATAGTTATAGAAATGAATCCA
AGAGTTTCAAGATCAAGTGCTTTAGCTTCTAAGGCAACGGGTATCCTATAGCAAAGTTGCGACACTTTTGGCA
GTAGGTTTTAGCTTAGATGAGATTAAAAATGATATTACAGGAACCTCCTGCATCTTTCGAGCCTGTGATTGATTAT
ATTGTAACAAAAATTCCTCGCTTTACCTTTGAAAAATTTCCAGGAGCAAATACAACCTTTAGGTACAGCTATGAAA

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AGTGTGGGTGAGGTAATGGCTATAGGACGCACCTTTTAAAGAAAGTATACAAAAAGCACTTTGTTTCGCTTGAGCGT
TCTTTAAGTGCTTTTGATAGGGTAAAATTTGAAGATAGAAATGATCTTGTTTTTAAAATTCGCAATGCCAATGAA
AAGCGTTTACTTTATGTTGCTCAAGCTTTTAGGGAAGTTTTAGCGTAGAAGAACTTTATGAGCTTTGTAAAATA
GATCCTTGTTTTTAAACACAGATTAAAGAAATTGTAGATTTTGAAGAACAAATTGATATGGATATTTTAAACAAT
AAGGCTCTTTTGAGAAAAGCAAAAACCTATGGGCTTTTCAGATAAAATGATAGCCTTGCTTGTAATTTGAAAGAT
AATTTAGAATTAAGCCAAAATGATATTTATTATGTAAGAATGAAGCAAAAAATCATCGCAGAATTTAGTGAAGTG
GATACTTGTCGGGTGAATTTGAAGCCTTAACCTCTTATCTTTATTCAAGTATCAATGTAAGCGAACTCACTCAA
AGTAAAAACGATGCTAAGGATAAAAAAGAAAAAAAGTGATGATTATAGGTGGGGGGCCAAACCGTATAGGACAA
GGTATAGAATTTGACTATGCTTGCGTACATGCTTCTTTTGCGCTTAAAGATATGGGTATTAAAACTATTATGTAT
AATTGTAATCCTGAAACCGTTTCGACTGACTATGATACAAGTGATATTTTGTATTTTCGAGCCTATTGATTTCGAA
CATTTAAGAGCGGTGATTGAGCGTGAAAAACCTGATGGAGTGATTGTGCATTTTGGTGGACAAACTCCTTTGAAA
TTTGCTAAGCGTTTAAAGTGCTTTTGGAGCTAAGATTATAGGTACTAGCGCAAGAGTAATTGATATGGCAGAAGAT
AGAAAGAAATTTGCCGAATTTATTACAAAGCTAGGTATCAATCAGCCAAAAAATCTACTGCAACAAGCGTAGAA
GAAGCGGTTCTTAAGGCTAGTGATATAGGGTATCCTGTGCTTGTAAGACCAAGTTATGTTTTAGGTGGGCGTGCG
ATGCGCGTGGTAAATGATGAGGCTGAACCTTAGACTCTATATGCAAGAAGCTGTGGATGTAAGCGATAAAAGCCCT
GTTTTGATCGATCAGTTTTTAGACAATGCTACAGAAATTGATGTTGATGCGATTTGTGATGGCAAAGATGTTTAT
GTTGCAGGAATTATGGAGCACATAGAAGAAGCAGGAATTCATTTCGGGTGACAGTGCTTGTTCTTTGCCGCCCTTGC
AATATCGATGAAAAAATGCAAGAATTTATTGCACAAAAAACCGCAGATATTGCTTTAAATTTGGGAGTTGTAGGA
CTTTTAAATATACAATTTGCTTTACATAATAATGAGCTTTATATGATAGAGGTAAATCCTAGAGCTAGTCGTACC
ATACCTTTTGTTAGTAAAGCTACGGGTATTTCCTTTAGCAAAAGTGGAACGCGTGATGTGGCAAGGAAATTTA
AAAGAAGCTTTAAAATTTTATGATACTTTTAAAGTGGTTAATTTTGATACTAAAATTTTACGCCCTAAAACCTCCA
AAATATATGAGCGTGAAAGAAGCAGTATTTCCATTTGCAAACTTAGTGGAAGTGATTTAGAATTAGGTCTTGAA
ATGCGTTCAACGGGTGAAGTTATGGGTATAAGCAAGGATTTTGCAATTCCTATGCGAAAAGTCAAATTCATCG
TTTAATCATCTTCCAGAGCAAGGCGTGGTATTTATCTCCTTAAAAGATAAGGATAAAAAATATACCAAAAAATC
GCTGCAGAATATGTAAAGCTTGGCTTTAAGCTTATGGCAACAGGGGGAACCTTGCAAGGAAATTTTAGAAAGTGGT
TTTGAGTGCGAACTTGTAACATAAAATTTTCAAGAGGACGCCCCAATGTTGAAGATAAATTGAAAAATGGAGAAAT
CACTTAGTTATCAATACAAGCGATAGTCACAGTTTTTAAAGGCGATACGAAAAAATTCGTGAAAATATTATTCGT
TTTAAATACCTTATTTTACAAATTTACGATCAGCTTTAGCAGGTGCAAAATCGATTAAAGCTATACAGAGTAAA
TCTTGCCTAGATGTAAAGAGTTTGCAAGAGTGGCTTAAATCTTGA

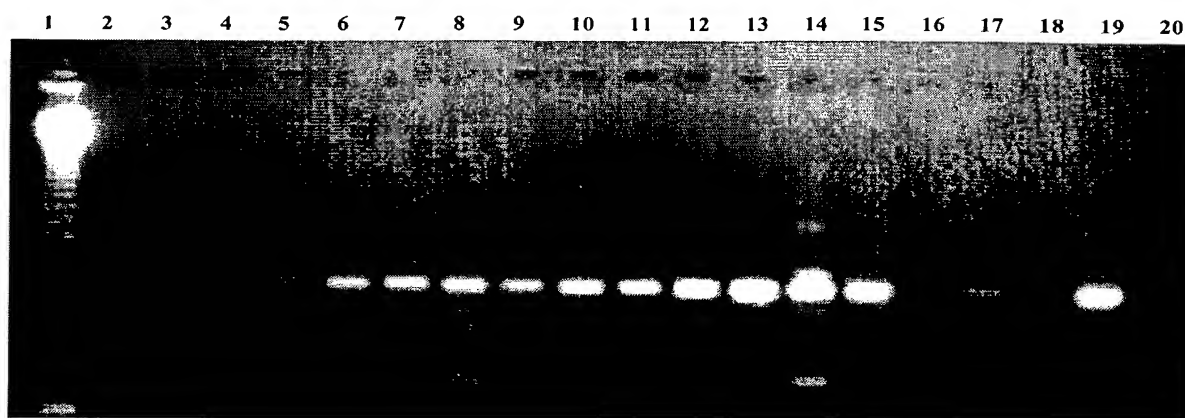
255. *Corynebacterium diphtheriae* (SEQ ID NO. 255)

ATGCCAAAGCGCAATGACATCAAACACGTCCTGGTTATCGGTTCCGGTCCAATCGTTATCGGACAAGCGTGTGAG
TTTGACTATTCCGGAACACAAGCGTGCCGAGTTCTTAAAGAAGAAGGACTTCGCGTCACTTTGATCAACTCGAAT
CCGGCGACAATCATGACGGATCCAGAGTTTGCTGATCATAATATGTTGAGCCGATTGAGCCGGAATATATTGAA
AAGATTTTTGAAAAAGAGATCGCTGAGGGACACCCCGTTGATGCTGTCTTGGCAACACTTGGTGGGCAAACGGCA
TTGAATGCCGCTATCAAATTAGATCGTCGCGGATCTCTCGAAAAATACAACGTAGAACTCATCGGTGCAGACATC
GACGCCATTGAGCGCGGCGAGGACCGCCAGAAATTCAAAGATATCGTTGCGAAAATTGGCGGCGAATCAGCGCGT
TCCCGTGTATGCCACAATATGCAAGAGGTATATGACACCGTTGAAGAGCTCGGCCTTCCGGTAGTTGTACGCCCT
TCCTTCACTATGGGCGGTTTGGGGTCCGGACTTGCTTCAATCAAGAGGATCTCGAACGAATTGCCGGCGGTGGA
CTCGCAGCGTCTCCCGAAGCAAACGTGCTTATTGAAGAATCAATTCCTGGCTGGAAGAATATGAGCTTGAGCTC

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ATGCGTGATGGTGCTGATAACGTTGTGGTTATTTGTTCCATTGAAAATGTTGATGCACTAGGCGTACACACAGGT
GATTCTGTTACTGTGCGACCTGCTTTGACTCTGACTGATCGTGAATACCAAAGATGCGTAATCAAGGCATCGCG
ATTATTCGTGAAGTAGGGGTCGACACCGGTGGATGTAACATCCAATTTGCGGTAAATCCACGTGATGGTCGTTTG
ATCACCATTGAGATGAATCCTCGTGTATCTAGGTCATCCGCCCTTGTCATCGAAAGCAACGGGATTCCCCATCGCT
AAGATTGCTGCCAAGTTGGCTATCGGATACACGCTGGATGAAATTACTAATGACATCACCGGTGTTACGCCGGCG
GCTTTCGAGCCAACGCTCGATTACGTAGTAGTCAAGTCTCCGCGCTTTGCGTTTGAGAAGTTCACAGGATCCGAC
GACACATTGACTACAACGATGAAGTCCGTTGGTGAGGCAATGGCTCTTGCCGTAATTACATCGCGGCGTTGGGT
AAAGTCATGCGTTTCGCTAGAAAACAAGCAAGTTGGTTTCTGGACAACAAGTGATGAATTCCTTGCTGGGGATCGC
GCTAAGAATCTTGACGCAGTGTTAGAAGATCTGAAACGCCCGACAGAAGGGCGGATGTATGACGTGGAGCTGGCT
CTTCGCCTTGCGGCTCAATTGAAGAAGTACATCAAGCGTCTGGGCTTGATCCATGGTTCTTGCGGAGCTTCAG
TCATTAATAGATTTCCGAGAATCCTTGATGAAGGCACCGGTGCTGGATGAGCCGTTGCTTCGAAAAGCCAAATTC
TTCGGATTGTCTGACCGCCAAATCGCGGCCCTTCGTCCCGAATTTGCAGGGGAAGACGGCGTTTCGTGCTTGCGA
TGGTCAATTGGGAGTACGGCCAGTATTTAAGACTGTAGATACGTGCGCTGCAGAATTTGAAGCTACGACTCCATAC
CATTATTCAGCATATGAACTCGATCCAGCTGCTGAATCGGAAGTACGTCTCAAACCTGAAAAAGACAAGATCATC
ATTTTGGGATCAGGTCCGAACCGAATTGGCCAAGGTATTGAGTTTGACTACTCATGTGTTTCATGCTGCGCTCGAA
CTTTCACGCGTGGGGTATGAGACAGTTATGGTTAACTGCAACCCAGAAACCGTGTGACAGATTATGACACCGCT
GACCGTCTGTATTTGAGCCACTGACATTTGAAGATGTTATGGAGGTCTACCACGCCGAATCAGAATCTGGACAT
GTTGCCGGTGTGATCGTTCAGCTTGGCGGACAACTCCACTTGGACTAGCCGAAAAGCTTCGTGATGCGGGTGTC
CCGGTCATTGGTACTACTCCAGAGGCTATCGATCTAGCTGAAGATCGAGGAGAATTCGGTGAAGTATTGCGTAAA
GCGCAATTGCCAGCTCCAGCTTTCCGTACCGCTACATCATTTGAGGAAGCTAAAACCTGTTGCCAATAACATTGGT
TACCCAGTATTAGTTCGTCCATCTTACGTCTTGGGCGGCCGTGGCATGGAAATCGTATACGACGAAAATTCCTTG
CACGCGTACATCGAGCGAGCTACCGAGATCACGAGTGATCACCCAGTGCTCGTGGATCGCTTTTGTAGATAATGCG
ATTGAAATTGACGTTGATGCGCTTTGTGATGGCGAAAATGTCTACCTTGCTGGTGTATGGAACACATTGAAGAA
GCTGGTATTCACCTCCGGTGACTCTGCTTGTGCGCTGCCACCTATGACGCTAGGTGCCGAAGATATCGAAAATGTC
CGTCGCTCAACAGAAGCGTTGGCACATGGTATCGGCGTTAAAGGATTGATGAATGTTCAATATGCCTTGAAGGAT
GACATTCTTTATGTGATTGAGGCCAACCTCGTGATCTCGTACAGTGCCTTTTGTCTCCAAAGCTACGGGTGTC
CACTTAGCAAAAGCAGCAGCGCAATCATGACTGGGGCAACGATTCCTGAGCTTCAAGCGGAGGGAATGATTCCA
ACCGGTTACGATGGTGGTTCTTTGCCAGAGAATTCGCCGATTGCGGTGAAGGAAGCAGTACTTCCGTTCAATCGA
TTCCGTCGTCCTGATGGCACAATGTTGGATACTTTGCTAAGTCTGAGATGAAATCAACGGGCGAAGTCATGGGG
CTGGCTGATAATTTTGGTGCTGCATATGCTAAGGCAGAACAGGCGGCTTTTGGTGCACTTCCAACCTGAAGGCACT
GTCTTCGTATCAGTAGCAAACCGCGATAAGCGTACTTTGATTTTCCCAATTCAGCGCCTAGCTTCACTTGGATTC
CGAGTACTGGCAACATCAGGCACAGCCGGAATGCTACGTGCGAATGGTATTGAATGCGAAGTTGTATTGAAGCAG
ACCCAAGTGCAGGAAGCACGACAAAACGGCACTGAGGGGCAGCGTTCGTTAGTGGATATGATTAAAGCCGGCGAG
GTGGACCTCATTCTTAATACACCTGCAGGGTCTTCAGGAGCGCGTCACGACGGTTACCAGATTCGCGCAGCGGCA
GTCAACGTTGGCGTTCTCTGGTTACTACCGTGCAAGGTGTTACTGCGGCAGTACAGGGAATCGAAGCGCTTAGG
GCTGGTGAGCTCAGCGTTCGAGCGCTGCAAGAGCTAGATCATTCGGTGACTCGATGA

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Figure 10. Amplification of molecular marker VI (pgi) in Gram-negative bacteria

1. DNA Ladder (123 bp)
2. *Pseudomonas aeruginosa*
3. *Pseudomonas diminuta*
4. *Stenotrophomonas maltophilia*
5. *Pseudomonas pseudoalcaligenes*
6. *Burkholderia cepacia*
7. *Pseudomonas putida*
8. *Pseudomonas syringae*
9. *Providencia stuartii*
10. *Proteus mirabilis*
11. *Proteus vulgaris*
12. *Citrobacter freundii*
13. *Enterobacter aerogenes*
14. *Klebsiella oxytoca*
15. *Klebsiella pneumoniae*
16. *Haemophilus influenzae*
17. *Legionella pneumophila*
18. *Serratia liquefaciens*
19. *Serratia marcescens*
20. Negative control

Figure 11. Molecular marker VI (pgi) sequences amplified from different Gram negative bacteria (SEQ ID NOs 256-277).

256. *Providencia stuartii* (SEQ ID NO. 256) *PSTU*
TATGGTNNGCGATTGGCCTATCCATTATCTTGTAACCGTGGGTATGACAATTTTGTTTCAGCTCCTCGAAGGGGCT
CATGCAATGGATAAGCACTTTACCCAAACGGCTTTTGAAAAGAATATTCCTGTTCTCCTTGGCTTAATTGGCATT
TGGTATAACAACCTTTTTTGAGTCGGAACTGAAGCGATTCTGCCATATGATCAATATATGCACCGTTTTGCGGCT
TATTTCCAACAAGGAAATATGGAGTCAAATGGTAAGTATATTGACCGTAATGGCAACAAAGTTTCTTATCAAACG
GGGCAATTATTTGGGGTGAACCGGGCACGAACGGCCAACATGCCTTTTATCAATTGATCCATCAAGGAATAAA
ATGATCCCTTGTGATTTTATTGCGCCAGCAGTAACGCATAATCCACTCGGTGATCATCACGATAAATTACTGTCTG
AACTTCTTCGCC

257. *Enterobacter cloacae* (SEQ ID NO. 257) *ECLC*
CTTTGTGGTNCTGCGATCGGCCTGTCTATCATTCTCTCCGTGGGCTTCGACAACCTTTGTTGAGCTGCTCTCCGGC
GCGCACGCGATGGACAAACACTTCTCCACCACCGCACCTGAGAAAAACCTGCCGGTGCTGCTGGCGCTGATCGGT
ATCTGGTACAACAACCTTCTCGGCGCAGAGACCGAAGCGATCCTGCCGTACGACCAGTACATGCACCGCTTCGCG
GCTTACTTCCAGCAGGGCAATATGGAATCCAACGGTAAATACGTTGACCGTAACGGCAACGCGGTGGATTACCAG
ACTGGCCCAATCATCTGGGGTGAGCCAGGCACCAACGGTCAGCACGCGTTCTACCAGCTGATTCACCAGGGGACC
AAAATGGTACCGTGCGATTTTCATCGCCCCGGCTATCACCCACAATCCACTGTCTGATCACCATCCTAAACTGCTG
TCTAACTTCTTCGCC

258. *Proteus mirabilis* (SEQ ID NO. 258) *PMIR*
CTTATGGTNNGCAATTGGTTTATCCATTGTATTATCTATTGGTTATGACAACCTTTGAGCAGTTACTGTCCGGTGC
TCATGCTATGGATAATCACTTTAGAACCACTGAAGCTGAAAATAATATTCGATGATATTGGCGCTTATTGGCAT
TTGGTATAACAATTTTTTTGGTACCGAACTGAAGCGATTCTGCCATACGATCAATATATGCACCGTTTTGCTGC
TTACTTCCAACAAGGTAATATGGAATCCAATGGTAAATATATCGACCGTGATGGAAACAAAGTCAGTTACCAAAC
CGGACCTATTATTTGGGGAGAGCCGGGACTAATGGTCAGCATGCGTTTTATCAATTAATTCATCAAGGAACCAA
ACTGATCCCTTGTGATTTTATTGCACCAGCGATCAGCCATAATCCATTATCTGATCATCATGCAAACTAATGTC
GAACTTCTTCGCAA

259. *Proteus vulgaris* (SEQ ID NO. 259) *PVUL*
TTATGGTNNGCTATTGGTTTGTCTATCGCTCTTTCCGTTGGTTATGATAATTTGAGCAATTATTGGAAGGTGCCC
ATGCAATGGATAACCATTTCCAAACGACAGCTGCTGAAAATAACCTACCAATGATCCTCGCGCTGATTGGCATT
GGTATAACAATTTTTTTGGTACAGAACTGAAGCGATTCTGCCCTATGATCAATACATGCATCGTTTTGCAGCCT
ATTTCCAACAAGGCAATATGGAGTCAAATGGTAAGTATATTGATCGCGATGGTAACGCAGTTAACTATCAAACG
GACCTATTATTTGGGGTGAACAGGAATAATGGTCAGCATGCGTTTTACCAATTAATTCATCAGGGTACAAAAA
TGATCCCTTGTGATTTTATTGCGCCTGCAATTAGTCATAATCCATTAAGTGATCACCATGCTAAGTTGATGTCTA
ACTTCTTCGCNA

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260. *Enterobacter aerogenes* (SEQ ID NO. 260) EAER

CTGTGGTCCGCCTCGGTCTGTCTATCATTCTGTCCGTCGGCTTCGACAACTTCGTTTCAGCTGCTGTCCGGCGCCC
ACGCCATGGACAAACACTTCTCTACCACGCCGGCTGAGAAAAACCTGCCGGTACTGCTGGCGCTGATTGGTATCT
GGTACAACAATTTCTTCGGCGCCGAAACCGAAGCAATTCTGCCGTACGATCAGTACATGCATCGCTTTGCCGCTT
ACTTCCAGCAGGGCAACATGGAATCCAACGGTAAGTACGTTGACCGTAACGGCAACGTCGTGGATTACCAGACTG
GCCCTATCATCTGGGGCGAGCCGGGGACTAACGGTCAGCACGCGTTCTATCAGCTGATCCACCAGGGCACCACAAA
TGGTACCGTGCGATTTTCATCGCCCCGGCTATCACCCATAACCCGCTGTCTGACCACCATCAGAACTGCTGTCTA
ACTTCTTCGCAA

261. *Klebsiella pneumoniae* (SEQ ID NO. 261) KPNE

CTGTGGTCCGGCGATTGGTCTGTCCATCATTCTCTCCGTGGGCTTCGACAACTTCGTTGAGCTGCTGTCCGGCGCG
CATGCGATGGATAAGCACTTCTCCACCACTCCGGCGGAGAAAAACCTGCCGGTGTCTGCTGGCGCTGATCGGCATC
TGGTACAACAACCTTCTTCGGTGCGGAAACCGAAGCGATTCTGCCGTACGACCAGTACATGCACCGCTTTGCCGCT
TACTTCCAGCAGGGCAACATGGAGTCCAACGGTAAGTATGTTGACCGTAACGGCCACGCGGTAGACTACCAGACT
GGCCCAATCATCTGGGGTGAGCCGGGCACCAACGGTCAGCACGCGTTCTACCAGCTGATCCACCAGGGCACCACAAA
ATGGTACCGTGCGATTTTCATCGCTCCGGCTATCACCCACAACCCGCTGTCTGACCACCATCAGAACTGCTGTCT
AACTTCTTCGCNAA

262. *Escherichia coli* 0157 :H7 (SEQ ID NO. 262) ECO157

TTTGTGGTNGCGATTGGCCTGTCGATTGTTCTCTCCATCGGCTTTGATAACTTCGTTGAACTGCTTTCTGGCGCA
CACGCGATGGACAAGCATTTCTCCACCACGCCTGCCGAGAAAAACCTGCCTGTACTGTTGGCGCTGATTGGCATC
TGGTACAACAATTTCTTTGGTGCGGAAACTGAAGCGATTCTGCCGTATGACCAGTATATGCACCGTTTCGCGGCG
TACTTCCAGCAGGGCAATATGGAGTCCAACGGTAAGTATGTTGACCGTAACGGTAACGTTGTGGATTACCAGACT
GGCCCGATTATCTGGGGTGAACCAGGCACTAACGGTCAGCACGCGTTCTACCAGCTGATCCACCAGGGAACCAAAA
ATGGTACCGTGCGATTTTCATCGCTCCGGCTATCACCCATAACCCGCTCTCTGATCACCACCAGAACTGCTGTCT
AACTTCTTCGCNAA

263. *Escherichia coli* K12 (SEQ ID NO. 263) ECOK12

CTTTGTGGTNGCGATTGGCCTGTCGATTGTTCTCTCCATCGGCTTTGATAACTTCGTTGAACTGCTTTCCGGCGC
ACACGCGATGGACAAGCATTTCTCCACCACGCCTGCCGAGAAAAACCTGCCTGTACTGCTGGCGCTGATTGGCAT
CTGGTACAACAATTTCTTTGGTGCGGAAACTGAAGCGATTCTGCCGTATGACCAGTATATGCACCGTTTCGCGGCG
GTACTTCCAGCAGGGCAATATGGAGTCCAACGGTAAGTATGTTGACCGTAACGGTAACGTTGTGGATTACCAGAC
TGGCCCCGATTATCTGGGGTGAACCAGGCACTAACGGTCAGCACGCGTTCTACCAGCTGATCCACCAGGGAACCAA
AATGGTACCGTGCGATTTTCATCGCTCCGGCTATCACCCATAACCCGCTCTCTGATCATCACCAGAACTGCTGTC
TAACTTCTTCGCNAA

264. *Citrobacter freundii* (SEQ ID NO. 264) CFRE

NTGTGGTCTGCAATCGGCCTGTCCATCATCCTGTCCGTAGGCTTCGACAATTTTGTGAGCTGCTCTCCGGCGCG
CATGCGATGGACAAACACTTCTCCACCACCCCGCTGAGAAAAACCTGCCGGTGTCTGCTGGCGCTGATCGGTATC

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TGGTACAACAACCTTCTTCGGTGCCGAAACCGAAGCGATTCTGCCGTATGACCAGTATATGCACCGTTTCGCGGCC
TACTTCCAGCAGGGCAACATGGAATCCAACGGTAAATACGTTGACCGTAACGGCAATGCGGTGGATTACCAGACT
GGCCCAATCATCTGGGGTGAGCCGGGTACTAACGGCCAGCATGCGTTCTACCAGCTGATCCACCAGGGCACCAAA
ATGGTGCCGTGCGATTTTCATCGCGCCGGCAATCACCACAACCCGCTGTGCGATCACCATCCGAAACTGCTGTCT
AACTTCTTCGCAA

265. *Haemophilus influenzae* (SEQ ID NO. 265) HINF

CTTNGGTNGCCTTGGTCTTTCAATTGCGCTATCAATTGGCTTTGAAAACCTTTGAAGCGTTATTAAATGGCGCGCA
TGAAATGGATGAACATTTCCGCTCTACTCCAATCGAACAAAATATCCCAACCACTTTAGCATTAGTTGGTTTATG
GAATACCAATTTTCTTGGTGCGCAAACAGAAGCGATCTTACCTTATGATCAATATTTACATCGCTTCGCAGCTTA
TTTTCAACAAGGTAATATGGAATCAAATGGTAAATATGTGGATCGTGATGGCAATGTCATTAACAATTATCAAAC
TGGCCCTATCATTTGGGGAGAACCTGGTACAAACGGACAACACGCGTTCTATCAATTAATTCATCAAGGCACTAC
TTTAATTCCTTGTGATTTTATCGCACCCGCTCAAAGCCATAACCCATTGGCAGATCATCACAATAAATTGCTTTC
AAACTTCTTCGCAA

266. *Serratia marcescens* (SEQ ID NO. 266) SMAR

TGTGGTCGGCGATCGGTTTGTGCGATTGCGCTGTCCATCGGTTATGACAACTTCGAGCAGCTGCTGAGCGGCGCGC
ACGCCATGGACAAGCACTTCGCCGAAACGCCGGCGGAGAAAAACCTGCCGGTGTTGCTGGCGCTGATCGGTATTT
GGTACAACAACCTTCTTTGGCGCCGAAACCGAAGCCATTCTGCCGTACGATCAGTACATGCACCGTTTTGCCGCTT
ACTTCCAGCAGGGCAACATGGAATCCAACGGCAAGTACGTGATCGCAACGGCAACCCGGTGGATTACCAGACCG
GTCCCATCATTTGGGGCGAGCCGGGCACCAACGGCCAGCATGCGTTCTATCAGTTGATCCACCAGGGCACCAAGC
TGGTGCCGTGCGATTTTCATCGCGCCGGCCATCAGCCATAACCNCTGGGCGATCATCACGCCAAACTGCTGTCCA
ACTTCTTGCCAA

267. *Morganella morganii* (SEQ ID NO. 267) MMOR

GTGGTCGGCGATTGGTCTGTCTATCGTGCTCTCTGTGCGTTATGACAACTTCACGCAGTTGCTCGATGGTGCGTA
TGCCATGGACAAGCACTTCACCGAAACTGAATTCTCACAGAATATTCGGTGCTGCTGGCGCTGATTGGTCTGTG
GTACAACAATTTCTTCGGTGCGGAAACAGAAGCAATTCTGCCTTATGATCAGTACATGCACCGCTTTGCGGCCCTA
TTTCCAGCAGGGCAATATGGAGTCCAACGGGAAATATGTGGATCGTAACGGTAAGGTGGTTTCTCATCAGACCGG
TCCGTTATCTGGGGTGAGCCCGGCACCAACGGGCAGCATGCGTTTTATCAGCTGATCCATCAGGGTACCAAACCT
GATCCCGTGTGATTTTATCGCACCCGGCTCAGAGCCATAATCCGCTGGGGGATCATCACAGTAAACTGCTGTGCGAA
CTTCTTCGCAA

268. *Klebsiella oxytoca* (SEQ ID NO. 268) KOXY

GTGGTAGCCTCGGCCTGTCCATCATCCTGTCCGTGGGCTTCGACAACTTTGTTGAGCTGCTCTCCGGCGCGCACG
CGATGGATAAACACTTCTCCACCACCCCGGCTGAGAAAAACCTGCCGGTGCTGCTGGCGCTGATCGGTATCTGGT
ACAACAACCTTCTTCGGCGCTGAAACCGAAGCGATTCTGCCGTACGACCAGTATATGCACCGTTTTGCCGCTTACT
TCCAGCAGGGCAACATGGAATCCAACGGTAAATACGTTGACCGTAACGGCAACGCCGTGGATTACCAGACGGGCC
CAATCATCTGGGGCGAGCCGGGGACCAACGGTCAGCACGCGTTCTACCAGCTGATTACACAGGGGACCAAAATGG

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TGCCTTGC GACTTTATCGCGCCGGCGATTACGCATAACCCGCTGTCCGATCACCATCCGAAGCTGCTGTCTAACT
TCTTCGCCCAA

269. *Shigella sonnei* (SEQ ID NO. 269)**SSON**

TTTGTGGTNGCGATTGGCCTGTCGATTGTTCTCTCCATCGGCTTTGATAACTTCGTTGAACTGCTTTCTGGCGCA
CACGCGATGGACAAGCATTTCTCCACCACGCCTGCCGAGAAAAACCTGCCTGTCTGCTGGCGCTGATTGGCATC
TGGTACAATAATTTCTTTGGTGCGGAAACTGAAGCGATTCTGCCGTATGACCAGTATATGCACCGTTTCGCGGCG
TACTTCCAGCAGGGCAATATGGAGTCCAACGGTAAGTATGTTGACCGTAACGGTAACGTTGTGGATTACCAGACT
GGCCCGATTATCTGGGGTGAACCAGGCACTAACGGTCAGCACGCGTTCTACCAGCTGATCCACCAGGGAACCAAA
ATGGTACCGTGCGATTTCATCGCCCCGGCTATCACCATAACCCGCTCTCTGATCACCACCAGAACTGCTGTCT
AACTTCTTCGCAA

270. *Salmonella enteritidis* (SEQ ID NO. 270)**SENT**

GCTGTGGTCTGCNTCGGGCTGTCCATTATTCTGTCCGTCGGTTTCGACAACTTTGTGAGCTGCTTTCCGGCGCG
CACGCGATGGACAAGCATTTCTCCACCCTCCGGCGGAGAAAAACCTACCCATTCTGCTGGCGTTGATTGGCATC
TGGTACAACAATTTCTTCGGCGCGGAAACCGAAGCCATTCTGCCGTACGACCAGTATATGCACCGTTTCGCCGCC
TACTTCCAGCAGGGTAACATGGAATCCAACGGTAAATACGTTGACCGTAGCGGCAACGCCGTGGATTACCAGACA
GGCCCAATTATCTGGGGCGAACCAGGCACCAACGGTCAGCACGCGTTTTATCAATTGATTACCCAGGGTACTAAA
ATGGTGCCGTGTGATTTTATCGCCCCGGCTATCACCATAACCCGCTATCCGATCATCATCAGAAGCTGCTGTCT
AACTTCTTCGCAA

271. *Salmonella enterica hadar* (SEQ ID NO. 271)**SHAD**

CGCTGTGGTCTGCNTCGGGCTGTCCATTATTCTGTCCGTCGGTTTCGACAACTTTGTGAGCTGCTTTCCGGCGC
GCACGCGATGGACAAGCATTTCTCCACCCTCCGGCGGAGAAAAACCTACCCATTCTGCTGGCGTTGATTGGCAT
CTGGTACAACAATTTCTTCGGCGCGGAAACCGAAGCCATTCTGCCGTACGACCAGTATATGCACCGTTTCGCCGC
CTACTTCCAGCAGGGTAACATGGAATCCAACGGTAAATACGTTGACCGTAGCGGCAACGCCGTGGATTACCAGAC
AGGCCCAATTATCTGGGGCGAACCAGGCACCAACGGTCAGCACGCGTTTTATCAATTGATTACCCAGGGTACTAA
AATGGTGCCGTGTGATTTTATCGCCCCGGCTATCACCATAACCCGCTATCCGATCATCATCAGAAGCTGCTGTC
TAACTTCTTCGCAA

272. *Salmonella enterica brandenburg* (SEQ ID NO. 272) SBRA

NCGCTGTGGTCTGCCTCGGGCTATCCATTATTCTGTCCGTCGGTTTCGACAACTTTGTGAGCTGCTTTCCGGCG
CACACGCGATGGACAAGCATTTCTCCACCCTCCGGCGGAGAAAAACCTACCCGTTCTGCTGGCGTTGATTGGCA
TCTGGTACAACAATTTCTTCGGCGCGGAAACCGAAGCCATTCTGCCGTACGACCAGTATATGCACCGTTTCGCCG
CCTACTTCCAGCAGGGCAACATGGAATCCAACGGTAAATACGTTGACCGTAACGGCAACGCCGTGGATTACCAGA
CAGGCCCAATTATCTGGGGCGAACCAGGCACCAACGGTCAGCACGCGTTTTATCAATTGATTACCCAGGGTACTA
AAATGGTGCCGTGTGATTTTATCGCCCCGGCTATCACCATAACCCGCTATCCGATCATCATCAGAAGCTGCTGT
CTAACTTCTTCGNAA

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273. *Salmonella enterica* derby (SEQ ID NO. 273) SDER

GCTGTGGTCTGCNTCGGGCTGTCCATTATTCTGTCCGTCGGTTTCGACAACTTTGTGAGCTGCTTTCCGGCGCG
CACGCGATGGACAAGCATTCTCCACCACTCCGGCGGAGAAAAACCTACCCATTCTGCTGGCGTTGATTGGCATC
TGGTACAACAATTTCTTCGGCGCGGAAACCGAAGCCATTCTGCCGTACGACCAGTATATGCACCGTTTCGCCGCC
TACTTCCAGCAGGGTAACATGGAATCCAACGGTAAATACGTTGACCGTAACGGCAACGCCGTGGATTACCAGACA
GGCCCAATTATCTGGGGCGAACCAGGCACCAACGGTCAGCACGCGTTTTATCAATTGATTACACAGGGTACTAAA
ATGGTGCCGTGTGATTTTATCGCCCCGGCTATCACCCATAACCCGCTATCCGATCATCATCAGAAGCTGCTGTCT
AACTTCTTCGCNAA

274. *Salmonella enterica* virschow (SEQ ID NO. 274) SVIR

CGCTGTGGTCTGCCTCGGGCTGTCCATTATTCTGTCCGTCGGTTTCGACAACTTTGTGAGCTGCTTTCCGGCGCG
GCACGCGATGGACAAGCATTCTCCACCACTCCGGCGGAGAAAAACCTACCCATTCTGCTGGCGTTGATTGGCAT
CTGGTACAACAATTTCTTCGGCGCGGAAACCGAAGCCATTCTGCCGTACGACCAGTATATGCACCGTTTCGCCGCC
CTACTTCCAGCAGGGTAACATGGAATCCAACGGTAAATACGTTGACCGTAACGGCAACGCCGTGGATTACCAGAC
AGGCCCAATTATCTGGGGCGAACCAGGCACCAACGGTCAGCACGCGTTTTATCAATTGATTACACAGGGTACTAA
AATGGTGCCGTGTGATTTTATCGCCCCGGCTATCACCCATAACCCGCTATCCGATCATCATCAGAAGCTGCTGTC
TAACTTCTTCCAA

275. *Salmonella enterica* typhimurium (SEQ ID NO. 275) STPM

GCTGTGGTCTGCNTCGGGCTGTCCATTATTCTGTCCGTCGGTTTCGACAACTTTGTGAGCTGCTTTCCGGCGCG
CACGCGATGGACAAGCATTCTCCACCACTCCGGCGGAGAAAAACCTACCCATTCTGCTGGCGTTGATTGGCATC
TGGTACAACAATTTCTTCGGCGCGGAAACCGAAGCCATTCTGCCGTATGACCAGTATATGCACCGTTTCGCCGCC
TACTTCCAGCAGGGTAACATGGAATCCAACGGTAAATACGTTGACCGTAACGGCAACGCCGTGGATTACCAGACA
GGCCCAATTATCTGGGGCGAACCAGGCACCAACGGTCAGCACGCGTTTTATCAATTGATTACACAGGGTACTAAA
ATGGTGCCGTGTGATTTTATCGCCCCGGCTATCACCCATAACCCGCTATCCGATCATCATCAGAAGCTGCTGTCT
AACTTCTTCGCNAA

276. *Salmonella enterica* paratyphi B (SEQ ID NO. 276) SPTB

CGCTGTGGTCTGCNTCGGGCTGTCCATTATTCTGTCCGTCGGTTTCGACAACTTTGTGAGCTGCTTTCCGGCGCG
GCACGCGATGGACAAGCATTCTCCACCACTCCGGCGGAGAAAAACCTACCCATTCTGCTGGCGTTGATTGGCAT
CTGGTACAACAATTTCTTCGGCGCGGAAACCGAAGCCATTCTGCCGTATGACCAGTATATGCACCGTTTCGCCGCC
CTACTTCCAGCAGGGTAACATGGAATCCAACGGTAAATACGTTGACCGTAACGGCAACGCCGTGGATTACCAGAC
AGGCCCAATTATCTGGGGCGAACCAGGCACCAACGGTCAGCACGCGTTTTATCAATTGATTACACAGGGTACTAA
AATGGTGCCGTGTGATTTTATCGCCCCGGCTATCACCCATAACCCGCTATCCGATCATCATCAGAAGCTGCTGTC
TAACTTCTTCCAA

277. *Serratia liquefaciens* (SEQ ID NO. 277) SLIQ

NTGTGGTCGGCGATTGGCCTGTCTATCGCCCTGTCAGTGGGTTACGAGAATTTGAACAGTTGCTGAGCGGCGCG
CACGCGATGGACAAACACTTCGCGCAAACGCCGGCAGAGCAAAACCTGCCGGTGCTGCTGGCGTTGATCGGTATC
TGGTACAACAATTTCTTCGGTGCAGAAACCGAAGCTATCCTGCCGTACGACCAGTACATGCACCGTTTTCGCCGCT

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TACTTCCAGCAGGGCAACATGGAATCCAACGGTAAATATGTCGATCGCAACGGCAATCCGGTGGACTACCAGACC
GGCCAATCATCTGGGGCGAGCCGGGCACCAACGGGCAGCACGCGTTTTACCAACTGATCCACCAGGGGACCAAA
CTGGTGCCTTGTGACTTTATCGCGCCGGCCATCAGCCATAATCCGCTGAGCGACCACCATGCAAAACTGCTGTCG
AACTTCTTCGCCAA

Figure 12. Molecular marker VII (EG10839 & EG11396 or *sfrB* & *yigC*) in Gram-negative bacteria (SEQ ID NOs 278-303).

**278. *Neisseria meningitidis* serogroup A strain Z2491
(SEQ ID NO. 278)**

ACAGAAAATCCTCGAAGACACCCCTGCTGGAACAATGGCAGTGGCTCAAACCTAAAGAACCGTAAACATCCTGCGT
ACACAAATGCCGTCTGAAACGCCCCACGCTTCAGACGGCAGACCGTAAACCTACAACCCCAATTCCTCCCAAA
TCTCATCAATCTTAGCCGTAACCGCAGGGTCTTTTTTAATCACCCGTCCCCATTGCGGGTCGGTTTCGCCCCGGCC
ACTTGTTGGTCGCATCCAAACCCATTTTGCCGCCAAGTCCGCTGACGGGGCTGGCGAAGTCGAGGTAGTCGATGG
GCGTGTTTTCCATCAAAACGGTATCGCGCACGGGGTCCATGCGCGTGGTTACCGCCCAGATGACTTCTTTCCAGT
CGCGCACATCCACATCGTCATCCACCACAATGATGAATTTGGTGTACATAAACTGGCGCAGGAACGACCAGCAGC
CCATCATCACGCGCTTGGCGTGTCCGGCGTACTGTTTTTTCATGCTCACCACCGCCATGCGGTAGGAGCAGCCTT
CGGGCGGCAGGTAAAAATCGGTGATTTGCGGGAACTGCTTTTGCAAAGCGGTACGAACACTTCGTTCAACGCCA
CGCCAAAACGGCGGGTTCATCGGGCGGTTTGCTGTGTAGGTAGAGTGGTAAATCGGGTTTTCGCGCATGGTGA
TGCGTTCGACCGTAAACACGGGGAAATGGTCTCTGCTGTTGTAATAGCCCGTGTGGTCGCCGTATGGACCTTCCA
ACGCGGTTTTGTTTTGGATGGATGACGCTTCCAACACGATTTCTGCGCGGGCAGGCATTGCAAATCGTTGCCGA
TACATTTACCCAGTTCCGTCCGCGAACC GCGCAGCAGTCCGGCAAACCTGGTATTCGCTCAAGGTATCGGGAACGG
GCGTTACCGCGCCCAAAATGGTGGCAGGGTCGCAGCCGAGCACGACGGCGACGGGATACGGCGTATCGGGATTGA
GTTTGCGGAATTCCTGATAATCCAGCGCGCCGCCGCGATGCGACAGCCAGCGCATAATCAGCTTGTTTATGCCGA
TTAATTGTTGGCGGTAAATGCCGAGATTTTGCGGTTTTTGTGCGGCCCGCGCGTGACGGTCAAGCCCCACGTTA
CCAGCGGCGCAACGTCTTCGGGCCAGCAATGCTGAATCGGAAGTTGATACAAATCAACGTCTTCGCCCTTCCATA
CGATTTCTTGACACGGCGCATTTTTTACCACGTTTCGGCGCCATGCTCCAAATGTCTTTCAAGAGCGGCAGTTTGG
AAAACGCGTCTTTAATGCCTTTGGGCGGTTTCGGGTTCTTTCAAATACGCCAGCGTCTGCCCGATTTTCGCGCAGCT
TGGACACGCTGTCCGCGCCCATGCCATCGCCACACGTTTCGGGCGTGCCGAACAGGTTTGCCAACACGGGATAAT
CATAGCGGTACCGTCGGGCTTAAC TGGGTGTTCAAACAACAACGCCGGCCCTTCGGCGCGCAGCACGCGGTTCGG
CGATTTTCGGTCATTTCCAAATGCGGGGAAACGGGGTGCGCGATGCGTTTGAGTTTGCCCTGCTGCTCGAGCATGG
CGATGAAGTCGCGCAGGTCTTTGTATTTTCATATTCATCCTTTTTTGTCCTTTTATCCTGAGCAATCCGATTTCGGAT
ACCGCCCTATCCTTGCTGCGCTTCGGCATATTCTATGCCGTGATAAAAAGTCGCGTACCAGCGGATGTTTCGCTG
CCTTGATGGAGTTGCAACAAAGGACGTTGACCATCGGGTTGGGTAACGACATTGCAATGCAAACCGAAGGTGTGCG
GATTTCGTAAGGGGGCAGCCGTTGCAGATCATGCCGAAATAAACGGCGTTTTTCAGGGTTG

279. *Klebsiella oxytoca* (SEQ ID NO. 279)

ACGACCAGACGCCCATCATGACGCGTTTTGCGGTGACCGGCGTACTGCTTCTTCATCGTGACGACCGCCAGGCGAT
AGGAACAGCCTTCAGGCGGCAAATAGAAATCCACGATTTTCAGGAACTGCTTTTGAGAATGGGGACGAACACTT
CGTTCAGCGCAACGCCAGTACCGCCGGCTCATCCGGCGGGCGCCCGGTATAGGTCGAGTGATAGATGGCATCTT
CACGCTGAGTAATGTGGGTAACGGTAAAGACGGGGAAGTTATCCACTTCATTGTAGTAGCCAGTATGGTCGCCAT
AGGGGCCCTTCGGCGCCATTTCTCCGGCTTCAATATACCCTTCCAGCACGATCTCCGCGCTGGCGGGCACCTCAA
GATCGTTAGAGATGCACTTCACGACTTCGGTTTTGGTGCCGCGCAGTAGCCCGGCAAAAGCGTATTCGGAAAGAG
TATCCGGAACCGGAGTCACCGCCCCGAGAATGGTTGCCGGATCGGCGCCCAGCGCGACGGAGACGGGAAACGCT
CGCCAGGACGCGCCGCGCACCACTCCTGGAAGTCCAGCGCGCCGCCGCGATGCGATAGCCAAC

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280. *Salmonella enterica* subsp. *enterica* serovar***Paratyphi* A (SEQ ID NO. 280)**

ATGGACGCCATGAAATATCACGATTTACGCGACTTCCTGACGCTACTTGAGCAACAGGGGGAACATAAAACGCATC
ACGCTACCTGTGGATCCTCATCTGGAAATTACGGAAATCGCTGACCGCACGCTGCGTGCCGGTGGACCGGCGTTG
CTGTTTGAAAAGTCTTAAAGGTTACGCCATGCCGGTGCTGTGCAACCTTTTTGGCACGCCAAAACGCGTGGCGATG
GGCATGGGGCAGGATGATGTTTCCGCCTTACGGGAAGTGGGTAAATTATTAGCGTTTCTGAAAGAACCTGAGCCG
CCGAAAGGCTTTCGCGATCTGTTTGACAAGCTGCCGCAGTTTAAGCAAGTGCTGAATATGCCGACGAAACGGTTA
CGCGGCGCGCCTTGCCAGCAGAAAATCGCGTCTGGCGATGATGTGATTTAACGCGTCTTCCTGTCTATGACCTGT
TGGCCGGACGACGCCGCGCCGCTGATTACCTGGGGACTGACGGTAACGCGTGGCCCGCACAAAGAACGGCAAAAC
CTGGGCATTTATCGTCAGCAGTTGATAGGTAAAAATAAGCTGATTATGCGCTGGCTGTCTCACCGCGGCGGCGCG
TTGGATTTTCAGGAGTGGTTAGCCGCGCGTCCGGGTGAACGTTTCCCGGTCTCCGTGCGATTGGGCGCCGATCCG
GCGACGATACTTGGCGCCGTGACTCCTGTTCCCGATACTCTGTGCGAGTATGCCTTTGCGGGCCTGCTGCGCGGC
ACGAAAACCTGAAGTGGTTAAATGCCTTTCTAACGATCTGGAAGTGCCTGCCAGCGCCGAGATTATCCTTGAAGGT
TACATTGAGCCGGGAGAGATGGCGCCGGAAGGACCGTATGGCGATCATACGGGCTATTATAATGAAGTGGATAAC
TTTCCGGTCTTTACCGTCACGCATATTACGCAGCGTGAGGATGCCATCTATCACTCCACCTATACCGGGCGTCCG
CCCGATGAGCCTGCGGTATTAGGGGTGGCGCTCAATGAAGTCTTCGTGCCTATTCTGCAAAAACAGTTTCCGGAA
ATCGTCGACTTTTATCTGCCGCCGGAAGGGTGTCTTACCGCCTGGCGGTAGTGACGATGAAAAAGCAGTACGCT
GGTCATGCGAAACGCGTCATGATGGGCGTCTGGTCGTTTTTGCGCCAGTTTATGTATACGAAATTTGTTATCGTT
TGCGATGATGACGTTAACGCACGCGACTGGAATGATGTGATCTGGGCGATTACCACCCGTATGGACCCTGCGCGG
GATACGGTGCTGGTTGAAAATACGCCGATTGATTACCTGGATTTTGCCTCGCCGGTCTCCGGGCTGGGTTCAAAA
ATGGGGCTGGATGCCACAAACAAATGGCCGGGCGAAACCCAACGCGAGTGGGGTTCGTCTATTGTTAAAGATCCT
GAAGTTACCGCACGTATTGATGCGATTTGGGATGAGCTGGCTATCTTTAAATAA

281. *Salmonella typhimurium* LT2 (SEQ ID NO. 281)

GAGGCTACAATGGACGCCATGAAATATCACGATTTACGCGACTTCCTGACGCTACTTGAGCAGCAGGGGGGAACATA
AAACGCATCACGCTACCTGTGGATCCTCATCTGGAAATCACGGAAATCGCTGACCGCACGCTGCGTGCCGGTGGGA
CCGGCGTGTCTGTTTGAAAATCCTAAAGGTTACGCCATGCCGGTGCTGTGCAACCTTTTTGGCACGCCAAAACGC
GTGGCGATGGGCATGGGGCAGGATGATGTTTCCGCCTTACGGGAAGTGGGTAAATTATTAGCGTTTCTTAAAGAA
CCTGAGCCGCCGAAAGGCTTTCGCGATCTGTTTGACAAGCTGCCGCAGTTTAAGCAAGTGCTGAATATGCCGACG
AAACGGTTACGCGGCGCGCCTTGCCAGCAGAAAATCGCGTCTGGCGATGATGTGATTTAACGCGTCTTCCTGTC
ATGACCTGTTGGCCGGACGACGCCGCGCCGCTGATTACCTGGGGACTGACGGTAACGCGTGGTCCGCACAAAGAG
CGGCAAAACCTGGGCATTTATCGTCAGCAGTTGATAGGTAAAAATAAGCTGATTATGCGCTGGCTGTCTCACCGC
GGCGGCGCGCTGGATTTTCAGGAGTGGTTAGCCGCGCGTCCGGGTGAACGTTTCCCGGTCTCCGTGCGATTGGGC
GCCGATCCGGCGACGATACTTGGCGCCGTGACTCCTGTTCCCGATACTCTGTGCGAGTATGCCTTTGCGGGCCTG
CTGCGCGGCACGAAAACCTGAAGTGGTTAAATGCCTTTCTAACGATCTGGAAGTGCCTGCCAGCGCCGAGATTATC
CTTGAAGGTTACATTGAGCCGGGAGAGATGGCGCCGGAAGGACCGTATGGCGATCATACGGGCTATTATAATGAA
GTGGATAGCTTTCCGGTCTTTACCGTCACGCATATTACACAGCGTGAGGATGCCATCTATCACTCCACCTATACC
GGGCGTCCGCCCCGATGAGCCTGCGGTATTAGGGGTGGCGCTCAATGAAGTCTTCGTGCCTATTCTGCAAAAACAG
TTTCCGGAAATCGTCGACTTTTATCTGCCGCCGGAAGGGTGTCTTACCGCCTGGCGGTAGTGACGATGAAAAAG

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CAGTACGCTGGTCATGCGAAACGCGTCATGATGGGCGTCTGGTCGTTTTTGCGCCAGTTTATGTATACGAAATTT
GTTATCGTTTTGCGATGATGACGTTAACGCACGCGACTGGAATGATGTGATCTGGGCGATTACCACCCGTATGGAC
CCTGCACGGGATACGGTGCTGGTTGAAAATACGCCGATTGATTACCTGGATTTTGCCTCGCCGGTCTCCGGGCTG
GGTTCAAAAATGGGGCTGGATGCCACAAACAAATGGCCGGGCGAAACCAACGCGAGTGGGGTCGTCTATTGTT
AAAGATCCTGAAGTTACCGCGCGTATTGATGCGATTTGGGATGAGCTGGCTATCTTTAAATAA

282. *Escherichia coli* CFT073 (SEQ ID NO. 282)

ATGGACGCCATGAAATATAACGATTTACGCGACTTCTTGACGCTGCTTGAACAGCAGGGTGAGCTAAAACGTATC
ACGCTCCCGGTGGATCCGCACCTGGAAATCACTGAAATTGCTGACCGCACTTTGCGTGCCGGTGGGCCTGCGCTG
TTGTTGAAAACCTAAAGGCTACTCAATGCCGGTGCTGTGCAACCTGTTCCGTACGCCAAAGCGCGTGCGCATG
GGCATGGGGCAGGAAGATGTTTCGGCGCTGCGTGAAGTTGGTAAATTATTGGCGTTTCTGAAAGAGCCGGAGCCG
CCAAAAGGTTTCCGCGACCTGTTTGATAAACTGCCGCAGTTTAAGCAAGTATTGAACATGCCGACAAAGCGACTG
CGTGGTGCACCCTGCCAACAAAAATCGTCTCTGGCGATGACGTCGATCTCAATCGCATTCCCATTATGACCTGC
TGGCCGGAAGATGCCGCGCCGCTGATTACCTGGGGGCTCACCGTAACGCGCGGCCCGCATAAAGAGCGGCAGAAT
CTGGGCATTTATCGCCAGCAGCTAATTGGTAAAAACAACTGATTATGCGCTGGCTGTGCGATCGCGGCGGCGCG
TTGGATTATCAGGAGTGGTGTGCGGCGCATCCGGGCGAACGTTTCCCGGTTTCTGTGGCGCTGGGTGCCGATCCT
GCCACGATTCTCGGTGCAGTCACCCCGTTCCGGATACGCTTTCAGAGTATGCGTTTGCCGGATTGCTGCGCGGT
ACCAAGACCGAAGTGGTGAAGTGTATCTCCAATGACCTTGAAGTGCCCGCCAGTGCGGAGATTGTGCTGGAAGGG
TATATCGAACAAGGCGAACTGCGCCGGAAGGGCCGTATGGCGACCACACCGGTTACTATAACGAAGTCGATAGT
TTTCCGGTATTTACCGTGACGCATATTACCCAGCGTGAAGATGCGATTTATCATTCCACCTATACCGGGCGTCCG
CCAGATGAACCTGCGGTACTGGGTGTAGCACTGAACGAAGTGTTCGTGCCGATTCTGCAAAAACAGTCCCGGAA
ATTGTCGATTTTTATCTGCCGCCGGAAGGCTGTTCTTATCGTCTGGCGGTAGTGACGATCAAAAAACAGTACGCC
GGACACGCGAAGCGCGTCATGATGGGCGTCTGGTCGTTCTTACGCCAGTTTATGTACACTAAATTTGTGATCGTT
TGCGATGATGACGTCAACGCCCGCGACTGGAACGATGTGATTTGGGCGATTACCACCCGTATGGACCCGGCGCGG
GATACTGTTCTGGTAGAAAATACGCCTATTGATTATCTGGATTTTGCCTCGCCTGTCTCCGGGCTGGGTTCAAAA
ATGGGGCTGGATGCCACGAATAAATGGCCGGGTGAAACCCAGCGTGAATGGGGACGTCCCATCAAAAAGATCCA
GATGTTGTCGCGCATATTGACGCCATTTGGGATGAACTGGCTATTTTAAACAACGGTAAAAGCGCCTGA

283. *Escherichia coli* K12 (SEQ ID NO. 283)

ATGGACGCCATGAAATATAACGATTTACGCGACTTCTTGACGCTGCTTGAACAGCAGGGTGAGCTAAAACGTATC
ACGCTCCCGGTGGATCCGCATCTGGAATCACTGAAATTGCTGACCGCACTTTGCGTGCCGGTGGGCCTGCGCTG
TTGTTGAAAACCTAAAGGCTACTCAATGCCGGTGCTGTGCAACCTGTTCCGTACGCCAAAGCGCGTGCGCATG
GGCATGGGGCAGGAAGATGTTTCGGCGCTGCGTGAAGTTGGTAAATTATTGGCGTTTCTGAAAGAGCCGGAGCCG
CCAAAAGGTTTCCGCGACCTGTTTGATAAACTGCCGCAGTTTAAGCAAGTATTGAACATGCCGACAAAGCGGCTG
CGTGGTGCGCCCTGCCAACAAAAATCGTCTCTGGCGATGACGTCGATCTCAATCGCATTCCCATTATGACCTGC
TGGCCGGAAGATGCCGCGCCGCTGATTACCTGGGGGCTGACAGTGACGCGCGGCCACATAAAGAGCGGCAGAAT
CTGGGCATTTATCGCCAGCAGCTGATTGGTAAAAACAACTGATTATGCGCTGGCTGTGCGATCGCGGCGGCGCG
CTGGATTATCAGGAGTGGTGTGCGGCGCATCCGGGCGAACGTTTCCCGGTTTCTGTGGCGCTGGGTGCCGATCCC
GCCACGATTCTCGGTGCAGTCACTCCCGTTCCGGATACGCTTTCAGAGTATGCGTTTGCCGGATTGCTACGTGGC
ACCAAGACCGAAGTGGTGAAGTGTATCTCCAATGATCTTGAAGTGCCCGCCAGTGCGGAGATTGTGCTGGAAGGG

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TATATCGAACAAGGCGAACTGCGCCGGAAGGGCCGTATGGCGACCACACCGGTACTATAATGAAGTCGATAGT
TTCCCGGTATTTACCGTGACGCATATTACCCAGCGTGAAGATGCGATTTACCATTCCACCTATACCGGGCGTCCG
CCAGATGAGCCCGCGGTGCTGGGTGTCGCACTGAACGAAGTGTTTGTGCCGATTCTGCAAAAACAGTTCCCGGAA
ATTGTCGATTTTTACCTGCCGCCGGAAGGCTGCTCTTATCGCCTGGCGGTAGTGACAATCAAAAACAGTACGCC
GGACACGCGAAGCGCGTCATGATGGGCGTCTGGTCGTTCTTACGCCAGTTTATGTACACTAAATTTGTGATCGTT
TGCGATGATGACGTTAACGCACGCGACTGGAACGATGTGATTTGGGCGATTACCACCCGTATGGACCCGGCGCGG
GATACTGTTCTGGTAGAAAATACGCCTATTGATTATCTGGATTTTGCCTCGCCTGTCTCCGGGCTGGGTTCAAAA
ATGGGGCTGGATGCCACGAATAAATGGCCGGGGGAAACCCAGCGTGAATGGGGACGTCCCATCAAAAAAGATCCA
GATGTTGTGCGCATATTGACGCCATCTGGGATGAACTGGCTATTTTTAACAACGGTAAAAGCGCCTGA

284. *Salmonella enterica subsp. enterica serovar Typhi*
(SEQ ID NO. 284)

ATGGACGCCATGAAATATCACGATTTACGCGACTTCCTGACGCTACTTGAGCAGCAGGGGGAACATAAACGCATC
ACGCTACCTGTGGATCCTCATCTGGAAATCACGGAAATCGCTGACCGCACGCTGCGTGCCGGTGGACCGGCGTTG
CTGTTTGAAAATCCTAAAGGTTACGCCATGCCGGTGCTGTGCAACCTTTTTTGGCAGCCAAAACGCGTGGCGATG
GGCATGGGGCAGGATGATGTTTCCGCCTTACGGGAAGTGGGTAAATTATTAGCGTTTCTGAAAGAACCTGAGCCG
CCGAAAGGCTTTCGCGATCTGTTTGACAAGCTGCCGCAGTTTAAGCAAGTGCTGAATATGCCGACGAAACGGTTA
CGCGGCGCGCCTTGCCAGCAGAAAATCGCGTCTGGCGATGATGTGATTTAACGCGTCTTCTGTGATGACCTGT
TGGCCGGACGACGCCGCGCCGCTGATTACCTGGGGACTGACGGTAACGCGTGGCCCGCACAAAGAACGGCAAAAC
CTGGGCATTTATCGTCAGCAGTTGATAGGTAAAATAAGCTGATTATGCGCTGGCTGTCTCACCGCGGCGGCGCG
TTGGATTTTCAGGAGTGGTTAGCCGCGCGTCCGGGTGAACGTTTCCCGGTCTCCGTCGCATTGGGCGCCGATCCG
GCGACGATACTTGGCGCCGTGACTCCTGTTCCCGATACTCTGTGCGAGTATGCCTTTGCGGGCCTGCTGCGCGGC
ACGAAAACCTGAAGTGGTTAAATGCCTTCTAACGATCTGGAAGTGCCTGCCAGCGCCGAGATTATCCTTGAAGGT
TACATTGAGCCGGGAGAGATGGCGCCGGAAGGACCGTATGGCGATCATACGGGCTATTATAATGAAGTGGATAAC
TTTCCGGTCTTTACCGTCACGCATATTACGCAGCGTGAGGATGCCATCTATCACTCCACCTATACCGGGCGTCCG
CCCGATGAGCCTGCGGTATTAGGGGTGGCGCTCAATGAAGTCTTCGTGCCTATTCTGCAAAAACAGTTTCCGGAA
ATCGTCGACTTTTATCTGCCGCCGGAAGGGTGTCTTACC GCCTGGCGGTAGTGACGATGAAAAGCAGTACGCT
GGTCATGCGAAACGCGTCATGATGGGTGTCTGGTCGTTTTTGCGCCAGTTTATGTATACGAAATTTGTTATCGTT
TGCGATGATGACGTTAACGCACGCGACTGGAATGATGTGATCTGGGCGATTACCACCCGTATGGACCCTGCGCGG
GATACGGTGCTGGTTGAAAATACGCCGATTGACTACCTGGATTTTGCCTCGCCGGTCTCCGGGCTGGGTTCAAAA
ATGGGGCTGGATGCCACAAACAAATGGCCGGGGGAAACCCAACGCGAGTGGGGTCGTCCTATTGTTAAAGATCCT
GAAGTTACCGCGCGTATTGATGCGATTTGGGATGAGCTGGCTATCTTTAAATAA

285. *Escherichia coli* O157:H7 EDL933 (SEQ ID NO. 285)

ATGGACGCCATGAAATATAACGATTTACGCGACTTCTTGACGTTGCTTGAACAGCAGGGTGAGCTAAAACGTATC
ACGCTCCCGGTGGACCCGCATCTGGAAATCACTGAAATTGCTGACCGCACGCTGCGTGCTGGTGGGCCTGCGCTG
TTGTTTGAAAACCTTAAAGGGTACTCAATGCCGGTGCTGTGCAACTTGTTCCGTACGCCAAAGCGCGTAGCGATG
GGTATGGGCCAGGAAGATGTTTCAGCACTGCGTGAAGTCGGTAAATTATTAGCATTTCTGAAAGAACCAGAGCCG
CCAAAAGGTTTTTCGCGATCTGTTTGATAAGCTGCCGCAGTTTAAGCAGGTGTTAAACATGCCGACAAAGCGACTG
CGCGGTGCACCCTGCCAACAAAAATCGTCTCTGGCGATGACGTCGATCTCAACCGTATTCCCATTATGACCTGT

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TGGCCGGAAGATGCCGCGCCGCTGATTACATGGGGGCTAACCGTTACACGTGGCCCTCATAAAGAGCGACAGAAT
CTGGGCATTTATCGCCAGCAACTGATTGGTAAAAACAAGCTGATTATGCGTTGGCTGTGCGCATCGCGGCGGCGCG
CTGGATTATCAGGAGTGGTGTGCGGCGCATCCAGGTGAACGTTTCCCGATCTCTGTGGCGTTGGGCGCTGATCCG
GCAACCATTCTCGGTGCAGTCACACCAGTACCAGATACTTTGTGCGGAATACGCCTTTGCCGGATTGCTACGTGGC
ACCAAAACCGAAGTAGTGAAGTGTATTTCCAATGATCTCGAAGTGCCCGCCAGTGCGGAGATTGTGCTGGAAGGG
TATATCGAACAAGGCGAAATGGCGCCAGAAGGACCGTATGGTGACCACACTGGTTACTATAACGAAGTCGATAGT
TTCCCGGTATTTACCGTGACGCATATTACCCAGCGTGAAGATGCGATTTACCATTCCACCTATACCGGGCGTCCG
CCAGATGAACCCGCGGTACTGGGAGTGGCGTTGAACGAAGTATTTGTTCCCATTTCTGCAAAAGCAGTTCCCGGAA
ATTGTGCGATTTTTACCTGCCGCCGGAAGGCTGCTCTTATCGCCTGGCGGTAGTGACAATCAAAAAACAGTACGCC
GGACACGCGAAGCGCGTCATGATGGGCGTCTGGTCGTTCTTACGCCAGTTTATGTACACTAAATTTGTGATCGTT
TGCGATGATGACGTTAACGCACGCGACTGGAACGATGTGATTTGGGCGATTACCACCCGTATGGACCCAGCGCGG
GATACTGTTCTGGTAGAAAATACGCCTATTGATTATCTGGATTTTGCTCGCCTGTCTCCGGGCTGGGTTCAAAA
ATGGGGCTGGATGCCACGAATAAATGGCCGGGGGAAACCCAGCGTGAATGGGGACGTCCCATCAAAAAAGATCCA
GATGTTGTGCGCACATATTGACGCCATCTGGGATGAACTGGCTATTTTTTAACAACGGTAAAAGCGCCTGA

286. *Shigella flexneri* 2a str. 301 (SEQ ID NO. 286)

ATGGACGCCATGAAATATAACGATTTACGCGACTTCCTGACGCTGCTTGAACAGCAGGGTGAGCTAAAACGTATC
ACGCTCCCGGTGGATCCGCATCTGGAATCACTGAAATTGCTGACCGCACTCTGCGTGCTGGTGGGCCTGCGCTG
TTGTTGCAAAACCCTAAAGGCTACTCAATGCCGGTGCTGTGCAACCTGTTCCGTACGCCAAAGCGCGTGCGATG
GGCATGGGGCAGGAAGATGTTTCGACGCTGCGTGAAGTTGGTAAATTATTGGCGTTTCTGAAAGAGCCGGAGCCG
CCAAAAGGTTTCCGCGACCTGTTTGATAAACTGCCGCAGTTTAAGCAGGTGTTAAACATGCCGACAAAGCGACTG
CGTGGTGCGCCCTGCCAACAAAAAATCGTCTCTGGCGATGACGTGATCTCAATCGCATTCCCATTATGACCTGC
TGCCCGGAAGATGCCGCGCCGCTGATTACCTGGGGGCTGACCGTAACGCGCGGCCCGCATAAAGAGCGGCAGAAT
CTGGGCATTTATCGCCAGCAGCTGATTGGTAAAAACAACTGATTATGCGCTGGCTGTGCGATCGCGGCGGCGCG
CTGGATTATCAGGAGTGGTGTGCGGCGCATCCGGGCGAACGTTTCCCGGTTTCTGTGGCGCTGGGTGCCGATCCT
GCCACGATTCTCGGTGCAGTCACCCCCGTTCCGGATACGCTTTCAGAGTATGCGTTTGCCGGATTGCTACGCGGC
ACCAAAACCGAAGTAGTAAAGTGTATTTCCAATGACCTCGAAGTGCCAGCCAGTGCCGAAATCGTCTGGAAGGG
TATATCGATCCTGGTGAGATGGCGCCGGAAGGGCCGTATGGTGACCACACAGGTTACTATAATGAAGTCGATAAT
TTCCCGGTGTTTACCGTGACGCATATTACCCAGCGTGAAGATGCGATTTACCATTCCACCTATACCGGGCGTCCG
CCAGATGAGCCCGCGGTACTGGGCGTGGCGTTGAACGAAGTGTGTTGTACCGATTCTGCAAAAACAGTTCCCGGAA
ATTGTGCGATTTTTACCTGCCGCCGGAAGGCTGTTCTTATCGTCTGGCGGTAGTGACGATCAAAAAACAGTACGCC
GGACACGCGAAGCGCGTCATGATGGGCGTCTGGTCGTTCTTACGCCAGTTTATGTACACTAAATTTGTGATCGTT
TGCGATGATGACGTCAACGCACGCGACTGGAACGATGTGATTTGGGCGATTACCACCCGTATGGACCCGGCGCGG
GATACTGTTCTGGTAGAAAATACGCCTATTGATTATCTGGATTTTGCTCGCCTGTCTCTGGGCTGGGTTCAAAA
ATGGGGCTGGATGCCACGAATAAATGGCCGGGGGAAACCCAGCGTGAATGGGGACGTCCCATCAAAAAAGATCCA
GATGTTGTGCGCGCATATTGACGCCATCTGGGATGAACTGGCTATTTTTTAACAACGGTAAAAGCGCCTGA

287. *Pseudomonas aeruginosa* PAO1 (SEQ ID NO. 287)

ATGACGTTCAAGGATCTCCGCGATTTTCATCGCCCAGCTGGAGCAGCGCGGTGCGTTGAAGCGCATCCAGGTGCCG
ATTTCCCCCGTGCTCGAGATGACCGAGGTGTGCGACCGCACGTTGCGCGCCAAGGGCCCGGCATTGCTGTTCAAA

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AAGCCGACCGGCTTCGACATGCCGGTGCTCGGCAACCTGTTCTGGTACGCCGAGCGCGTGGCGCTGGGCATGGGC
GCCGAGGACGTGCGCGCACTGCGCGAGATCGGCAAGCTGCTGGCGCAACTCAAGGAGCCCGAGCCGCCGAAGGGC
CTCAAGGACGCCTGGGCCAAGCTGCCGATGTACAGGAAGGTCTGTCCATGGCGCCGAAGGTGCTCAAGGACGCC
CCCTGCCAGGAAGTGGTTCGAGGAGGGCGAGGACGTGACCTCGGCCGGCTGCCGGTCCAGACCTGCTGGCCGGGC
GATGTGCGGCCGCTGATCACCTGGGGCTGACCGTTACCCGCGGGCCGAACAAGGAACGGCAGAACCTGGGCATC
TACCGCCAGCAGGTGATCGGCCGCAACAAGGTGATCATGCGCTGGCTCAGCCATCGCGGCGGGCGCACTGGACTAC
CGCGAGTGGTGCCAGAAGCATCCGGGCCAGCCCTATCCGGTAGCCGTGGCGCTGGGCGCCGATCCGGCGACCATC
CTCGGTGCGGTGACGCCGGTGCCGGACACCCTTTCCGAATACGCTTTCGCCGGCCTGTTGCGCGGGCATCGTACC
GAGCTGGTCAAGTGTGCGCGGAGCGACTTGCAGGTGCCGGCCAGCGCCGAGATCGTCCTCGAAGGGGTGATCCAC
CCCGGCGAGATGGCCGACGAAGGCCCTATGGCGATCACACCGGTACTACAACGAGGTGATCGCTTCCCGGTG
TTCACCGTCGAGCGCTACCCGCCGGCAGAAACCGATCTACCACAGCACCTACACGGGGCGTCCGCCGGACGAG
CCGGCGATCCTCGGGGTGGCGCTGAACGAAGTGTTCGTGCCGATCCTGCAGAAGCAGTTCCCGGAAATCGTCGAT
TTCTACCTGCCGCCGGAAGGTTGTTCTACCGGATGGCGGTGGTGACCATGAAGAAGCAGTACCCAGGGCACGCC
AAGCGCGTGATGCTCGGGGTCTGGTCTTCTGCGGCAGTTCATGTACACCAAGTTCGTATCGTACCGACGAT
GACATCGATGCGCGCACTGGAACGATGTGATCTGGGCCATCACACGCGGATGGACCCCAAGCGCGACACGGTG
ATGATCGACAACACGCCCATCGACTACCTCGACTTCGCCTCGCCGTTTCCGGCCTCGGCTCGAAGATGGGGCTT
GATGCCACCCACAAGTGGCCGGGCGAGACCAGCCGCAATGGGGGCGCGCCATCGTCAAGGACGAAGCGGTGACA
CGGCGCATCGACGCCCTCTGGTCGAGCCTCGGGATCGACTGA

288. *Pseudomonas syringae* pv. *tomato* str. DC3000
(SEQ ID NO. 288)

ATGAAATTCAAAGATCTAAGGGATTTCTGTGCAGCAGTTGGAGCAGCGCGAGAGTTGAAACGCATTTCAGATGCCG
ATCTCGCTGTGCTGGAAATGACTGAAATCTGTGACCGTACCTTGCGCGCCAAAGGCCCGGCCCTGCTGTTTGAA
AACCCGGTTGGCTTTGATATTCCGGTGCTGGGCAACCTGTTCCGGCACGCCGAGCGCGTGGCCATGGGCATGGGC
GCGGAAGCCGTCACCGAGCTGCGCGAAATCGGCAAGTTGCTTGCGTTTCTCAAGGAGCCCGAGCCGCCCAAAGGC
CTGAAAGATGCCTGGTCCAAGCTGCCCATCTTCCGCAAAGTCATCGCCATGGCGCCCCAAGGTGCTCAAGGATGCA
CCCTGCCAGGAGATCGTCATCGAGGGTGATGACGTGATCTCGGCATGTTGCCGGTGCGAGACCTGCTGGCCGGGC
GATGTGCGCGCCGCTGATCACCTGGGGCTGACCGTGACCAAAGGCCCGAACAAAGGAGCGGCAGAACCTCGGTATT
TATCGCCAGCAGGTATCGGCCGCAACAAGATCATCATGCGCTGGCTCAGCCATCGCGGTGGCGCGCTTGACTTC
CGCGACTGGTGCGTCAAGCATCCTGGCGAGCCTTATCCGGTGCCGTCGCACTGGGCGCGGACCCGGCGACCATT
CTCGGTGCCGTGACGCCGGTGCCGACAGCCTGTCCGAATACGCCTTCGCCGGGCTACTGCGTGGCTCGCGCACC
GAGCTGATCAAGTGCCGTGGCAGCAACCTGCAAGTGCCAGCCAGTGCCGAAATCGTGCTTGAGGGCGTGATTCAT
CCGGGCGAGATGGCCAACGAAGGCCCTACGGCGATCACACCGGTTATTACAACGAAGTCGACAGCTTTCGGGTG
CTACCGTCGAGCGCATACCCACCGCATCAAGCCGATCTACCACAGCACCTACACGGGGCGTCCACCGGACGAG
CCGGCTATCCTGGGTGTGGCGCTGAACGAAGTGTTCGTGCCGATTCTGCAGAAGCAGTTTCCGGAAATCGTCGAT
TTCTACCTGCCGCCCGAGGGGTGCTCTTACCGCATGGCGGTGGTGACTATCAAGAAACAGTACCCCGGCCATGCC
AAGCGCGTGATGCTGGGCGTCTGGTCTTCTGCGCCAGTTTATGTACACCAAATTTGTGATCGTACCGATGAC
GACATCAATGCGCGTGAATGACGTGATCTGGGCCATCACACCCGATGGACCCCAAGCGCGACACGGTC
ATGATCGACAACACGCCCATCGATTACCTCGATTTTGCCTCTCCGGTGTCTGGATTGGGATCAAAAATGGGCCTG

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GATGCCACTAACAAATGGCCAGGGGAAACCACCCGCGAATGGGGCAGGGCGATCGTCAAGGACGAAGCCACCACG
CGCCGGGTGGACGAGATCTGGACTCAGTTGGGAATAGACTGA

289. *Yersinia pseudotuberculosis* IP 32953 (SEQ ID NO. 289)

ATGATCAGCATGAAATACCGTGACTTACGTGACTTCCTCTCATTACTGGAACAGAGGGGGGAACCTTAAACGCATT
AGCCAGCCCATTGATCCTTATTTGGAAATGACAGAAATTGCCGATCGCACGTTACGTGCTGGTGGGCCTGCGTTA
CTTTTTGAGAACCCTAAAGGTTACAGCATGCCCGTGTTGTGTAATCTGTTTGGCACCGCTAAGCGAGTCGCCATG
GGGATGGGGCAAGAAGATGTCAGCGCCCTGCGAGATGTTGGTAAATTATTGGCCTTCCTGAAAGAACCCGATCCC
CCAAAAGGTTTCCGTGACTTATTTGATAAGCTGCCAAAATTTAAGCAGGTATTGAATATGCCAACGAAACGCTTG
AACTCGGCCCCGTGTCAGGAGCAAGTTTGGCAAGGTGAGGATGTTGATTTAAGTCGCATCCCTGTGATGCACTGC
TGGCCAGAAGATGCCGCACCACTAGTCTCTTGGGGGTGACTATTACACGTGGTCCCCACAAAGAACGGCAGAAT
CTAGGCATCTATCGCCAGCAGGTATTGGGTAAAAACAAATTAATTATGCGTTGGCTATCGCATCGTGGTGGTGCG
CTGGATTATCAGGAGTGGTGTGAGGCACACCCCTGGTGAACGTTTTCCGGTCGCTGTCGCCTTGGGAGCAGACCCT
GCTACGATCTTAGCCGCAGTGACCCCGGTACCAGACACGCTGTCTGAATATGCCTTTGCCGGCTTGTTACGCGGC
CATAAACGGAAGTGGTGAAGTGTCTTTCCAATGACCTTGAAGTTCCTGCAAGTGCAGAAATTGTATTGGAAGGA
TATATCGAACAAGGTGATATGGCTCCGGAAGGTCCTTATGGTGATCATACGGGCTATTACAATGAAATAGATAAT
TTCCCCGTGTTTACCGTCACGCATATTACACAGCGCCAAGACGCAATTTATCATTCAACCTATACGGGCCGACCA
CCGGATGAACCTGCGGTAATGGGGGTGGCACTGAACGAAGTCTTTGTACCTATTTTGCAAAGCAATTCCCCGAA
ATTGTTGATTTCTACTTGCCACCAGAAGGGTGCTCATACCGGTTGGCGGTGGTAACCATCAAGAAACAATATGCA
GGCCATGCCAACGCGTGATGATGGGAGTATGGTCGTTTTTACGCCAGTTTATGTATACCAAGTTTGTTATTGTT
TGTGATGACGATATTAATGCTCGTGATTGGAATGATGTAATTTGGGCGATCACCACCCGGATGGACCCATCCCCG
GATACGGTGTTAATTGAAAATACACCGATAGATTATTTGGATTTGCCTCACCGGTTTCCGGTTTGGGATCGAAA
ATGGGGCTGGATGCCACCAACAAATGGCCAGCAGAGACTCCGCGTGAATGGGGGCGTCCAATTAAGATGGACGAA
GACGTCCGTGCCCCGTATTGATGCTCTGTGGGATGAGCTGGCCATTTTCAGTGACAAAGACGCGAAACGCTAA

**290. *Neisseria meningitidis* serogroup B strain MC58
SEQ ID NO. 290)**

ATGAATATGAAATACAAAGACCTGCGCGACTTCATCGCCATGCTCGAGCAGCAGGGCAAACCTCAAGCGCGTCGCA
CACCCCATTTCCTCGTATTTGGAAATGACCGAAATCGCCGACCGCGTGCTGCGTGCCGAAGGGCCGGCGTTGCTG
TTTGAAAACCCGATTAAGCCCGACGGTACGCGCTACGGTTATCCCGTGTTGGCAAACCTGTTCCGGCACGCCCGAA
CGTGTGGCGATGGGCATGGGCGCGGACAGCGTGTCCAAGCTGCGTGAAATTGGGCAGACGCTGGCGTATTTGAAA
GAACCCGAACCGCCCAAAGGCATCAAAGATGCGTTTTCCAACCTGCCGCTGCTGAAAGACATTTGGAGCATGGCG
CCGAACGTGGTGAAAAACGCGCCGTGTCAGGAAATCGTGTGGGAAGGCGAAGACGTTGATTTGTATCAACTCCG
ATTCAGCATTGCTGGCCGGAAGACGTTGCGCCGCTGGTAACGTGGGGCTTGACCGTCACGCGCGGGCCGCACAAA
AAACGCCAAAATCTCGGCATTTACCGCCAACAACCTCATCGGCAAAAAACAAGCTGATTATGCGTTGGCTGTGCGAT
CGCGGCGGCGCGTTGGATTATCAGGAGTTCGCAAACTCAATCCCGATACGCCGTATCCCGTCGCCGTGCTACTC
GGCTGCGACCCCGCCACCATTTTGGGCGCGGTAACGCCTGTTCCCGATACCTTGAGCGAATACCAGTTTGCCGGA
CTGCTGCGCGGTTGCGGGACGGAGCTGGTGAATGTATCGGCAACGATTTGCAAGTGCCTGCCCGCGCAGAAATC
GTGTTGGAAGGCGTCATCCATCCGAACGAAACCGCGTTGGAAGGCCCGTACGGCGACCACACCGGCTATTACAAC
GAGCAGGATTATTTCCCTGTGTTTACGGTGAACGCATCACCATGCGCGAAAACCCGATTTACCATTGACCTAC

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ACGGGCAAACCGCCCGATGAACCCGCCGTTTTGGGCGTGGCGTTGAACGAAGTGTTTCGTACCGCTTTTGCAAAAG
CAGTTCCCCGAAATCACCGATTTCTACCTGCCGCCGAAGGCTGCTCCTACCGCATGGCGGTGGTGAGCATGAAA
AAACAGTACGCCGGACACGCCAAGCGCGTGATGATGGGCTGCTGGTCGTTTCCTGCGCCAGTTTATGTATACCAA
TTCATCATCGTGGTGGATGACGATGTGAACGTGCGCGACTGGAAAGAAGTCATCTGGGCGGTACCCACGCGCATG
GACCCCGTGCGCGACACTGTTTTGGTAGAAAACACGCCCATCGATTATCTCGACTTCGCCAGCCCCGTCAGCGGA
CTCGGCGGCAAAATGGGTTTGGATGCGACCAACAAATGGCCGGGAGAAACCGACCGCGAATGGGGACGCGTCATC
AAAAAAGACCCTGCGGTTACGGCTAAGATTGATGGGATTTGGGAGGAATTGGGGTTGTAG

291. *Neisseria gonorrhoeae* FA 1090 (SEQ ID NO. 291)

ATGAAATACAAAGACCTGCGCGACTTCATCGCTATGCTCGAGCAGCAGGGCAAGCTCAAGCGCGTCGCCACCCC
GTTTCCCCGCATTTGGAAATGACCGAAATTGCCGACCGCGTGTTGCGCGCCGAAGGGCCGGCGTTGTTGTTTGAA
AACCCGGTTAAGCCCGACGGTACGCGCTATGATTATCCCGTGTTGGCGAACCTGTTCCGCCACCCCCGAACGTGTG
GCGATGGGCATGGGCGCGGACAGCGTGTCCAAGCTGCGCGAAATCGGGCAGACGCTGGCGTATTTGAAAGAACCC
GAACCGCCCCAAGGCATCAAAGACGCGTTTTCCAAACTGCCGCTGTTGAAAGATATTTGGAGCATGGCGCCGAAC
GTGGTGAAAAACGCGCCGTGTCAGGAAATCGTGTGGGAAGGAGAAGACGTTGATTTGTATCAGCTTCCGATTCAA
CATTGCTGGCCGGAAGACGTTGCGCCGCTGGTAACGTGGGGCTTGACCGTCACGCGCGGGCCGCACAAAAAACGC
CAAAATCTCGGCATTTACCGTCAACAACATCATCGGCAAAAACAAGCTGGTTATGCGCTGGCTGTGCGATCGCGGC
GGCGCGTTGGATTATCAGGAATTCGCAAACTCAATCCCGATACGCCGTATCCCGTCGCCGTCTACTCGGTTGC
GACCCCTCCACCATTTTGGGCGCGGTAACGCCCGTTCCCGATACCTTTGAGCGAATACCAGTTTGCCGGACTGCTG
CGCGGTTGCGGACGGAGCTGGTGAAATGTATCGGCAGCGATTTGCAAGTGCCTGCCCGTGCTGAAATTGTATTG
GAAGGCGTGATTATCCTCAAACGAAACCGCGTTGGAAGGCCCATACGGCGACCACACGGGCTATTACAACGAGCAG
GGCCATTTCCCTGTGTTTACGGTGAACGCATCACCATGCGCGAAAACCCGATTTACCACTCTACCTACACAGGC
AAACCGCCCGACGAACCTGCCGTTTTGGGCGTGGCGTTGAACGAAGTGTTTCGTACCGCTTTTGCAAAAGCAGTTC
TCCGAAATCACCGATTTCTACCTGCCGCCGAAGGCTGTTCTACCGCATGGCGGTGGTCAGCATGAAAAAACAG
TACGCCGGACACGCCAAGCGCGTGATGACGGGCTGCTGGTCGTTTCCTGCGCCAGTTTATGTACACCAAATTCATC
ATCGTGGTGGATGACGATGTAAACGTGCGCGACTGGAAAGAAGTCATCTGGGCGGTAACCACGCGCATGGACCCC
GTCCGCGACACCGTTTTGGTGGAAAACACGCCCATCGACTACCTCGACTTCGCCAGCCCCGTCAGCGGACTCGGC
GGCAAAATGGGTTTGGATGCGACCAAGCAATGGCCGGGAGAAACCGACCGCGAATGGGGACGGGTAATCAAAAA
GACCCTGCGGTTACGGTTAAATTTGATGGGATTTGGGGGAAATTGGGGTTGTAG

292. *Yersinia pestis* C092 (SEQ ID NO. 292)

ATGATCAGCATGAAATACCGTGACTTACGTGACTTCCTCTCATTACTGGAACAGAGGGGGGAACCTAAACGCATT
AGCCAGCCCATTGATCCTTATTTGGAAATGACAGAAATTGCCGATCGCACGTTACGTGCTGGTGGGCCTGCGTTA
CTTTTTGAGAACCCTAAAGGTTACAGCATGCCCGTGTTGTGTAATCTGTTTGGCACCGCTAAGCGAGTCGCCATG
GGGATGGGGCAAGAAGATGTACGCGCCCTGCGAGATGTTGGTAAATTATTGGCCTTCCTGAAAGAACCCGATCCC
CCAAAAGGTTCCGTGACTTATTTGATAAGCTGCCAAAATTTAAGCAGGTATTGAATATGCCAACGAAACGCTTG
AACTCGGCCCCGTGTCAGGAGCAAGTTTGGCAAGGTGAGGATGTTGATTTAAGTCGCATCCCTGTGATGCACTGC
TGGCCAGAAGATGCCGACCACTAGTCTCTTGGGGGTTGACTATTACACGTGGTCCCCACAAAGAACGGCAGAAT
CTAGGCATCTATCGCCAGCAGGTATTGGGTAAAAACAAATTAATTATGCGTTGGCTATCGCATCGTGGTGGTGCG
CTGGATTATCAGGAGTGGTGTGAGGCACACCCTGGTGAACGTTTTCCGGTCGCTGTGCGCTTGGGAGCAGACCTT

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GCTACGATCTTAGCCGCAGTGACCCCGGTACCAGACACGCTGTCTGAATATGCCTTTGCCGGCTTGTTACGCGGC
CATAAAACGGAAGTGGTGAAGTGTCTTTCCAATGACCTTGAAGTTCCTGCAAGTGCAGAAATTGTATTGGAAGGA
TATATCGAACAAGGTGATATGGCTCCGGAAGGTCCTTATGGTGATCATACGGGCTATTACAATGAAATAGATAAT
TTCCCCGTGTTTACCGTCACGCATATTACACAGCGCCAAGACGCAATTTATCATTCAACCTATACGGGCCGACCA
CCGGATGAACCTGCGGTAATGGGGGTGGCACTGAACGAAGTCTTTGTACCTATTTTGCAAAGCAATTCGCGGAA
ATTGTTGATTTCTACTTGCCACCAGAAGGGTGCTCATACCGGTTGGCGGTGGTAACCATCAAGAAACAATATGCA
GGCCATGCCAAACGCGTGATGATGGGAATATGGTCGTTTTTACGCCAGTTTATGTATACCAAGTTTGTTATTGTT
TGTGATGACGATATTAATGCTCGTGATTGGAATGATGTAATTTGGGCGATCACCACCCGGATGGACCCATCCCGC
GATACGGTGTTAATTGAAAATACACCGATAGATTATTTGGATTTGCGCTCACCAGTTTCCGGTTTGGGATCGAAA
ATGGGGCTGGATGCCACCAACAAATGGCCAGCAGAGACTCCGCGTGAATGGGGGCGTCCAATTAAGATGGACGAA
GACGTCCGTGCCGTATTGATGCTCTGTGGGATGAGCTGGCCATTTTCAGTGACAAAGACGCGAAACGCTAA

293. *Pseudomonas putida* KT2440 (SEQ ID NO. 293)

TTGATTGGGGCCGCCTTGCGGCCCTTCGCGGGCAAGCCCGCTCCTGCACAGGTCATTGCGGCCCTTGTAGGAGCG
GGCTTCCGCGAAGGGATGCAAAGCGGCCCCAATGCATTTTCACCCCAAACAAGGCCCGAACGGCGCTACACTCT
GCACCCCGACCGATACGGCCAACACGAGGCTCCTGCATGCAGTATCGCGACTTGCGCGACTTCATTTCGTGGCCTG
GAACAGCGCGCGAGCTCAAGCGCATCCAGGTACCGATCTCCCCGTCTGGAAATGACCGAGGTCTGCGACCGC
ACCCTGCGCGCCAAGGGCCCGGCATTGTTGTTTCGAAAAGCCCACCGGCTTCGACATCCCAGTGCTGGGCAACCTG
TTCGGTACCCCGAGCGGGTGGCCATGGGCATGGGCGCCGAGTCGGTCAGCGAACTGCGGGAAATCGGCAAGCTG
CTGGCCTTCTCAAGGAGCCTGAGCCGCCCAAGGGCCTGAAGGACGCCTGGTCGAAGCTGCCGATCTTCAAGAAG
GTCGTGTCGATGGCGCCAAAAGTGGTCAAGGACGCGGTGTGCCAGGAAGTGGTGGTCGAGGGTGACGATGTGAC
CTTGGCACGCTGCCGATTTCAGCACTGCTGGCCTGGCGACGTGGCGCCGCTGATTACCTGGGGCCTCACCGTGACC
CGTGGCCCGAACAAGGACCGCCAGAACCTGGGCATCTACCGCCAGCAGGTGATCGGCCGCAACAAGGTGATCATG
CGCTGGCTCAGCCATCGTGGCGGCGCCCTCGATTACCGAGAGTGGTGCGAGAAGAACCCCGGCCAGCCGTTTCCG
GTCGCCGTGGCCCTGGGCGCTGACCCAGCGACCATTTCTCGGCGCGGTGACCCCGGTCCCGGACACCCTTTCCGAG
TACGCCTTCGCCGGCCTGCTGCGAGGCAATCGCACCGAGCTGGTCAAGTGCCGTGGCAGCAACCTGCAGGTACCG
GCAACCGCCGAGATCATTTCTGGAAGGGGTGATCCACCCAGGCGAAATGGCCCCGGAAGGCCCTTACGGCGATCAC
ACGGGCTACTACAACGAAGTGGACAGTTTCCCGGTGTTACCGTTGAGCGCATCACCCACCGGCAAAAACCGATC
TACCACAGCACCTACACGGCCGCGCCGAGATGAGCCGGCCATTCTCGGCGTGGCGCTGAACGAAGTGTTCGTG
CCGATCCTGCAGAAGCAGTTCCCGGAAATCACCGACTTCTACCTGCCGCCGGAAGGCTGCTCGTACCGCATGGCG
GTGGTGACCATGAAGAAACAGTACCCAGGCCACGCCAAGCGCGTAATGCTGGGTGTGTGGTCGTTCTGCGACAG
TTCATGTACACCAAGTTCGTTATTGTACCGATGACGATATCAACGCTCGTGACTGGAACGATGTGATCTGGGCC
ATTACCACGCGCATGGACCCCAAGCGTGATACGGTAATGATTGACAATACCCCGATCGACTACCTGGACTTTGCG
TCACCGGTGTGCGGGCTGGGTTCGAAGATGGGCCTGGACGCTACGCACAAGTGGCCGGGCGAGACTACACGCGAA
TGGGGCCGGGTTCATCGTCAAGGATGAGGCCGTACCCGCCGTATCGATGAGCTGTGGGATCAGTTGGGAATAGAT
TGA

294. *Serratia marcescens* ATCC 13880 (SEQ ID NO. 294)

CAGACGCCCATCATCACGCGTTTCGCATGGCCGGCGTACTGTTTTTTCATGGTCACTACCGCCAGGCGGTAAGAG
CACCCCTCCGGCGGCAGATAGAAATCGACGATTTCCGGGAAGTCTTTTGCAGGATCGGTACGAACACTTCATTC

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AGCGCCACGCCCAGGATCGCCGGCTCATCCGGCGGGCGGCCGGTGTAGGTGAGTGGTAGATCGCGTTGCGGCGC
TGGGTGATGTGAGTAACGGTGAACACCGGGAACCTGGTCGATTTTCATTGTAGTAACCGGTGTGGTCGCCGTAGGGG
CCTTCCGGCGCCATTTACCCGGCTCGATATAGCCTTCAAGCACGATTTCCGGCGCTGGCGGGCACTTCCAGATCG
TTGGAAAGGCACTTGACCACTTCGGTTTTGTTGCCGCGCAGCAACCCGGCAAAGGCGTATTCGGACAAGGTATCA
GGCACCGGCGTGACCGCACCGAGGATGGTAGCAGGATCGGCGCCCAGCGCCACCGCAACCGGGAAACGCTCGCCC
GGGTGCGCCTGGCACCACTCCTGATAATCCAGCGCGCCGCCGCGATGCGACAGCCAACGCAT

295. *Burkholderia mallei* ATCC 23344 (SEQ ID NO. 295)

ATGAAATACAGAGATTTACGCGATTTTCATCCATGGCCTCGAGCAGCGCGCGAGTTGCGGGCGGTCACCCAGCCC
GTATCGCCCGTCCTCGAAATGACCGAACTCTGCGACCGCGTGCTGCGCGCGGGCGGCCCGCACTCCTGTTTCGAC
GCGCCGGCCGCGCCACCGGTTTCCGGTGCTCGGCAATCTGTTGCGCACGCCGCGGCGCGTTCGCGCTCGGCATGGGC
GTCGACGCCGACGACGAAGCGGCGCTCGCGTCGCTGCGCGACATCGGCCGCCTGCTGTCCGCGCTCAAGGAGCCG
GACCCGCCGAAGCGCCTGAAAGACGCGGGCAAGTTGCTGTGCTCGCGAAGGCCGTGTGGGACATGGGCCCCGAAG
ACGGTCTCCGCGCCGCCGTGCCAGGAGATCGTCTGGGAAGGCGACGACGTCGATCTGCACAAGCTGCCGATCCAG
ACCTGCTGGCCGGGCGACGCCGGGCCGCTGCTCACGTGGGGCCTGACCGTCACGCGCGGGCCGAACAAGACGCGC
CAGAATCTGGGCATCTACCGGCAGCAACTGATCGGACGCAACAACTGATCATGCGCTGGCTCGCGCATCGCGGC
GGCGCGCTCGATTTCCGCGAATTCGCGCTGAAGCATCCGGGCCAGCCCTATCCCGTCGCCGTCGTGCTCGGCGCC
GATCCGGCGACGATGCTCGGGGCCGTACGCCCCGTGCCCGATTTCGCTGTCCGAATACCAGTTTCGCGGGCCTGCTG
CGCGGCGCGCGCACCGAGCTCGCGAAATGCGTGACGCCCGGCGTCGACGCGCTGCAGGTGCCGGCGCGCGCGGAA
ATCGTGCTCGAAGGCTTCATCCACCCGAGCAAGGCGCGCCCGCGCGCCGAAGGCGCGCCGCCGCGGCCG
GCCGCGGGCGCGCGCGGCCGGCTACGAGCATGCGCTCGAGGGCCCGTACGGCGATCACACCGGCTACTACAACGAG
CAGGAATGGTTTTCCGGTCTTACGGTCGAGCGGATCACGATGCGCCGCGATGCGATCTACCACTCGACGTACACC
GGCAAGCCGCCGACGAGCCGGCCGTGCTCGGCGTCGCGCTGAACGAAGTGTTTCGTGCCGCTGCTGCAGAAGCAG
TTCGCCGAGATCACCGATTTCTATCTGCCGCCGAGGGTTGCAGCTACCGGATGGCGATCGTCCAGATGAAGAAG
AGTTACGCGGGACACGCGAAGCGGGTGATGTTTCGGCGTCTGGAGCTTCCTGCGGCAGTTTCATGTATACGAAGTTC
ATCGTGCTGTCGACGAGGACGTGAACGTGCGCGACTGGAAGGAAGTGATCTGGGCGATCACGACGCGCGTCGAT
CCGGCGCGGACACGGTGCTCGTCGAGAACACGCCGATCGACTATCTCGACTTCGCGTCGCCCGTCGCCGGCCTC
GGCTCGAAGATGGGGCTCGATGCGACCAACAAGTGCGCGGGCGAAACCCAGCGCAATGGGGCCGGCCGATCGAG
ATGGACGCCCGCGTGAAGGCGCGCTCGATCGTCTGTGGACGGAGATCGGCCTATCGTGA

296. *Burkholderia pseudomallei* K96243 (SEQ ID NO. 296)

ATGAAATACAAAGATTTACGCGATTTTCATCCATGGCCTCGAGCAGCGCGGCGAGTTGCGGGCGGTCACCCAGCCC
GTATCGCCCGTCCTCGAAATGACCGAACTCTGCGACCGCGTGCTGCGCGCGGGCGGCCCGCGCTCCTGTTTCGAC
GCGCCGGCCGCGCCACCGGTTTCCGGTGCTCGGCAATCTGTTTCGGCACGCCGCGGCGCGTTCGCGCTCGGCATGGGC
GTCGACGCCGACGACGAAGCGGCGCTCGCGTCGCTGCGCGACATCGGCCGCCTGCTGTCCGCGCTCAAGGAGCCG
GACCCGCCGAAGCGCCTGAAGGACGCGGGCAAGTTGCTGTGCTCGCGAAGGCCGTGTGGGACATGAGCCCGAAG
ACGGTCTCCGCGCCGCCGTGCCAGGAGATCGTCTGGGAAGGCGACGACGTCGATCTGCACAAGCTGCCGATCCAG
ACCTGCTGGCCGGGCGACGCCGGGCCGCTGCTCACGTGGGGCCTGACCGTCACGCGCGGGCCGAACAAGACGCGC
CAGAATCTGGGCATCTACCGGCAGCAACTGATCGGACGCAACAACTGATCATGCGCTGGCTCGCGCATCGCGGC
GGCGCGCTCGATTTCCGCGAATTCGCGCTGAAGCATCCGGGCCAGCCCTATCCCGTCGCCGTCGTGCTCGGCGCC

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GATCCGGCGACGATGCTCGGGGCCGTACGCCCCGTGCCCGATTGCTGTCCGAATACCAGTTCGCGGGCCTGCTG
CGCGGCGCGCGCACCGAACTCGCGAAATGCGTGACGCCCCGGCGTCGACGCGCTGCAGGTGCCGGCGCGCGCGGAA
ATCGTGCTCGAAGGCTTCATCCACCCGAGCAAGGCGCGCCCGCGCCGGCGCCGAAGGCGCGCCGCCGCGGCCG
GCCGCGGGCGCGGGCGGCCGGCTACGAGCATGCGCTCGAGGGCCCGTACGGCGATCACACCGGCTACTACAACGAG
CAGGAATGGTTTCCGGTCTTCACGGTCGAGCGGATCACGATGCGCCGCGATGCGATCTACCACTCGACGTACACC
GGCAAGCCGCCCCGACGAGCCGGCCGTGCTCGGCGTCGCGCTGAACGAAGTGTTGCTGCCGCTGCTGCAGAAAGCAG
TTCGCCGAGATCACCGATTTCTATCTGCCGCCGAGGGTTGCAGCTACCGGATGGCGATCGTCCAGATGAAGAAG
AGTTACGCGGGACACGCGAAGCGGGTGATGTTGCGCGTCTGGAGCTTCCTGCGGCAGTTCATGTATACGAAGTTC
ATCGTGGTCGTCGACGAGGACGTGAACGTGCGCGACTGGAAGGAAGTGATCTGGGCGATCACGACGCGCGTTCGAT
CCGGCGCGCGACACGGTGCTCGTCGAGAACACGCCGATCGACTATCTCGACTTCGCTTCGCCCCGTGCGCCGGCCTC
GGCTCGAAGATGGGGCTCGATGCGACCAACAAGTGCGCCGGGCGAAACCCAGCGCGAATGGGGCCGGCCGATCGAG
ATGGACGCCGCCGTGAAGGCGCGCGTTCGATCGTCTGTGGACGGAGATCGGCCTGTCTGTGA

297. *Bordetella parapertussis* (SEQ ID NO. 297)

TTGAAGTATCGCGACCTCCGAGATTTTCTTGCCCAGCTTGAACGCCAGGGCGAACTCAAACGCATCACCGCGCCG
GTCTCGACGCGGCTGGAAATGACCGAGATTGCCGACCGGGTGCTGCGCGCCGGCGGCCCGGCCCTGCTGTTTCGAG
AACGCCCCGCCACAACGACGCGCCGGCCGACATGCCGGTGCTGGCCAACCTGTTGCGCACGCCGCGGGGTCGCC
TGGGGCATGGGGCCGACGACGTGCGCGCCCTGCGCGAAACCGGCCAACTGCTGGCCTCCCTGCGCGAGCCCCGAA
GCGCCCCAAGGGCCTGCGCGACGCGCTGGCCAAGGTGTCCATGCTGAAAGCCGCCCTGTGGGACATGAGCCCCAAG
ACCGTGCGCAGCGCCGCTGCCAGGAAATCGTCTGGGAAGGCGCGACGTGACCTGGGCGCCTGCCCATCCAG
ACCTGCTGGCCGGGCGATGTGGCGCCCTGCTCGCCTGGGGCCTGGTGATCACGCGCGGGCCGAACGCCCGGCGG
CAGAACCTGGGTATCTACCGCCAGCAGCCGCTGGGGCCGAACAAGCTGATCATGCGCTGGCTGTGCGACCGCGGC
GGCGCGCTGGACTTCCGCGACACGCCCCAGGCCACCCGGGCAAGTCGTTTCCCATCGCCGTGGCGCTGGGTGCC
GACCCGGCCACCATCCTGGACGCGGTACGCCGGTGCCGGACACGCTGTCCGAATACCAGTTCGCCGGGCTGCTG
CGCGGCTCGCGCACCGAGGTGCTCAAGGCGCTGGGCAGCGACCTGTGCGTGCCGGCCTCGGCCGAGATCGTGCTC
GAGGGCCACCTGCTGCCGGCCGACGATCCGCGCGCCGTGCTGCCGCGGTGCCCGAGGGCGCAACCCGCCCCCCG
GCCACCGGCTACGAAATGGCCCTCGAAGGCCCTATGGCGACCATAACGGCTACTACAACGAGCAGGACTGGTTC
CCGGTGTTACGGTGGACCGCATACCATGCGGGCGAACCCCATCTACCACTCCACCTATACCGGCAAGCCGCC
GACGAGCCGGCCGTGCTGGGCGTGCGCTGAACGAGGTATTCGTGCCGCTGCTGCGCCGCCAGCTGCCCGAAATC
GTCGATTTCTACCTGCCCCCGGAAGGCTGCAGCTACCGCCTGGCGGTGGTGTCGATCCGCAAGCAGTACGCCGGC
CACGCCAAGCGCGTGATGTTGCGCCTGTGGAGCGTGCTGCGGCAGTTCATGTACACCAAGTTCATCGTGGTGGTC
GACGAAGACATCGACCCGCGCGACTGGACCGAAGTGGTCTGGGCCATGACCACGCGCATGGACCCCGTGCGCGAC
ACGGTGCTGGTCGAGAACACGCCGATCGATTACCTCGATTTGCCTCGCCGGTGTCGGGCTGGGCGGCAAGATG
GGGCTGGACGCCACCAACAAGTGCGCCGGGCGAAACCCAGCCGCGAATGGGGCACGCCCATACACATGGACGAGGCG
GTCAAGCGCCGGGTGGATGCCATGTGGGACACGCTGGGACTGTAG

298. *Bordetella bronchiseptica* RB50 (SEQ ID NO. 298)

TTGAAGTATCGCGACCTCCGAGATTTTCTTGCCCAGCTTGAACGCCAGGGCGAACTCAAACGCATCACCGCGCCG
GTCTCGACGCGGCTGGAAATGACCGAGATTGCCGACCGGGTGCTGCGCGCCGGCGGCCCGGCCCTGCTGTTTCGAG
AACGCCCCGCCACAACGACGCGCCGGCCGACATGCCGGTGCTGGCCAACCTGTTGCGCACGCCGCGGGGTCGCC

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TGGGGCATGGGGGCCGACGACGTGCGCGCCCTGCGCGAAACCGGCGAACTGCTGGCCTCCCTGCGCGAGCCCGAA
GCGCCCAAGGGCCTGCGCGACGCGCTGGCCAAGGTGTCCATGCTGAAAGCGCCCTGTGGGACATGAGCCCAAG
ACCGTGCGCAGCGCCGCTGCCAGGAAATCGTCTGGGAAGGCGCCGACGTGACCTGGGCCGCTGCCCATCCAG
ACCTGCTGGCCGGGCGATGTGGCGCCCCCTGCTCGCCTGGGGCCTGGTGATCACGCGCGGGCCGAACGCCCGGCGG
CAGAACCTGGGTATCTACCGCCAGCAGCCGCTGGGGCCGAACAAGCTGATCATGCGCTGGCTGTGCGACCGCGGC
GGCGCGCTGGACTTCCGCGACCACGCCCAGGCCACCCGGGCAAGCCGTTTCCCATCGCCGTGGCGCTGGGTGCC
GACCCGGCCACCATCCTGGGCGCGGTACGCGCGGTGCCGGACACGCTGTCCGAATACCAGTTCGCCGGGCTGCTG
CGCGGCTCGCGCACCGAGGTGCTCAAGGCGCTGGGCAGCGACCTGTGCGTGCCGGCCTCGGCCGAGATCGTGCTC
GAGGGCCACCTGCTGCCGGCCGACGATCCGCGCGCCGTGCTGCCGCGGTGCCGAGGGCGCCAACCCGCCCCCG
GCCACCGGCTACGAAATGGCCCTCGAAGGCCCTATGGCGACCATAACCGGCTACTACAACGAGCAGGACTGGTTC
CCGGTGTTACGGTGGACCGCATCACCATGCGGGCGCAACCCATCTACCACTCCACCTATACCGGCAAGCCGCCC
GACGAGCCGGCCGTGCTGGGCGTGGCGCTGAACGAGGTATTCGTGCCGTGCTGCGCCGCCAGCTGCCCGAAATC
GTCGATTTCTACCTGCCCCCGGAAGGCTGCAGCTACCGCCTGGCGGTGGTGTCGATCCGCAAGCAGTACGCCGGC
CACGCCAAGCGCGTGATGTTGCGCCTGTGGAGCGTGCTGCGGCAGTTCATGTACACCAAGTTCATCGTGGTGGTC
GACGAAGACATCGACCCGCGCGACTGGACCGAAGTGGTCTGGGCCATGACCACGCGCATGGACCCCGTGCGCGAC
ACGGTGCTGGTTCGAGAACACGCCGATCGATTACCTCGATTTGCGCTCGCCGGTGTCGGGCCTGGGCGGCAAGATG
GGGCTGGACGCCACCAACAAGTGGCCGGGCGAAACCAGCCGCGAATGGGGCACGCCCATACACATGGACGAGGCG
GTCAAGCGCCGGGTGGATGCCATGTGGGACACGCTGGGACTGTAG

299. *Bordetella pertussis* Tohama I (SEQ ID NO. 299)

TTGCCGGGATCTGCCTTGAAGTACCGCGACCTCCGAGATTTTCTTGCCCAGCTCGAACGCCAGGGCGAACTCAAA
CGCATACCGCGCCGGTCTCGACGCGGCTGGAAATGACCGAGATTGCCGACCGGGTGCTGCGCGCCGGCGGGCCCG
GCCCTGCTGTTTCGAGAACGCCCCGCCACAACGACGCGCCGGCCGACATGCCGGTGCTGGCCAACCTGTTTCGGCAGC
CCGCGGCGGGTGCCTGGGGCATGGGGGCCGACGACGTGCGCGCCCTGCGCGAAACCGGCGAACTGCTGGCCTCC
CTGCGCGAGCCCGAAGCGCCCAAGGGCCTGCGCGACGCGCTGGCCAAGGTGTCCATGCTGAAAGCCGCCCTGTGG
GACATGAGCCCCAAGACCGTGCGCAGCGCCGCTGCCAGGAAATCGTCTGGGAAGGCGCCGACGTGAGCTGAGC
CGCCTGCCCATCCAGACCTGCTGGCCGGGCGACGTGGCGCCCTGCTCGCCTGGGGCCTGGTGATCACGCGCGGG
CCGAACGCCGGCGGCAGAACCTGGGCATCTACCGCCAGCAGCCGCTGGGGCCGAACAAGCTGATCATGCGCTGG
CTGTGCGACCGGGGCGGCGCGCTGGACTTCCGCGACCACGCCAGGCCACCCGGGCAAGCCGTTTCCCATCACC
GTGGCGCTGGGCGCCGACCCGGCCACCATCCTGGGCGCGGTACGCCGGTGCCGGACACGCTGTCCGAATACCAG
TTCGCCGGGTGCTGCGCGGCTCGCGCACCGAGGTGCTCAAGGCGCTGGGCAGCGACCTGTGCGGTGCCGGCCTCG
GCCGAGATCGTGCTCGAGGGCCACCTGCTGCCGGCCGACGATCCGCGCGCCGTGCTGCCGTGGTGCCCGAGGGC
GCCAACCCGCCCCCGGCCACCGGCTACGAAATGGCGCTCGAAGGCCCTATGGCGACCATAACGGCTACTACAAC
GAGCAGGACTGGTTCCCGGTGTTACGGTGGACCGCATCACCATGCGGCGCAACCCCATCTACCACTCCACCTAT
ACCGGCAAGCCGCCCCGACGAGCCGGCCGTGCTGGGCGTGGCGCTGAACGAGGTATTCGTGCCGTGCTGCGCCGC
CAGCTGCCCCGAGATCGTCGATTTCTACCTGCCCCCGGAAGGCTGCAGCTACCGCCTGGCGGTGGTGTCGATCCGC
AAGCAGTACGCCGGCCACGCCAAGCGCGTGATGTTGCGCCTGTGGAGCGTGCTGCGGCAGTTCATGTACACCAAG
TTCATCGTGGTGGTTCGACGAAGACATCGACCCGCGCGACTGGACCGAAGTGGTCTGGGCCATGACCACGCGCATG
GACCCCGTGCGCGACACGGTGCTGGTTCGAGAACGCGCCTATCGATTACCTGGATTTGCGCCTCGCCGGTGTCGGC

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CTGGGCGGCAAGATGGGGCTGGACGCCACCAACAAGTGGCCGGGCGAAACCAGCCGGAATGGGGCACGCCCATACACATGGACGAAGCGGTCAAGCGCCGGGTGGATGCCATGTGGGACACGCTGGGACTGTAG

300. *Legionella pneumophila* subsp. *pneumophila* str. *Philadelphia 1*

(SEQ ID NO. 300)

ATGAAGTATTCAGATCTGAGAGATTTTCATAGCCCAACTTGAATCACGTGAATTATTTAAACGTATTGATTATCCTGTATCACCTCATCTTGAGATGACCCTAGTCAGCGATAAAGTGTTGCGCTCAGGAGGGCCAGCCCTTCTGTTTACC AATACCCCAATTACAACATGCCTGTACTGACCAATCTTTTTGGTACGGTAGAGCGCGTGGCTTTGGGAATGGGT GAGGAATCAATAGTGGCTTTGAGGGAGATTGGAAAATTATTGGCTGCTTTAAAGGAGCCCGATCCTCCCAAAGGC TTCAAAGACGCTTTTAGCAAGTTGCCCTTATTGAAACAAGCGCTGAATATGGCACCCAAATATGTCAGTGGAGCC GAGTGCCAGACTCATGTGTGGGAAAAGGATGAAGTGGATTTAACCTTATTGCCCATCCAAACGTGTTGGCCCGGA GATGTTGCTCCTCTAATTACCTGGGGTTTGGTTACTACTCGTGGCCACACCAGTCCAGAGAAAACATGGGCATC TATCGCCAGCAACTATTAAGTAAAAACAAATTGATCATGCGCTGGTTATCTCACCGCGGAGGTGCTTTGGATTAC CAGGCCTGGCAACAAGAATATCCCAAAGAGCGTTTCCCTGTTGCGGTGACTTTAGGCGCTGATCCAGCCACCATA CTGGCAGCAGTTACTCCCGTTCCTGATACTTTGTCTGAATACGCTTTTGCGGGCTTGCTTAGAGGACAACGAACT CGGTTGACTCGATGCATTGGCAATGATTTGCATGTTCCAGCCAGCGCAGAAATTGTTTTGGAAGGTTATCTGGAG CCAGGAAATGAGGCGCCCGAAGGGCCTTATGGCGATCACACCGGTTATTATAATGAAGTCCAATCTTTTCTGT TTTACGGTAGAGCGTATTACTCATCGCGATAAACCTATTTACCACAGTACTTATACCGGAAGACCGCCAGATGAG CCAGCCATTTTGGGAGTTGCCTTAAATGAAGTGTTCATTCCTTGTACAAAAACAATTCAGAGATTGTGGAT TTTTATTTGCCGCCAGAAGGATGCTCTTATCGTTTGGCTGTAGTCACTATAAAAAAGCAATATCCAGGACATGCT AAACGTATTATGATGGCTGTTTGGTCTTCTTGCGCCAGTTTATGTATACCAAGTTCGTCATTGTTTGTGATGAT GATGTGGACGCGCGCAATTGGCAAGATGTCATATGGGCAATGACCACACGCATGGATCCGTCCCGCGATACAGTC ATGGTAGAAAATACACCCATTGATTATCTGGACTTCGCTTCCCCAGTTTCAGGATTGGGTTCAGATGGGTATG GATGCTACCAGTAAATGGCCAGGAGAAACACAAAGAGAATGGGGTAAACCAATTACGATGGATGAAGATGTGCTT AATAGAGTAAATGGTTATTGGTCCTTATTAGGATTTAAATAA

301. *Klebsiella pneumoniae* ATCC 13883 (SEQ ID NO. 301)

AATGGCGCAGGAACGACCAGACGCCCATCATTACGCGCTTGGCATGTCCCGCTACTGTTTTTTCATGGTCACCA CCGCCAGGCGATAGGAGCACCTTCCGGCGGCAGATAGAAATCAACGATTTCCGGGAAGTCTTTTGCAGGATCG GCACAAAGACTTCATTCAGCGCCACGCCCAGCACCGCTGGCTCATCGGGCGGTCCGGCGGTATAGGTAGAATGAT AAATCGCGTCTTCACGCTGGGTAATATGGGTACCCTAAATACCGGAAGCTGTCCACTTCATTATAGTAACCGG TGTGATCGCCATACGGGCCTTCCGGCGCCATTTACCGGCCCTCAATGTAGCCTTCAAGCACAAATTTCCGCGCTGG CCGGCACTTCAAGGTCATTGGAAACGCACTTAACCACTTCGGTCTTGGTGCCGCGCAGCAGGCCTGCGAAAGCAT ATTCCGACAGGGTATCGGGCACCGGCGTCAACGCGCCAAGAATGGTTGCCGGATCGGCGCCAAGCGCCACGGAAA CCGGGAAGCGTTCGCCCCGACGCGCCGCGCACCCTCTGGAAATCCAGCGCGCCGCGCGATGAGACAGCCA

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302. *Serratia liquefaciens* ATCC 27592 (SEQ ID NO. 302)

CCCATCATTACGCGTTTAGCATGACCAGCATACTGTTTCTTGATGGTCACCACCGCCAGACGATAAGAACAGCCT
TCGGGCGGCAGATAGAAATCGACAATTTCCGGGAACTGCTTTTGAGAAATGGGAACGAAGACTTCGTTTCAGCGCC
ACGCCCAGCACCGCAGGCTCATCCGGCGGACGGCCGGTGTAGGTCGAGTGGTAAATGGCATCGCGACGCTGGGTG
ATGTGAGTGATGGTAAATACCGGGAAGTGGTCGATCTCGTTGTAGTAACCGGTGTGATCGCCATACGGGCCTTCC
GGTGCCATTTACCCGGTTCAATGTAGCCTTCCAACACGATTTCCGCGCTGGCCGGCACTTCCAAATCGCAGGAG
AGGCACTTGACCACTTCGGTTTTGTTGCCACGCAGCAGCCCCGGCAAAAGCATATTCAGACAGGGTATCCGGTACC
GGCGTCACCGCGCCGAGGATAGTGGCGGGATCCGCCCCCTAATGCCACCGCAACCGGGAAACGCTCACCAGGGTGC
GCCTGACACCATTCTGATAATCCAACGCGCCGCCACGGTGGGACAGCCAACT

303. *Brucella melitensis* (SEQ ID NO. 303)

CCCGAAGCACCCGAAACACCGATGACGATCCGCTTCATATCCGTTTGTCCCTGTCGAGGCCGAGTTCATCCCAGA
TCGCGTCCACACGGGCGATGGTTTCTTCATTCATGGCCAGAACCTTGCCCCATTCGCGGTCCGTTTCAGGACCGA
TCTTGTTGGTGGCGTCAAGACCGAGCTTTCCGCCAAGGCCGGAGCGTGGCGAGGCGAAATCCAGATAATCGACCG
GCGTGTGGAAAGTGTACACAGTCGCGGCTTGTCATCAAAGCGGGTGGCAAGCGCCACATCACATCGTCCCAGT
TGTGTACATCGATATCGGGATCGACGGCGATAATGAGCTTGGTATAGCTGAACTGCGGCAGCATGGACCAAAGCC
CCATCATCACGCGCCGCGCCTGCCCCGATAACGCTTGTCGATGGAAACCACCATGGCGCGGTAGGAACAGGCGG
CAGGCGGCAGCCAGAGATCGGCTATCTCGGGAACTGCTTGCGCACGACAGGCACGAAAAGCTGGTTCATCACCT
CGCCAAGCCGCGAAGGCTCGTCCGGCGGGCGCTCCGTATAGGTGGAAAGATAGACCGGCTTCTTGCGCATGGTGA
TCGCCGTACCTGCATGACGGGAAACGCTCCACGCTGTTATAATAGCCGGTATGGTCCCCATAAGGCCCTTCGG
GCGCGGTTTGTGTAGCGGAAACCCGACCTTCAAGAACGATTTCTGCATTGGCGGGCACCATCAGCGGCACCGTGC
GCCCTGCGTGACACACGGCCTGCGCCCGCCAGAAGGCCGGAAATGCAAGCTCGCTCATGCCTTCCGGCAGCG
GCATAACTGCGGCCAGAATGGTCGCCGGGTCAACGCCGATGGCAATTGCAACCGGCATGTCCTCACC GCGCTTTT
GCCACATGCGATGGTGGCGCGCGCCCGCGATGCGCGAGCCAGCGCATGATAAGCCGGTTCTCTCCAGTTTCT
GCATCCGGTAAATGCCGACATTGACATCGGAGGGATCGTCCGGCGCGCGTGTGATAACGAGCGGCCAGGTGATGA
GCGGCGCAGGCTCGCCCGGCCAGCACCATTTGGATCGGCAGCGTGTGAGATTGACCGATGCGCCTTCCATCACAA
GGCCATGAACCGGCGCCCGGCTCACCTGGCGCGGGCGCATGTTGAGGGCTGCCTTGCCCATCGGCAGCTTTTCCC
ATATTTACCGGCCGAACGCGGCGGCTTCGGCGCACGCAATTCGGCCAGCATTTTCAGCCAGAAGCGGCAATTCCT
CCGGCAGACGCCCAAGCCCCCAGGCGATACGCCGCTCGGACCCGA

Figure 13. Molecular marker VIII (hypothetical protein yleA) in Gram-negative bacteria (SEQ ID NOs 304-325).

304. *Haemophilus influenzae* (SEQ ID NO. 304)

TTAGCCGTGATAACGCCCTACGCCTAATTCATCTTCTTTACGTGTGCGATTCACTACTTCTTGTGGAGATTGCGC
AATACGTAATCCCATTTTCATCTTCAGTACGCACCACTTCGCCACGTAACGAATTAGTATAAACATCAGTGATTTT
CACATCCACAACTTACCGATCATTTCTGGAGAACCTTGGAATTAACAATACGATTCGTTTCAGTACGTCCCGT
CAATTCATAATATCTTTCTTCGATGGGCCTTCACTAACACGCGCTGCTCTGTGCCAAGCATAACGACGGCTAAA
TTGTGCCGCTTGTTGATTAATACGCTCTTGATGACATAAAGACGCTGTTTCTTTTCATCTCCCGTGACATCATC
TGGCATATCTGCTGCTGGCGTACCTGGTGGGCTGAGTACACAAAAGTGAAGCTCATATCAAAGTTTACTTGTGC
AATCAAATTCATAGTTTGTCTCAAATCTTCCGCCGTTTACCAGGGAAACCAACAATAAAGTCAGAGCTGATTTG
AATATCTGGGCGCACAGCACGAAGTTTACGAATAATGGATTTATATTCTAATGCGGTATGAGCACGTTTCATCAT
TGTTAATACACGGTCAGAACCTGCTTGCACTGGAAGATGTAAGAACTCACTAATTCAGGCGTATCACGATACAC
ATCAATAATATCATCGGTAAATTTCTATTGGATGACTGGTTGTGAAACGTAAACGGTCAATACCATCAATTGATGC
GACAAGACGAAGCAACTCAGCAAAGCTGCAAATTTGACCATCATGCGTTGGCCACGATAAGCATTTCATTTTG
ACCAAGTAGATTGACCTCACGCACACCTTGTTCCGCAAGTTGCGCAATTTCAAATAGCACATCATCTACAGGACG
GCTAACTTCTTCTCCACGAGTATAAGGCACAACACAAAAGTACAGTATTTATTACAGCCTTCCATAATGGAAAC
AAATGCCGTTGGGCCTTCTGCGCGAGGTTCTGGTAAGCGGTCAAATTTCTCAATTTTCAGGGAACTTACGTCTAC
GACGGAACTTTTTCCACCACGAATTTGATTAATCATTTTCAGGCAAGCGATGCAAAGTTTGCGGGCCAAAAATAAT
ATCCACATAAGGCGCACGATGGCGAATATGTTCCCTTCTTGAGAGGCTACACAGCCGCCACACCAATCACTAA
ATTTGGATTATTTTTCTTTAATTTCTTTCCACGCCCAAGTTGGTGGAACTTTTTCTTGTGCTTTTTTCACGAAT
AGAACAGGTATTTAATAATAATACGTCTGCTTCTTCAGGTGCTTCCGTGAGTTCTAATCCGTGGGTGCTTAATAA
AAGATCAGCCATTTTAGATGAATCATATTCATTCATCTGGCAGCCCCAAGTTTTAATATGTAATTTTTGAGTCAT

305. *Pasteurella multocida* (SEQ ID NO. 305)

CTACGCGTGATAACGTCCCACGCCGAGTTCATCTTCTTTACGAGTACGATTAATCACCATTTGTGGCGATTGAAC
AACGCGAAGTCCCATTTGTTCTTCAGTTCTAACGACTTCACCACGCAGTGAGTTAGTAAACACATCCGTGATCTT
GATATCAACAACTTCCCAATCATATCAGGCGTGCCACAAAATTGACGATACGATTAGTTTCTGTACGCCCTGT
GAGTTCCATTAAATCTTTTTTCGAGGGTCTTCCACTAACACGCGCTGTTCTGTGCCTAACATTGCTCGACTAAA
TTGCGCGGCTTGATTGTTAATGCGTTGTTGCAACACATATAAACGTTGTTTCTTCTCTTCTGTGCATCATC
AGGCATATCTGCTGCTGGCGTGCTGGACGTGCTGAATAAATGAAGCTGAACTCATATCAAATTTACTTGTGC
AATTAAATTCATGGTTTGCTCGAAATCTTCTGCTGTTTCGCCCCGGGAAACCGACAATAAAATCTGAGCTAATTTG
AATCTCTGGACGCACCGCTCTTAACCTCCGAATAATCGATTTATATTCTAATGCCGTATGATTGCGTTTCATCAT
AGATAACACACGATCAGAACCCTTTGTACAGGTAAGTGAAGAACTCACCAACTCTGGCGTATCACGGTACAC
ATCAATAATGTCATCAGTGAATCAATTGGGTGACTGGTGGTAAAACGTAAACGGTCAATACCATCAATAGCGGC
TACTAAACGTAACAATTCGCAAAAGTACAAATACCGTCATCATGAGTTGCACCACGATAAGCGTTCACGTTTTG
TCCTAATAAATTCATTCACGCACGCCTTGCTCTGCCAACTGTGCAATTTCAAATAATACATCATCCACTGGACG
ACTGACTTCTTCACCACGCGTATAAGGCACGACACAGAATGAGCAATATTTATTACAGCCTTCCATAATGGATAC
GAAAGCAGTTGGACCTTCTGCACGCGGTTCTGGTAAACGGTCAATTTTTCAATTTCTGGAAAAGTACATCGAC
TACTGAGCTTTTACCACCTCTGATCTGATTGATCATTTTCAGGTAAACGATGTAAGGTTTGTGGTCCAAAAATAAT

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ATCGACATAAGGAGCACGAGTACGAATGTGTTCTCCTTCTTGTGAGGCAACACAGCCCCAACACCGATAACGAG
TCCCGGCTTATGTTTCTTTAATTCTTTCCAACGTCTAATTGATGGAAAACTTTTCTGTGCTTTTTCACGAAT
TGAGCAAGTGTTTAACAATAACACATCCGCTTCTTCCGGAATTTCTGTAACTCTAAGCCGTGAGTACTGTTTAA
GAGATCTGCCATTTTAGATGAATCATATTCATTCATCTGACAACCCACGTTTTAATATGTAATTTTTGCGTCAT

306. *Haemophilus ducrei* (SEQ ID NO. 306)

TTACAGATTTACTGCGTATTTGCCTACACCTAAATCATCTTCCTTACGGGTCCGTGCAATGACACTTGATGCTGA
TTCAACAATACGTAAACCCATTTGATCTTCTGTTCTGATCACTTCACCGCGTAATGAGTTTGAGTAAACATCGGT
GATTTTAATATCTACGAATTTGCCGATCATATTTGGTGTGCCGATGAAATTAACCTACACGATTGGTTTCTGTACG
ACCCGTTAATTCATAATATCTTTTTTAGATGGGCCTTCAACCAAATTCGTTGTTCAAGTCCCAAGCATTAAAGCG
ACTAAATTGCATCGCTTGATGGTTAATTCGTTGTTGTAAGTGTGCTAAGCGGTCTTTTTTCTCATTTTCAGACAC
ATCATCAGGTAAGTCTGATGCAGGCGTACCTGGACGCGCAGAGTAGATAAAGCTAAAGCTCATATCAAATTTGAC
TTGTTCAATAATTTTCATTGTTTGTTCAAAGTCTTCCGCTGTTTCGCCAGGAAAGCCAACAATGAAATCTGAGCT
AATTTGGATATTTGGACGAACCGCACGTAATTTACGAATAATGGCTTTGTATTCTAATGCGGTGTGGTTACGTTT
CATCATGGTTAAACACGATCGGCGCCACTTTGGATAGGTAAATGCAAGAAGCTGACCAATTCTGGAGTATCACG
ATACACTTCAATAATGTCTCGTGAATTCAATGGGGTGGCTTGTGGTATAACGTAAGCGGTCAATACCATCAAT
GGCGGCAACTAAACGTAATAATTCTGCAAAAGTGCAAAATGCCACCATCAAAGGTTTCACCACGGTAAGCATTAAAC
GTTTTGACCCAGCAAGTTAACTTCACGAACGCCTTGCTCTGCTAATTGTGCGATTTTGAATAAGACATCATCAAC
AGGGCGGGAAACTTCTTCACCACGGGTATAAGGCACTACACAGAATGAGCAGTATTTATTACAGCCTTCCATAAT
TGATACGAAAGCAGTTGGACCTTCTGCTTTGGGTTCTGGTAAGCGGTGCAATTTTTCAATTTCTGGGAAGGAGAT
ATCGACTACTGCACGATCGCTGATCGGATCTGGTTGATCATTTCTGGTAAGCGGTGCAATGTTTGTGGCCCAA
TACTATATCAACAAAAGGGGCACGTTTCACGGATATGTTTACCTTCTTGTGAAGCAACACAGCCACCAACGCCAAT
AATTAAATCGGGTTTGTCTTTTTCCAGTTTTTCCAACGACCAAGTTGTGAAAAGACTTTTTCTTGTGCTTTTTTC
ACGAATTGAGCAAGTATTCAATAATAAAATATCCGCTTCTTCAGGTTTATCGGTTAATTCTAATCCGTGTGTTGA
GTTTAAGAGATCTGCCATTTTTGATGAGTCATACTCATTCATTTGGCAACCCCAAGTTGTGATATGTAATTTTGC
CAT

307. *Vibrio parahaemolyticus* (SEQ ID NO. 307)

TTATGGCGTAAAGTAGCTACACCTAGCTCATCTTCGCGACGTGTTTTCGCCATCATTTGTGTTGGAGAAATCAC
ACTACGAAGGTCCATGTCTTTTTCTGTACGTACTAGCTCACCACGTAGCGAGTTTGCAAATACGTCCGTAATCTT
CACGTCAACGAAGTACCAATTAGGTCTGCGCTACCTTCAAAGTTTACTACACGGTTGTTTTCTGTACGAGCGCG
CAGTTCCATTAGGTTTTTCTTAGAAGGGCCTTCAACCAGTACACGCTGCTCAGTAGCAAGCATTAGGCGTGAGTA
ACGCATTGCTTGTGCATTGATGGTTTGTGTCAGCTCGTATAGACGCTCTTCTTCACTTGCTCTGGTATATCACA
AGGGTAATCTGCCGAGGTGTACCTGGACGAGGTGAGAAGATAAAGCTGAAGCTCATGTCAAAGTCTACGTCTTT
GATTAGCTTCATTGTGTCTTGAAGTCTTTGTCTGTTTACCAGGGAAACCAACAATAAAGTCAGAACTGATTTG
GATATCAGGACGCGCTTTACGTAGTTTACGGATGATCGACTTGTACTCGATAGCTGTGTGAGGACGCTTCATCAT
CGTTAGAATACGGTCACTACCACTTTGTACTGGCAGGTGTAGGAACTCACAAGCTCCGGGGTATCTTCGTAAAC
CGCGATGATGTCGTCTGTAACTCTAGCGGGTGGCTAGTCGTGAAACGAATACGGTCGATACCATCGATAGATGC
AACGAGACGAAGCAGTTCAGCAAAAGAGCAGATCTCGCCGTCGTGCATAGGGCCACGGTATGCGTTTACGTTTTG
ACCTAGTAGGTTAACTTCACGTACACCTTGTTCCGCTAGCTGTGCAATCTCGAATAACACGTATCCATTGGACG

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ACTAACTTCTTCACCACGAGTGTATGGTACAACGCAGTAAGTGCAGTATTTTGAACAGCCTTCCATGATAGAAAC
AAACGCCGTCGCACCTTCTGCACGTGGCTCAGGTAGGCGGTGGAACCTTTTCAATCTCTGGGAACGAAATGTCCAT
TACCGGTGCATCGTCAGTTTGAGATTGTTTGATCATCTCAGGTAGGCGGTGCAGAGTTTGAGGGCCAAAGATCAC
GTCAACGTATGGTGCACGCTCACGGATGTGGTCACCTTCTTGTGTTGCTACACAACCACCTACACCGATAACTAC
GCCAGGTTTTTTATCTTTTAGTGTTTTCCAACGGCCTAGCTGGTGGAAAACCTTCTCTTGCCTTTTTTCACGGAT
CGAACAGGTGTTAAGTAGAAGTACGTCTGCTTCCTCTGGCTCTTCCGTCAGCTCATAGCCGTTTGCAGCATTAAG
CAGGTCGGCCATTTTTGATGAATCGTATTCGTTTCATCTGGCAGCCCCAGGTTTTAATTAGCAGTTTCTTACTCAT

308. *Yersinia pestis* (SEQ ID NO. 308)

GAATTTACCAATCATGTGCGGTGAACCCCTCAAAGTTCACGACGCGGTTGTTTTCCGTACGCCCCGCCAGTTCCAT
GACATTTTTGCGAGAGGTACCCTCCACCAAACACGCTGTACTGTCCCTACCATCTTACGGCTAATTTCCATCGC
CTGTTGGCTAATGCGTTGTTGCAGGATATGTAGCCGCTGTTTTTCTCTCTTCCGGACACATTGTTGGGTAAATC
AGCCGCTGGTGTGCCGGGACGCGGGGAGTAAATAAAGCTGTAGCTGGTATCAAAATGAATATCTGCGACCAGTTT
CATGGTCTGTTCAAATCCTGCTGGGTTTTACCAGGGAAGCCGACAATAAAATCAGAACTTATCTGGATATCAGG
GCGTGCTTGACGCAGTTTGCGGATGATGGCTTTGTATTCCAAGGCGGTATGGGCACGCTTCATCATGGTCAAAT
ACGGTCAGAACCGCTTTGTACCGGCAAATGCAGGAAGCTCACCAATTCAGGCGTATCGCGATAAACATCAATGAT
ATCGTCAGTAACTCAATGGGGTGGCTGGTGGTAAATCGTACCCTATCGATACCATCAATCGCCGCAACCAAACG
CAACAGCTCGGCAAACCTACAGATATCGCCATCGTAGGTTGCCCCGCGGTAGGCGTTAACATTCTGGCCGAGTAA
GTTGACTTCACGTACGCCTTGAGCGGCTAACTGGGCGATTTCAAAAAGAATGTCATCGCTTGACGGCTGACTTC
CTCGCCTCGGGTGTAGGGTACGACACAGAATGTACAATATTTATTGCAGCCTTCCATGATCGAAACAAACGCAGT
TGGGCCTTCAGCCCGTGGTTCTGGCAAACGGTCAAATTTTTCAATTTCCGGGAAAACCTGATATCCACGACAGGGCT
ATTCGTTCCCTTGACGTGGTTAATCATTTCCGGTAAACGATGCAGCGTTTGTGGCCCCGAAGATGACATCGACACA
GGGGGCGCGCTGGCGCAATTGTTACCTTCCTGTGACGCCACGCAACCACCGACCCCAATAATCAACTGCGGGTT
TTTCTCTTTCAATAATTTCCATTGCCCTAGCAGGCTGAATACTTTTTCTGTGCTTTTTCCCGGATAGAACAGGT
ATTTAGCAGCAGTAAATCCGCTTCTTCCGGGATGGTGGTAACTGGTAGCCATGGGTACTGGCCAAGAGATCTGC
CATTTTAGATGAATCGTATTCATTCATCTGGCAACCCAGGTTTTGATATGCAGTTTTTTAGTCATCGGGTTAT
CATCATCAAAATCACCTCGTTCCGTGCGGTACTCCGTTGTGGTAGATAATCTCCGTTGTAGTAGAGAGTCGCAAA
GGCTTCGTCGTTAGGGAGCATTGTAGTCATTTGCCTCTGCGATGACCACCGCAGAACCGTTGAGTTATTCTGTTG
AGTGATAAAAAATCCGTTACACTGCGGTTAGACAAAACCTTGCTAATG

309. *Vibrio cholerae* (SEQ ID NO. 309)

TCTTCACTTCTTCCGACAGATCGCAAGGATAGTCAGCGGCGGGTGTGCCTGGACGAGGTGAGAAAATAAAGCTAA
AGCTCATGTGAAATCGACATCGCGGATCAGCTTCATGGTGTCTTGAAATCTTTGTGCGTTTTCCCTGGGAAGC
CAACGATAAAATCAGAGCTGATTTGAATATCTGGGCGTGCTTTACGTAGCTTACGGATGATGGATTTGTACTCAA
TCGCCGTATGTGGACGCTTCATCATAGTCAGAATGCGATCGCTCCCACTTTGTACTGGCAAGTGCAGGAAGCTCA
CCAGCTCAGGCGTGTCTTCGTACACTGCAATAATGTCATCGGTAAATTCGAGTGGGTGGCTAGTGGTAAAGCGGA
TACGATCGATGCCGTCAATGGTGGCGACCAAACGCAGTAATTCAGCGAAAGAGCAAATGCCGCCATCGTGAGTGG
CACCACGGTAAGCGTTGACGTTTTGACCCAGCAGGTTAACTTCACGCACCCCTTGCTCGGCAAGCTGAGCGATCT
CGAACAGGACATCGTCCATAGGACGGCTGACTTCTTCACCGCGTGTGTAAGGCACTACGCAGTAAGTACAGTATT
TTGAGCAGCCTTCCATGATAGAAACGAACGCCGTTGGGCCTTCGCACGTGGCTCAGGCAGGCGGTGCAATTTTT

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CAATCTCAGGGAAAGAGATATCCATCACGGGCGCGTCGCTGGTTTGCGATTGTTTAATCATTTCTGGCAGACGAT
GCAGCGTCTGTGGGCCGAAGATGACATCCACATAAGGCGCACGATCGCGAATCGAGTCACCTTCTTGAGTAGCAA
CACAGCCACCGACACCGATCACGACACCTGGCTTCTTGTCTTTCAGGGTTTTCCAACGACCGAGTTGGTGGAAGA
CTTTTTCTGCGCCTTTTTCACGAATCGAACAGGTGTTTAGGAGTAAACGTCAGCTTCCTCGGGTATTTCTGTCA
GCTCATAGCCGTTTGCAGCATTAAGCAGGTCAGCCATTTTCGATGAATCGTACTCGTTCATCTGGCAGCCCCAAG
TTTTAATTAGCAGTTTCTTACTCATCTCACTTTCGCTCGTTCAATAGTTCTTCAATCATTTGAGCTGTAGCTCAC
ATTCTAGCCGCCCTCTCGGCGGTAAGCGGCGTATTGTACTGCTTTAAAAACCGACTGACTAGTAATTGGCGGAAT
TCTCTTGTAACCCCTTG

310. *Escherichia coli* souche K12 (SEQ ID NO. 310)

TTACGGCTGATAATAACCCACGCCAAGGTCGTTTTCTTTGCGGGTACGGGCAATCACTGATTCGGGTGTTTCTGC
CACGCGCAGACCCATTTTCATCTTCAGTACGCACCACTTTACCGCGCAGAGAGTTCCGGGTAGACGTCGGTAATTC
TACATCGACGAATTTACCGATCATATCCGGCGTGCCTTCGAAGTTGACCACGCGGTTATTTTCCGTACGCCCGGA
AAGCTCCATGATGCTCTTACGCGATGTACCTTCTACCAGAATACGCTGGGTGGTGCCGAGCATCCGGCGGCTCCA
CGCCATCGCTTGCTGATTAATGCGCTCTTGCGAATATACAGACGCTGCTTCTTCTCTTCTTCCGGAACATCATC
AACCATATCGGCGGCTGGTGTACCCGGACGTGCAGAGAAGATAAAGCTGTAGCTCATGTGCGAAATTGACGTCGGC
AATCAGCTTCATCGTTTTTCTCGAAGTCTTCGGTGGTTTCGCCAGGGAAGCCAACGATGAAATCAGAACTGATCTG
AATATCTGGACGCGCCGCACGCAGTTTACGGATGATCGCTTTGTACTCCAGCGCCGTATGGGTACGGCCCATCAG
GTTTCAGAATGCGATCGGAACCGCTCTGTACCGGCAGATGCAGGAAGCTCACCAGCTCCGGCGTGTGCGGATACAC
TTTCATGATACGTCGGTGAATTCGATCGGATGGCTGGTGGTAAAGCGAATACGATCGATCCCGTCGATCGCAGCA
ACCAGACGCAGCAGATCGGCAAACGATCCGGTGGTGCCGTCGTAGTTTTTACCACGCCAGGCGTTCACGTTCTGA
CCGAGCAGGTTGACTTCACGCACGCCCTGAGCCGCAAGCTGGGCAATCTCAAACAGAATATCGTCGGACGGACGG
CTTACCTCTTACCACGGGTGTAAGGCACCACGCAGTAGGTGCAATATTTATTGCGCCCTTCATGATGGAGACA
AACGCGGTGCGCCCTTCGGCGCGCGGTTCCGGTAGACGGTCAAACCTCTCGATTTCCGGGAAGCTGATATCTACA
ACCGGGCTGCGGTGCGCCACGCACGGAGTTGATCATCTCCGGCAGACGGTGCAGCGTTTGCGGCCCCAAAAATAATA
TCGACATAGTGGGCGCGCTGGCGAATGTGCTCGCTTCTTGCGATGCCACGCAGCCACCGACGCCGATAATCAGG
TCTGGATTCTTCTCTTTTAACAGTTTCCAGCGACCCAACTGATGGAAGACTTTTTCCTGAGCCTTCTCGCGGATT
GAGCAGGTGTTTCAGCAGCAGCACATCCGCTTCTTCCGCCACGTCGGTCAGTTGATAGCCGTGGGTGGCATCCAGC
AGATCGGCCATCTTCGATGAATCGTACTCGTTCATCTGACAGCCCCAGGTTTTAATATGGAGTTTTTTGGTTCAT

311. *Escherichia coli* souche 0157:H7 (SEQ ID NO. 311)

TTACGGCTGATAATAACCCACGCCAAGGTCGTTTTCTTTGCGAGTACGGGCAATCACCGATTCTGGTGTTTCTGC
CACGCGCAGACCCATTTTCATCTTCAGTACGCACCACTTTACCGCGCAGAGAGTTCCGGGTAGACGTCGGTAATTC
TACATCGACGAATTTACCGATCATATCCGGCGTGCCTTCGAAGTTGACCACGCGGTTATTTTCCGTACGCCCGGA
AAGCTCCATGATGCTCTTACGCGATGTACCTTCTACCAGAATACGCTGGGTGGTGCCGAGCATCCGGCGGTYCCA
CGCCATCGCTTGCTGATTGATACGTTCTTGCGAATATACAGACGCTGCTTCTTCTCTTCTTCCGGAACATCATC
AACCATATCGGCGGCTGGTGTACCCGGACGTGCAGAGAAGATAAAGCTGTAGCTCATGTGCGAAATTGACGTCGGC
AATCAGCTTCATCGTTTTTCTCGAAGTCTTCGGTGGTTTCGCCAGGGAAGCCGACGATGAAGTCAGAACTGATCTG
AATATCTGGACGCGCCGCACGCAGTTTACGGATGATCGCTTTGTACTCCAGCGCCGTATGGGTACGTCCCATCAG
GTTTCAGAATGCGATCGGAACCGCTCTGTACCGGCAGATGCAGGAAGCTCACCAGCTCCGGCGTGTGCGGATACAC

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TTTCGATGATATCGTCGGTGAATTCGATCGGATGGCTGGTGGTAAAGCGAATACGATCGATCCCGTCGATCGCAGC
AACCAGACGCAACAGATCGGCAAACGATCCGGTGGTGCCGTCGTAGTTTTTACCACGCCAGGCGTTCACGTTCTG
ACCGAGCAGGTTGACTTCACGCACGCCCTGAGCCGCAAGCTGGGCAATCTCAAACAGAATATCGTCAGACGGACG
GCTTACCTCTTACCACGGGTGTAAGGCACCACGCAGTAGGTGCAATATTTATTGCAGCCTTCCATGATGGAGAC
AAACGCGGTGCGCCCTTCGGCGCGCGGTTCGGGTAGACGGTCAAACCTCTCGATTTCCGGGAAGCTGATATCTAC
AACCGGGCTGCGGTGCGCCGCGCACGGAGTTGATCATCTCCGGCAGACGGTGACGCGTTTGCGGCCAAAAATAAT
ATCGACATAGTGGGCGCGCTGGCGAATGTGCTCGCCTTCTTGCGATGCCACGCAGCCACCGACGCCGATAATCAG
GTCTGGATTCTTCTCTTTTAACAGTTTCCAGCGACCCAAGTATGGAAGACTTTTTCTGAGCCTTCTCGCGGAT
TGAGCAGGTGTTTACGAGCAGCACATCCGCTTCTTCCGCCACGTCGGTCAGTTGATAGCCGTGGGTGGCATCCAG
CAGATCGGCCATCTTCGATGAATCGTACTCGTTCATCTGACAGCCCCAGGTTTTTAATATGGAGTTTTTTGGTCAT

312. *Pseudomonas aeruginosa* (SEQ ID NO. 312)

CCGCCGTACGGTCGTGCGCCTCAATGCAGGGTGCTGTCGATCAGGGTACCGCGCAGCGAGTGCGGCAGCGCGTCG
TCGATGTGCACCTGGGCGAACTGGCCGATCAGGCGTGATTTGTCGCAGCGGAAGTTGACGATCCGGTTGTTCTCG
GTGCGCCCCCTGGAGCATGCCTGGGTCTTCTTCGAGAAGTCGGTGACCAGGATCCGCTGGGTGCTGCCGACCATG
CGCCGGCTGATCTCGTAGCCTTGCTGGTGGATGCGGCTCTGGAGGATCTGCAGGCGCTGTTTCTTCACTTCTTCC
GGCAGGTGCTCGGCGAGGTGCGGCGCGGGCGTGCCGGGCGCGCGCTGTAGATGAAGGAGAAGGAGAAGTCGAAG
CCGACGTCCTCCACCAGCTTCATGGTCTGCTCGAAGTCCTTCTCGGTTTCGCCGGGAAACCGACGATGAAGTCG
GAGCTGATGCAGATGTCCGGTACCGCGGCCTTCAGCTTGCGGATACGCGACTTGTATTCCAGCACGGTATGGTTG
CGCTTCATCGCCGCCAGCACGCGGTGCGAGCCCGACTGCACCGGCAGGTGGATGAATTTACCAGCTCCGGCACC
TCGGCGTGCGCCTGGATCAGCGCGTGGGAGAATTCAGCGGGTGCGAGGTGGTATAGCGGATGCGCTCGATACCG
TCGACGGCGGCGACCACCCGAGCAGTTGCGGCGAAGTCGGCCAGGCGGCCATCGTGGGTGAGGCCGCGGAAGCCG
TTGACGTTCTGTCCAGCAGGGTGACTTCGCGGACGCCGTTCTCGGCCAGGTGGATCACTTCGGCGATCACGTCG
TCGAATGGTGGCTGACTTCCTCGCCGCGGGTGTAAGGGCACACGCAGAAGCTGCAGTACTTGCTGCAGCCTTCC
ATCACCGAGACGAAGGCGGTGGGGCCATCGACCCGCGGTTCCGGCAGGCGGTGCAATTTCTCGATTTCCGGGAAG
GACACGTCGACCTGCGGCTTGCGCGTGCTGCGCGCGGCGTCGATCATTTCCGGCAGGCGGTGACGGGTCTGCGGG
CCGAAGACCACGTCGACATAGGGCGCGCGCTCACGGATCGCGGCGCCTTCCTGGCTGGCCACGCAGCCGCCGACG
CCGATCACCGAGTCGGGATTCTGCTGCTTCAGCTCGCGCCACATGCCGAGCTTGAAAACACCTTTTCTGGGCC
TTCTCGCGGATCGAGCAGGTATTGAGCAGGATGACGTCGGCCTCGGCGGCGTTTTTCGGTCACCTCGAGGGCTTGG
TGTTACCGAGCAGGTCCGCCATTCGCGACGAGTCGTAATCGTTTCATCTGGCAGCCGTGGGTTTTGATGAAAAGC
TTCTTGCCCATGCGCTTCGTCGGACAGTTGAAAAGGACCGCGCATTATAGAGGGCGGGGCCCCCGGTTCTTAGC
GTTGCTGGCCGAAAGGCTGTGCTATGATTGCGGCCCTTCATTTTCCGGCATTGCTTTCCCCGCCATGAACAAGCG
CGAAAACCCCATCTACAAGGTGATTTTCTCAACCAGGGCCAGGTCTTCGAGATGTATGC

313. *Bordetella pertussis* (SEQ ID NO. 313)

TCATTCGGCTCCGGATGTGTGCGGTTTCGATGCCGGCGACACGGCCGCGCAGCGAGTTGGTGTGGGCGTGGGTGAC
GACGACGTCGACCATGTGGCCGATCAGGCGCGGCACGCCGGGAAAGTTGACGATACGGTTGTTCTCGGTACGGCC
CATCAGCTCGTTGGGGTCGCGCCGCGAAGGGCCTTCGACCAGCACGCGCTGGCGGGTGCCGATCATGCCCTGGGC
GATGGCCGCGGCTGCTGGTTGATGAGCGCCTGCAACTGCTGCAGGCGGCGCAGCTTGACGTCCTGCGGCGTGTC
ATCGTGCAGGTGCGGCGCCGGCGTGCCGGGCGGCGCGAATACACGAACGAGAACGAGGTGTGGAAGCCGACGTC

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CTCGATCAGCTTCATGGTCTTCTGGAAGTCCTCCTCGGTCTCGCCCGGAAACCAACGATGAAGTCCGAGGACAG
CGTCAGGCTGGGGCGCGCAGCGCGCAGGCGGCGCACCACGGAATTGAACTCCAGCGCGGTGTAGCCGCGCTTCAT
GGCCGCCAGCACCCGGTCGCTGCCGGCCTGCACCGGCAGGTGCAGGAACGACACCAGCTTGGGCAGCCGTGCGTA
GGCGTCGACCATGCGCTGGGTCAATTCCTTCGGATGCGAGGTGGTGTAGCGGATCCGTTGATACCGGGAATCTC
GTGCACGTATTCCAGCAGCATGGCGAAATCGGCGATTTGCGCGCTGTGCGCCATGGCGCCGCGGTAGGCGTTGAC
GTTCTGGCCCAGCAGCGTGAATTCCTTGACGCCCTGGTCGGCCAGGTGCGCGACCTCGAGCAGGACGTGCTCGAA
GGGGCGCGACACTTCTTCGCCGCGCGTGTAGGGCACCACGAGAAGCTGCAATACTTGCTGCAGCCTTCCATGAT
GGACACGAACGCGGTGGCGCCGTGACGCGCGGCGGGGCGAGGGCGTCAACTTCTCGATCTCGGGGAAGCTGAT
GTCGACCTGCGACACGCCCTGGGCGCGGCGGCGCTTGATCAGGTGCGGCAGCCGGTGCAGGGTCTGCGGGCCGAA
CACCACGTGACATAGGGCGCGCGCTTGACGATGGCCTCGCCTTCCTGGCTGGCCACGCAGCCGCCACGCCGAT
CACCAGGTTGGGGTTCTGCTTCTTGAGGTGCTGTACCCGGCCCAGGTGCGAGAACACCTTCTCCTGCGCCTTCTC
GCGCACGGAACAGGTGTTGAACAGGATGACATCGGCATCCTCGGGGTTGTGCGTCACTCCAGGCCCTGGTCGGC
GCGCAGCACGTGCGCCATCTTGTCCGAGTCGTACTCGTTTCATCTGGCAGCCGAAGGTGCGGATATACAA

314. *Bordetella parapertussis* (SEQ ID NO. 314)

TCATTCGGCTCCGGATGTGTGCGTTTCGATGCCGGCGACACGGCCGCGCAGCGAGTTGGTGTGGGCGTGGGTGAC
GACGACGTGACCATGTGGCCGATCAGGCGCGGCACGCCGGGAAAGTTGACGATACGTTTCTCGGTACGGCC
CATCAGCTCGTTGGGGTCGCGCCGCGAAGGGCCTTCGACCAGCACGCGCTGGCGGGTGGCGATCATGCCCTGGGC
GATGGCCGCGGCCCTGCTGGTTGATGAGCGCCTGCAACTGCTGCAGGCGGCGCAGCTTGACGTCCTGCGGCGTGT
ATCGTGCAGGTGCGCGGCGGCGTGC CGGGCGGCGGAATACGAACGAGAACGAGGTGTGAAGCCGACGTC
CTCGATCAGCTTCATGGTCTTCTGGAAGTCCTCCTCGGTCTCGCCCGGAAACCGACGATGAAGTCCGAGGACAG
CGTCAGGCTGGGGCGCGCAGCGCGCAGGCGGCGCACCACGGAATTGAACTCCAGCGCGGTGTAGCCGCGCTTCAT
GGCCGCCAGCACCCGGTCGCTGCCGGCCTGCACCGGCAGGTGCAGGAACGACACCAGCTTGGGCAGCCGTGCGTA
GGCGTCGACCATGCGCTGGGTCAATTCCTTCGGATGCGAGGTGCTGTAGCGGATCCGTTGATACCGGGAATCTC
GTGCACGTATTCCAGCAGCATGGCGAAATCGGCGATTTGCGCGCTGTGCGCCATGGCGCCGCGGTAGGCGTTGAC
GTTCTGGCCCAGCAGCGTGAATTCCTTGACGCCCTGGTCGGCCAGGTGCGCGATCTCGAGCAGGACGTGCTCGAA
GGGCCGCGACACTTCTTCGCCGCGCGTGTAGGGCACCACGAGAAGCTGCAATACTTGCTGCAGCCTTCCATGAT
GGACACGAACGCGGTGGCGCCGTGACGCGCGGCGGGGCGAGGGCGTCAACTTCTCGATCTCGGGAAAGCTGAT
GTCGACCTGGGACACGCCCTGGGCGCGGCGGCGCTTGATCAGGTGCGGCAGCCGGTGCAGGGTCTGCGGGCCGAA
CACCACGTGACATAGGGCGCGCGCTTGACGATGGCCTCGCCCTCCTGGCTGGCCACGCAGCCGCCACGCCGAT
CACCAGGTTGGGGTTCTGCTTCTTGAGGTGCTGTACCCGGCCCAGGTGCGAGAACACCTTCTCCTGCGCCTTCTC
GCGCACGGAACAGGTGTTGAACAGGATGACATCGGCATCCTCGGGGTTGTGCGTCACTCCAGGCCCTGGTCGGC
GCGCAGCACGTGCGCCATCTTGTCCGAGTCGTACTCGTTTCATCTGGCAGCCGAAGGTGCGGATATACAATTTGCC
CAGGCCCTGGGCGGTGGTGGCCGCGGTGCCGGCATCGGACGGGCTGGCGCCGTGCGGTTTGACAGTGGTTTTCTTG
CAT

315. *Burkholderia pseudomallei* (SEQ ID NO. 315)

TCAGTGCCTGGCGGCGCTCGCGTCGCCGTGCGCGAGCACGAGCTCGCCGCGCAGCGAGTGGGGATACGCGTGATT
GATCTTCACGTCGATCATCTGGCCGATCAGGCGCGGGTGC GCGGCGCTCGGCGCGGGAAAATTCACGACCCGGTT
GTTCTCGGTGCGGCGCGGAGCTCGTTCCGATCCTTGCGCGACGGCCCTCGACGAGGATTCGCTCGACCTTGCC

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GAGCATCGACTGGCTGATCCTCGCGACGTTCTCCTCGATCGTCGCCTGCAGATGTTGCAGGCGCTTGAGCTTGAG
CTCGCGCGGCGTGTCTGTCGGCGAGATTCGCGGCCGCGTGC CGGGCCGCGGGCTGTAGATGAACGAGAAGCTCGT
GTCGTAGCTCATCTCGTGAACGAGCGCCATCGTCTTGTCGAAGTCGGCGTCGGTCTCGCCGGGGAAACCCACGAT
GATGTCCGTGGACAGCGACAGATTCGGGCGGATCGCGCGCAGCTTGCGGATCACCGATTTGTATTTCGAGCACGGT
GTAGCCGCGCTTCATCGCCATCAGGATGCGGTCCGAGCCGTGCTGGACGGGCAGGTGCAGATGGTCGACGAGCTT
CGGCACCTTCGCGTAGACGTCGAGCAGGCGCTGCGTGAACCTCTTCGGATGCGATGTCGTGTAGCGGATCCGCTC
GATGCCGGGGATGTCGGCGACATATTCGATCAGCGTCGCGAAATCGGCGATCTCGGCCGAGCCGGCCGCGATCGC
GCCGCGGTAGGCGTTACGTTCTGGCCGAGCAGCGTGA CTTCGCGCACGCCCTGGTCGGCGAGGCCCGCGACCTC
GGTCAAGACGTCGTCGAGCGGGCGCGACACTTCATCGCCGCGCGTGTACGGCACGACGCAGTAGCTGCAGTACTT
CGAGCAGCCTTCCATGATCGACACGAACGCGCTCGGCCCTTCGACGCGAGCGGGCGGCAGATGGTCGAACTTCTC
GATTTGGGGAACTGATGTCGACCTGCGCGCGGCCGCTTTCGCGGCGCGCGTCGATCATCTGCGGCAGGCGGTG
CAGCGTTTGGGGCCGAACACGAGATCGACGTACGGCGCGCGCGACGATCGACGCGCCTTCTGGCTCGCCAC
GCAGCCGCCGACGCCGATCAGCAGGTCCGGCTTCGCTTCTTCAGCTCGCGCACGCGGCCGAGATCGGAGAACAC
CTTCTCCTGCGCTTTTCTCGCACCGAGCAGGTGTTGAACAGGATGATGTCCGCGTCTTCGGGGTGTGGTCTT
CTCGAGGCCCTCGGCCGATTGAGCACGTGACCATCTTGTGCGAGTCGTACTCGTTCATCTGGCAGCCGAAGGT
TTTTACGTAACTTTCTTGGTCAT

316. *Vibrio vulnificus* (SEQ ID NO. 316)

TTATGGCGTAAATGTCGCTACACCTAGCTCATCTTCGCGGCGTGT TTTGGCCATCATTTGTGTTGGCGAAATCAC
GCTACGTAGGTCCATATCTTTTTCAGTACGTACAATCTCACCACGCAGTGAGTTCGCAAATACATCGGTAATTTT
CACATCAACGAAGTACCAATCAGATCTGCGCTACCTTCAAAGTTTACTACACGGTTGTTTCTGTACGAGCACG
TAGCTCCATCAAGTTCTTCTTAGAAGGGCCTTCAACCAGTACACGCTGCTCTGTGCCTAGCATGAGGCGAGAGTA
ACGCATGGCTTGTGCGTTGATTTGTTGTTGCAGTTCGTACAAGCGCTCTTTCTTCGTCTCTTCTGAAAGATCACA
TGGGTAATCTGCCGCGAGGATACCAGGGCGAGGAGAGAAGATGAAGCTGAAGCTCATGTCAAAGTCGACATCTTT
GATCAGCTTCATGGTGTCTTGAAATCTTTGTCGCTTTCACCTGGGAAGCCAACAATAAAGTCAGAACTGATTTG
GATATCAGGACGCGCTTTACGCAGTTTACGAATGATCGACTTGTATTGATGCCAGTGTGAGGACGCTTCATCAT
CGTCAGAATGCGATCGCTACCACTTTGTACTGGTAGATGAAGGAAGCTCACCAGCTCTGGCGTATCTTCGTAGAC
AGCGATGATATCATCGGTGAACTCAAGTGGGTGGCTGGTGGTAAAGCGAATACGGTCGATACCATCGATAGACGC
AACAAGGCGAAGCAGTTCTGCAAAAGAACAGATTTACCATCGTGCCTTGGGCCACGGTATGCGTTTACGTTTTG
GCCTAGCAGGTTGACTTCGCGAACACCTTGCTCGGCAAGTTGCGCGATTTGTAAGCACATCGTCCATTGGGCG
GCTGACTTCTTACCACGAGTGTAAGGCACTACGCAGTAAGTACAGTACTTAGAACAGCCTTCCATGATAGAAAC
GAATGCGGTTGCGCCTTCTGCACGTGGTTCTGGCAGACTGTCAAACCTTCTCGATTTCTGGGAATGAAATGTCCAT
CACTGGTGCATCTTCACTTTGTGATTGTTTGATCATTTTCAGGAAGACGGTGCAAGGTTTGCGGGCCAAAGATAAC
GTCAACAAAAGGTGCAGTTTACGAATGTGATCGCCTTCTGTGTTGCTACACAACCACCAACACCGATCACGAC
GCCTGGCTTTTTATCTTTGAGTGTTTTCCAACGGCCAAGCTGGTGGAACACTTTTTCTTGCGCCTTTTTCAGGAT
CGAACAGGTGTTAAGTAATAGAACATCTGCTTCTTCTGGTTCTTCTGTCAATTTCGTAGCCATTTGCTGCGTTT
CAGATCCGCCATTTTCGATGAATCGTATTCGTTTCTGGAACCCCAAGGTTTAAATTAGCAGTTTCTTACTCAT

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317. *Vibrio fischeri* (SEQ ID NO. 317)

CTATGGCGTAAAAGTACCTACACCAAGATCATCTTCACGACGTGTCTTTTCCATCATTTCTGCTGGAGTCATAAC
AACACGTAAACCCATGTCTTTTTCTGTACGAAGTAGTTACACACGCAGTGAGTTCGCAAATACATCTGTGATTTT
AACATCAACAAATTGACCAATAAGATCCGCTGAACCTTCAAAGTTTACAACACGGTTGTTTTTCAGTACGAGCAGC
AAGTTCCATCAGGTTTTTCTTCGATGGGCCTTCAACTAATACACGTTGCTCAGTGTCTAGCATTAGACGAGAGTA
GCGCATTGCTTGGCTGTTTACTTGCTGTTGCAGTTCAGCTAGGCGATCTTTCTTCTCTTGTTTCAGGGATATCACA
TGGATAATCAGCAGCAGGTGTTCTTGACGCGCAGAGAAGATGAAACTAAAGCTCATGTGGAAGTCGACATCTTT
AATCAGTTTTCATTTGTATCTTGGAAGTCTTTGCGCGTTTCACCAGGGAAGCCAACAATAAAGTCAGAACTGATTTG
AATATCAGGACGAGCCTTACGTAATTTACGAATGATTGATTTGTATTCAATCGCTGTGTGAGGGCGCTTCATCAT
AGTTAGAATACGATCAGAACCCTTTGAACAGGTAAGTGTAAAGAACTTACTAGCTCTGGCGTATCTTCGTATAC
AGCGATGATGTCATCACCAACTCTAATGGGTGGCTTGTTGTAAAGCGTAAACGGTCGATACCATCGATAGATGC
AACCATACGTAATAATTCAGCAAATGTGCAGATATCACCGTCGTGCATTGGACCACGGTACGCGTTAACGTTTTG
ACCCAATAGTTTTACTTCACGTACGCCTTGCTCTGCAAGCTGTGCAATTTCAAATAATACGTCATCAAGAGGACG
GCTTACTTCTTCACCACGAGTGTATGGAACAACACAGTAAGTACAGTACTTAGAACACCCTTCCATAATAGAAAC
GAACGCTGTTGCACCTTCTGCTTTTGGTTTCAGGAAGGTTATCGAACTTTTCGATCTCTGGGAATGAAATATCCAT
TACTGGTTTTTTCATTTGATTGAGATTGGCGGATCATTTTCAGGTAAACGGTGTAAGTTTGTGGACCAAAAATTAC
GTCAACGTATGGAGCTCGTTGGCGAATATGATCACCTTCTTGAGTTGCAACACAACCACCAACACCGATCACTAG
ATCTGGTTTTTTATCTTTTAGGTTTTTCCAGCGGCCTAATTGGTGAAACACTTTCTCTTGCTTTTTTCACGAAT
AGAGCAGGTATTTAATAGTAGAACGTCAGCTTCTGTTGGTTCTTCTGTTAATTCATAACCATTTGCGGCACCTAA
AAGGTCGGCCATTTTAGATGAATCGTATTCGTTTCATCTGACAGCCCCAGGTTTTGATCAGCAGTTTCTTAGTCAT

318. *Yersinia pseudotuberculosis* (SEQ ID NO. 318)

TTAAGGCTGATAAATACCTACACCAATTTCAATTTCTTTACGGGTGCGAGCAATCACCGATTGCGGTGACTCGTG
GGTTCGCAGGTCCATCTGATCTTCTGTACGCAGTAAAATGCCGCGCAGTGAAGTGGCATAAACGTTAACAATTTT
GACATCAACGAATTTACCAATCATGTGGGTGAACCTCAAAGTTACGACGCGGTTGTTTTCCGTACGCCCGGC
CAGTTCCATGACATTTTTGCGAGAGGTCCCCTCCACCAAAACACGCTGTACTGTCCCTACCATCTTACGGCTAAT
TTCCATCGCCTGTTGGCTAATGCGTTGTTGCAGGATATGTAGCCGCTGTTTTTTCTCCTCTTCGGACACATTGTC
GGGTAAATCAGCCGCTGGTGTGCCGGGACGCGGGGAGTAAATAAAGCTGTAGCTGGTATCAAATGAATATCTGC
GACCAGTTTCATGGTCTGTTCAAAATCCTGCTGGGTTTCACCAGGGAAGCCGACAATAAAATCAGAACTTATCTG
GATATCAGGGCGCGCCTGACGCAGTTTGGCGATGATGGCTTTGTATTCCAGGGCGGTATGGGCACGCTTCATCAT
GGTCAAAATACGGTCAGAACCCTTTGTACCGGCAAATGCAGGAAGCTCACCAATTCAGGCGTATCGCGATAAAC
ATCAATGATATCGTCAGTAACTCAATGGGTGGCTGGTGGTAAATCGTATCCTATCGATACCATCAATGGCCGC
AACCAAACGCAACAGCTCGGCAAACTACAGATATCGCCATCGTAGGTTGCCCCGCGGTAGGCGTTAACATTCTG
GCCGAGTAAGTTGACTTCACGTACGCCTTGAGCGGCTAACTGGGCGATTTCAAAAAGAATGTCATCGCTTGACG
GCTGACTTCCCTCGCCTCGGGTGTAGGGTACGACACAGAATGTACAATATTTATTGCAGCCTTCCATGATCGAAAC
AAACGCAGTTGGGCCTTCAGCCCGTGGTTCTGGCAAACGGTCAAATTTTTCAATTTCCGGGAAAACCTGATATCCAC
GACAGGGCTATTCGTTCCCTGCACGTGGTTAATCATTTCCGGTAAACGATGCAGCGTTTGTGGCCCGAAGATGAC
ATCGACACAGGGGGCGCGCTGGCGCAATTGTTACCTTCTGTGACGCCACGCAACCACCGACCCCAATAATCAA
CTGCGGGTTTTTCTCTTTCAATAATTTCCATTGCCCTAGCAGGCTGAATACTTTTTCTGTGCTTTTTCCCGGAT

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AGAACAGGTATTTAGCAGCAGTAAATCCGCTTCTTCCGGGATGGTGGTTAACTGGTAGCCATGGGTACTGGCCAA
GAGATCTGCCATTTTAGATGAATCGTATTCATTCATCTGGCAACCCAGGTTTTGATATGCAGTTTTTTAGTCAT

319. *Salmonella enterica subspecies paratyphi A*

(SEQ ID NO. 319)

TTAAGGCTGGTAGAATCCTACGCCCAGCTCATTTTCTTTACGGGTACGGGCAATGACGGACTCCGGCGTTTCGGC
GACGCGCAGCCCCATTTTCATCTTCGGTACGCACCACTTTTCCGCGCAGGGAGTTTCGGATAGACGTCAGTAATTTTC
CACATCGACAAACTTACCAATCATCTCCGGCGTGCCTTCAAAGTTCACCACCCGATTGTTTTTCGGTACGGCCAGA
CAGTTCCATAATGTTTTTACGTGACGTGCCTTCCACCAGAATGCGCTGTGTCTGTGCCGAGCATACGGCGGCTCCA
TGCCATCGCCTGCTGATTGATACGCTCTTGCAGAATATACAGACGCTGCTTTTTCTCTTCTTCCGGTACGTCATC
AACCATATCGGCAGCCGGCGTTCCCGGACGCGCAGAGAAGATAAAGCTGTAGCTCATATCAAAGTTGACGTCAGC
GATAAGCTTCATGGTTTTTTTCGAAATCATCGGTAGTTTCGCCAGGGAATCCGACGATAAAGTCAGAGCTTATCTG
AATGTCCGGCCGCGCCGCGCAGTTTACGGATGATTGCTTTATATTCCAGCGCAGTGTGGGTGCGCCCCATCAG
ATTCAACACGCGATCGGAACCGCTCTGTACCGGCAGATGCAGGAACTGACCAGCTCCGGCGTATCGCGGTACAC
CTCGATAATATCGTCGGTGAACCTCAATCGGATGGCTGGTGGTAAAGCGAATACGGTCAATGCCGTCGATGGCGGC
AACCAGACGCAGCAGATCGGCAAAGGTGCCAGTGGTGCCGTCGTAGTTTTCTCCGCGCCAGGCGTTAACGTTCTG
GCCCCACAGGTTGACCTCACGCACGCCCTGCGCCGCTAACTGGGCGATTTTGAACAGGATATCGTCTGAGGGACG
GCTGACTTCTTACCGCGGGTATACGGCACACGCAGTAAGTACAATATTTATTGCAGCCTTCCATGATAGAAAC
GAAAGCGGTTCGGGCCTTCTGCGCGCGGTTCCGGCAAACGGTTCGAACCTTCTCGATTTCCGGGAAGCTGATATCGAC
CACCGGGCTGCGGTGCGCCACGCACGGAGTTAATCATCTCCGGCAGGCGGTGTGAGGTTTTCGCGACCAAAAAATAAT
GTCGACGTAATGGGCGCGTTGACGAATGTGCTCGCCTTCTTGGGAAGCCACGCAGCCGCCGACGCCGATAATCAG
ATCGGGATTTTTCTCTTTTAAACAGTCTCCAGCGACCTAATTGATGGAAGACTTTTTCTGAGCCTTCTCGCGGAT
TGAGCAGGTATTCAACAGCAGCACATCCGCCTCTTCCGCCACGTGCGTCAGTTGATAGCCGTGGGTGGCGTCCAG
CAGATCGGCCATCTTCGATGAATCGTACTCGTTCATCTGACAGCCCCAGGTTTTAATATGGAGTTTTTTAGTCAT
CGACTTGCTCTTGCGAAATAGTGGCTGAAAAGCAGGGCGCAT

320. *Salmonella typhimurium* (SEQ ID NO. 320)

TTAAGGCTGGTAGAATCCTACGCCCAGCTCATTTTCTTTACGGGTACGGGCAATGACGGACTCCGGCGTTTCGGC
GACGCGCAGCCCCATTTTCATCTTCGGTACGCACCACTTTTCCGCGCAGGGAGTTTCGGATAGACGTCAGTAATTTTC
CACATCGACAAACTTACCAATCATCTCCGGCGTGCCTTCAAAGTTCACCACCCGATTGTTTTTCGGTACGGCCAGA
CAGTTCCATAATGTTTTTACGCGACGTGCCTTCCACCAGAATGCGCTGTGTCTGTGCCGAGCATACGGCGGCTCCA
TGCCATCGCCTGCTGATTGATACGCTCTTGCAGAATATACAGACGCTGCTTCTTCTTCTTCCGGCACGTCATC
AACCATATCGGCAGCCGGCGTTCCCGGACGCGCAGAGAAGATAAAGCTGTAGCTCATATCAAAGTTGACGTCAGC
GATAAGCTTCATGGTTTTTTTCGAAATCATCGGTAGTTTCGCCAGGGAATCCGACGATAAAGTCAGAGCTTATCTG
AATGTCCGGCCGCGCCGCGCAGTTTACGGATGATTGCTTTATATTCCAGCGCAGTGTGGGTGCGCCCCATCAG
ATTCAACACGCGATCGGAACCGCTCTGTACCGGCAGATGCAGGAACTGACCAGTTCCGGCGTATCGCGGTATAC
CTCGATAATATCGTCGGTGAACCTCAATCGGATGGCTGGTGGTAAAGCGAATACGGTCAATGCCGTCGATGGCGGC
AACCAGACGCAGCAGATCGGCAAAGGTACCGGTGGTGCCGTCGTAGTTTTCTCCGCGCCAGGCGTTAACGTTCTG
GCCCAGCAGGTTGACCTCACGCACGCCCTGCGCCGCTAACTGGGCGATTTTGAACAGGATATCGTCTGAGGGACG
GCTGACTTCTTACCGCGGGTATACGGTACCACACAGTAAGTACAATATTTATTGCAGCCTTCCATGATAGAAAC

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GAAAGCGGTCGGGCCTTCTGCGCGGGTCCGGCAAACGGTCGAACTTCTCGATTTCCGGGAAGCTGATATCGAC
CACCGGGCTGCGGTGCGCCACGCACGGAGTTAATCATCTCCGGTAGGCGGTGTAAGGTTTGCGGGCCAAAAATAAT
GTCGACGTAATGGGCGCGTTGACGAATGTGCTCGCCTTCCTGGGAAGCCACGCAGCCGCCGACCCGATAATCAG
ATCGGGATTTTTCTCTTTTAACAGTCTCCAGCGACCTAATTGATGGAAGACTTTTTCTGAGCCTTCTCGCGGAT
TGAGCAGGTATTCAACAGCAGCACATCCGCCTCTTCCGCCACGTCGGTCAGTTGATAGCCGTGGGTGGCGTCCAG
CAGATCGGCCATCTTCGATGAATCGTACTCGTTCATCTGACAGCCCCAGGTTTTAATATGGAGTTTTTTAGTCAT

321. *Shigella flexneri* (SEQ ID NO. 321)

TTACGGCTGATAATAACCCACGCCAAGGTCGTTTTCTTTGCGGGTGCGGGCAATCACCGACTCCGGTGTTTCTGC
CATGCGCAGACCCATTTTCATCTTCAGTTCGCACCACCTTACC CGCGCAGAGAGTTGCGGTAGACGTCGGTAATTTCT
TACATCGACGAATTTACCGATCATATCCGGTG TGCCCTCGAAGTTGACCACGCGGTTATTTTCGGTACGCCCCGA
AAGCTCCATGATGCTCTTACGCGAAGTCCCTTCTACCAGAATACGCTGGGTGGTGCCGAGCATCCGACGGCTCCA
TGCCATCGCTTGCTGATTGATACGTTCTTG CAGAATATACAGACGCTGCTTCTTCTTCTTCCGGAACATCATC
AACCATATCGGCGGCAGGCGTTCTTGACGTGCAGAGAAGATAAAGCTGTAGCTCATGTGAAATTGACGTCGGC
AATCAGCTTCATCGTTTTCTCGAAGTCTTCGGTGGTTTCGCCAGGGAAGCCAACAATGAAGTCAGAACTGATCTG
AATATCCGGACGCGCCGCACGCAGTTTACGGATGATCGCTTTGTACTCCAGCGCCGTATGGGTACGTCCCATCAG
GTT CAGAATGCGATCGGAACCGCTCTGTACCGGCAGATGCAGGAAGCTCACCAGCTCAGGCGTGTCGCGGTACAC
TTCGATGATATCGTCGGTGAATTTCGATCGGATGGCTGGTGGTAAAGCGAATACGATCGATCCCGTCGATCGCAGC
AACCAGACGCAACAGATCGGCAAACGATCCGGTGGTGCCGTCGTAGTTCTCACCACGCCAGGCATTACATTTCTG
ACCGAGCAGGTTGACTTCACGCACGCCCTGAGCCGCAAGCTGGGCAATCTCAAACAGAATATCGTCAGACGGACG
GCTTACCTCTTACCACGGGTGTAAGGCACCACGCAGTAGGTGCAATATTTATTGCAGCCTTCCATGATGGAGAC
AAACGCGGTTCGGCCCTTCGGCGCGCGGTTCCGGCAGACGGTCAAACCTTCTCGATTTCCGGGAAGCTGATATCTAC
AACCGGGCTGCGGTGCGCGCGCACGGAGTTGATCATCTCCGGCAGACGGTGCAGCGTTTGCGGGCCAAAAATAAT
ATCGACATAGTGGGCGCGCTGGCGAATGTGCTCGCCTTCTTGCGATGCCACGCAGCCACCGACGCCGATAATCAG
GTCTGGATTCTTCTCTTTTAACAGTTTCCAGCGACCCAACCTGATGGAAGACTTTTTCTGAGCCTTCTCGCGGAT
TGAGCAGGTGTT CAGCAGTAGCACATCCGCTTCTTCCGCCACGTCGGTCAGTTGATAGCCGTGGGTGGCATCCAG
CAGATCGGCCATCTTCGATGAATCGTACTCGTTCATCTGACAGCCCCAGGTTTTAATATGGAGTTTTTTGGTCAT

322. *Pseudomonas syringae* (SEQ ID NO. 322)

TTACTGTAGCAGCGAGCCACGCAACGAGTGGGGCTGCGCATCATCAATGTGTACGTCGGCAAAC TGCCCGATCAG
GCGGGGATTGTGCGCAGCGAAAATTGACAATCCGGTTGTCTCGGTGCGACCTTG CAGTTCGCCGGGGTCTTTCTT
TGAGTAATCTGTAACCAGAATACGCTGGATGCTGCCAACCATCTGTGCGGTGATCTCGAAACCCTGTTGGTT CAG
GCGATGTTGCAACGCGGCCAGTCGCTCTTTTTT CAGCGCTTCCGGCGTGTCGTCTTTCAGGTCAGCGGCCGGTGT
GCCGGGGCGCGGGCTGTAAATGAACGAGAACGAGAAGTCGAAACCGGCGTCTTCGATCAGCTTCATGGTGTTGTC
GAAATCCTTTTTCGGTTTTACCGGGGAAGCCAACGATGAAGTCGGAACCTGATGCTGATACCGGCACTGCCGCCCCG
AAGCTTGCGTAGCCTGGACTTGTATTCCAGCGTGGTGTGGTTGCGTTTCATGGCCGCCAGAATGCGGTCCGAACC
TGACTGCACCGGCAAATGCAGGTGCTTGACCAGTTCCGGCAGCTCGGCGTGCGCTGAATCAGGCTGTGCGAAAA
CTCAGACGGGTGCGAGGTTGTGTAACGAATGCGGTGCGATGCCATCGACGACGGCAACTGCCCGAATCAGATCAGC
CAAGTCGGCGACTCGCCCGTCATGGGTGGTGCCGCGATAACCGTTGACGTTCTGCCCCAGCAGTGTGACTTCGCG
CACGCCGTGTTGCGCCAGGTGAGTGACCTCGGT CAGCACGTCATCGAACGGTCGGCTGACTTCTTCGCCGCGCGT

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GTAGGGCACCACGCAGAAGGTGCAGTACTTGCTGCAGCCTTCCATCACCGACACGTAAGCACTCGGGCCATCCAC
GCGCGGCTCGGGCAAGTGGTCAATTTTTTCGATCTCGGGGAATGAAACATCGACCTGCGGCAAGCGGGTGATGCG
CGCTGCGTCGATCATTTCCGGCAGGCGGTGCAATGTTTGCGGGCCGAACACCACGTCCACGTAGGGCGCGCGGT
GCGGATGGCCGCGCCTTCTGGCTGGCAACACAGCCGCCGACGGCAATCACCATCTCGGGGTGGCCAGTTTCAG
CTCACGCCAGCGCCGAGCTGCGAATAGACCCGGTCTTGCGCACGCTCGCGAATCGAGCAGGTGTTGAGCAGGAT
CACGTGCGCGTCTTCCGCGCGAGCGGTGACTTCCAGAGCCTGATGTTGCCCAGCAGATCGACCATGCGCGAGCT
GTCGTACTCGTTCATCTGGCAACCGTGGGTTTCGATGTAAAGCTTCTTGCCAT

323. *Burkholderia mallei* (SEQ ID NO. 323)

TCAGTGCGTGGCGGCGCTCGCGTCGCCGTGCGCGAGCACGAGCTCGCCGCGCAGCGAGTGCGGATACGCGTGATT
GATCTTCACGTGATCATCTGGCCGATCAGGCGCGGGTGCGCGGCGCTCGGCGCGGAAAATTCACGACCCGGTT
GTTCTCGGTGCGGCCGCGAGCTCGTTCGGATCCTTGCGCGACGGCCCCCTCGACGAGGATTCGCTCGACCTTGCC
GAGCATCGACTGGCTGATCCTCGCGACGTTCTCCTCGATCGTCGCCTGCAGATGTTGCAGGCGCTTGAGCTTGAG
CTCGCGCGGCGTGTCTGTCGGCGAGATTGCGGGCCGGCGTGCCGGGCGCGGGCTGTAGATGAACGAGAAGCTCGT
GTCGTAGCTCATCTCGTGAACGAGCGCCATCGTCTTGTCGAAGTCGGCGTCGGTCTCGCCGGGAAACCCACGAT
GATGTCCGTGGACAGCGACAGATTGCGGCGGATCGCGCGCAGCTTGGCGATCACCGATTTGTATTGAGCACGGT
GTAGCCGCGCTTCATCGCCATCAGGATGCGGTCCGAGCCGTGCTGGACGGGCAGGTGCAGATGGTTCGACGAGCTT
CGGCACCTTCGCGTAGACGTGAGCAGGCGCTGCGTGAACCTTTTCGGATGCGATGTCGTGTAGCGGATCCGCTC
GATGCCGGGGATGTGCGCGACATATTCGATCAGCGTCGCGAAATCGGCGATCTCGGCCGAGCCGGCCGCGATCGC
GCCGCGGTAGGCGTTCACGTTCTGGCCGAGCAGCGTGACTTCGCGCACGCCCTGGTTCGGCGAGGCCGCCACCTC
GGTCAAGACGTCGTGAGCGGGCGCGACACTTCATCGCCGCGCGTGTACGGCACGACGCAGTAGCTGCAGTACTT
CGAGCAGCCTTCCATGATCGACACGAACGCGCTCGGCCCTTCGACGCGAGCGGGCGGCAGATGGTTCGAACCTTCTC
GATTTTCGGGGAACGTGATGTGACCTGCGCGCGGCCGCTTTCGCGGCGCGCGTCGATCATCTGCGGCAGGCGGTG
CAGCGTTTTCGGGGCCGAACACGAGATCGACGTACGGCGCGCGCGACGATCGACGCGCCTTCTGGCTCGCCAC
GCAGCCGCCGACGCCGATCAGCAGGTCCGGCTTCGCTTCTTCAGCTCGCGCACGCGGCCGAGATCGGAGAACAC
CTTCTCCTGCGCCTTTTCTCGCACCGAGCAGGTGTTGAACAGGATGATGTCCGCGTCTTCGGGGTGTGGTTTT
CTCGAGGCCCTCGGCCGATTGAGCACGTGACCATCTTGTCGGAGTCGTACTCGTTCATCTGGCAGCCGAAGGT
TTTTACGTAACTTTCTTGGTTCAT

324. *Legionella pneumophila* (SEQ ID NO. 324)

TTAGGCTGGCTGCATCTCCTTTTCAAGCAGCCTTCTCGCAATGAATTAGGTAGTGCGTCACTAATTTGGACATC
TATAAATTGTCCAATTAAATGAGGTGGTCCATCAAAATTAACACGATTACATTACGTACGACCAGATAATTG
CTGTGAACTTTTCTTGAAAATCCGGTAACCAGAATTTTTTGCTTGCTGCCTATCATTGATTAAGTAAACGAGC
TGCAATTCATTAATAATCTGTTTTGTAAAATCTGTAAACGTTGCTTTTTGATCTCCATAGGCGTGTATCAGGTAA
ATTTGCTGCAGGAGTTCCTGGTCTTGGGCTGTATATAAAGCTGAAAGAGGTATCAAAACCGATTCATGCACAAG
ATCCATAGTGTCTTGAAATCTTTGTCTGTCTCTCCGGGAAAGCCTACAATAATGTCAGTAGATAAGCGAATGTC
TGGTCGAATTTTCTTAATTTACGAATTTTGGATTTAAATTCCAAAGCAGTGACCTCGTTTCATTAACGATAA
AATGCGATCGGATCCGCTTGTACCGGAAGGTGTAAATGATTGGCAAGCTCTGGAACCTCAGCGTAGGCATTAAT
CAAATTTTCAGAAAATGCCAAGGGATGTGATGTTGTGAAACGTATTCTTCTATTCCATCGATAGCGGCAATATA
ATGAATTAAACAGGGCAAGATCGGCTATATCCCCATTGTCCATAATACCTCTGTAATCGTTCACATTTTGGCCTAG

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TAAATTAATCTCTCTGACGCCCTTGACTGGCTAATTGATAACACTCAGCCAATACATCATCAAATGGTCTGCTGAT
TTCTTCGCCACGGGTGTAGGGACCACACAGAAGCTGCAATATTTACTACAGCCTTCCATTATAGATACAAAAGC
TG TAGGGCCTTCTGCTCTTGGTGCGGGTAAATGATCAAATTTCTCTATTTCTGGAAAGCTGATATCAACAACAGA
TTTATTTTTCTCAAGCCTTTCATTGAGCAGGGCAGGGAGCCTGTGTAATGTCTGTGGCCCAAATACGATATCAAC
AAACGGTGCTCTTTTTATGATGTCTGAGCCTTCCTGGCTCGCTACGCATCCTCCCACTCCAATGAGCACATGAGG
GTTTTTGGCTTTATATTCTCGCCATTGACCCAGTTGAGAAAAAACTTTTTCTGTGCTTTTTCTCGAATTGAGCA
TGTGTTTAATAAAAATAACATCGGCATCCTCGACTTGATCAGTTTTGACCAAACCATGGGAAGCGTAAAGTACTTC
TGCCATTTTAGAAGAATCGTATTCATTCATTTGGCAGCCATTTGTTTTAATATATAATTTTTTAACCAT

325. *Bordetella bronchiseptica* (SEQ ID NO. 325)

TCATTCGGCTCCGGATGTGTGCGTTTCGATGCCGGCGACACGGCCGCGCAGCGAGTTGGTGTGGGCGTGGGTGAC
GACGACGTCGACCATGTGGCCGATCAGGCGCGGCACGCCGGGAAAGTTGACGATACGGTTGTTCTCGGTACGGCC
CATCAGCTCGTTGGGGTCGCGCCGCGAAGGGCCTTCGACCAGCAGCGCTGGCGGGTGCCGATCATGCCCTGGGC
GATGGCCGCGGCCTGCTGGTTGATGAGCGCCTGCAACTGCTGCAGGCGGCGCAGCTTGACGTCCTGCGGCGTGTC
ATCGTGAGGTTCGGCGGCCGGCGTGCCGGGCCGGCGCGAATACACGAACGAGAACGAGGTGTGGAAGCCGACGTC
CTCGATCAGCTTCATGGTCTTCTGGAAGTCCTCCTCGGTCTCGCCCGGGAACCGACGATGAAGTCCGAGGACAG
CGTCAGGCTGGGGCGCGCAGCGCGCAGGCGGCGCACCACGGAAGTGAAGTCCAGCGCGGTGTAGCCGCGCTTCAT
GGCCGCCAGCACCCGGTCGCTGCCGGCCTGCACCGGCAGGTGCAGGAACGACACCAGCTTGGGCAGCCGTGCGTA
GGCGTCGACCATGCGCTGGGTCAATTCCTTCGGATGCGAGGTGCTGTAGCGGATCCGTTGATACCGGGAATCTC
GTGCACGTATTCAGCAGCATGGCGAAATCGGCGATTTGCGCGCTGTGCGCCATGGCGCCGCGGTAGGCGTTGAC
GTTCTGGCCCAGCAGCGTGACTTCCTTGACGCCCTGGTGGCCAGGTGCGCGACCTCGAGCAGGACGTCGTCGAA
GGGCCGCGACACTTCTTCGCCGCGCGTGTAGGGACCACGCGAGAAGCTGCAATACTTGCTGCAGCCTTCCATGAT
GGACACGAACGCGGTGGCGCCGTGACGCGCGGCGGGGCGAGGGCGTGAAGTCTCGATCTCGGGAAAAGCTGAT
GTCGACCTGCGACACGCCCTGGGCGCGGCGGCGCTTGATCAGGTGCGGCAGCCGGTGCAGGGTCTGCGGGCCGAA
CACCACGTCGACATAGGGCGCGCGCTTGACGATGGCCTCGCCCTCCTGGCTGGCCACGCAGCCGCCACGCCGAT
CACCAGGTGGGGTTCTGCTTCTTGAGGTGCTGTACCCGGCCCAGGTGCGAGAACACCTTCTCCTGCGCCTTCTC
GCGCACGGAACAGGTGTTGAACAGGATGACATCGGCATCCTCGGGGTTGTGGTCAGCTCCAGGCCCTGGTCGGC
GCGCAGCACGTCGGCCATCTTGTCCGAGTCGTAATCGTTTCATCTGGCAGCCGAAGGTGCGGATATACAATTTGCC
CAGGCCCTGGGCGGTGGTGGCCGGCGTGCCGGCATCGGACGGGCTGGCGCCGTGCGGTTTGACAGTGGTTTCTTG
CAT

Figure 14 represents marker I (purA) sequences amplified from different Gram-positive bacteria (SEQ ID NOs 326-359)

326 *Enterococcus faecalis* (SEQ ID NO. 326)

CTATTTGAAGGGCGCAAGGTGTCATGTTGGATATCGATCAAGGAACCTATCCATTTGTTACTTCCTCTAATCCAG
TAGCTGGTGGCGTAACATATCGGTAGTGGCGTTGGTCCATCAAAAATTAATAAAGTGGTTGGTGTCTGCAAAGCGT
ACACTTCACGTGTCGGTGACGGCCCATTCCCAACAGAATTATTTGATGAAACAGGAGAAACCATTCGTCGTGTCTG
GTAAAGAATACGGAACAACAACAGGACGTCCGCGTCGTGTCTGGTTGGTTGATTTCAGTAGTCATGCGTCATTCAA
AACGTGTATCAGGGATTACAACTTGTCTTAACTCGATTGACGTGTTAAGTGGTTTAGAAACGGTGAAAATTT
GTACAGCTTATGAACTTGATGGTGAATTAATTTATCATTATCCAGCAAGCTTGAAAGAATTAAGCCGCTGTAAAC
CAGTTTATGAAGAATTACCAGGTTGGTCTGAAGATATCACTGGTTGCAAACTTTAGCCGATTTACCAGCTAATG
CTCGTAACTATGTGCATCGGATTTTCAAGATTAGTTGGTGTGCGCATTTCAACATTCTCAGTAGGGCCAGACC

327 *Enterococcus gallinarum* (SEQ ID NO. 327)

CTCTTCGAGGTGCGCAAGGAGTTATGCTAGATATTGATCAAGGAACATATCCGTTTCGTAACATCCTCAAATCCAG
TAGCTGGTGGAGTAACCATTGGTAGTGGAGTGGGTCCTTCTAAAATCAATAAAGTAGTTGGTGTGTGTAAAGCAT
ATACTTCAAGAGTTGGTGACGGCCCATTCCCAACAGAACTTTTTGATGAAACAGGCAATCAAATTCGTGAAGTTG
GCCGTGAATATGGTACGACAACCTGGTCTCCACGTCGTGTTGGTTGGTTGACTCTGTTGTCATGCGTCATTCAA
AACGTGTTTCTGGTATCACGAATCTGTCTTTAAATTCAATTGATGTTTTGAGCGGCTTGGAACGTGAAAAATTT
GTACTGCTTATGAATTAGATGGAGAATTGATTTATCATTATCCTGCAAGTCTAAAAGAATTGAATCGTTGTAAAC
CAGTCTATGAAGAGTTACCAGGCTGGTCAGAAGATATTACTGGATGCAAAACATTAGCTGATCTTCTGAAAATG
CACGTAACATATGTACATCGTATCTCTGAATTAGTTGGGGTTCGTATCTCAACATTCTCAGTAGGTCCTGACC

328 *Enterococcus flavescens* (SEQ ID NO. 328)

CTTTTTGAAGGTGCTCAAGGCGTGATGCTGGATATCGACCAAGGAACCTATCCTTTTCGTGACATCATCCAACCCC
GTTGCTGGGGGAGTCACTATTGGTAGTGGTGTGGGTCCTTCAAAAATCAACAAAGTCGTTGGTGTCTGCAAAGCT
TACACCTCTCGGGTAGGAGATGGTCCTTTCCCAACGGAAGTGTGTTGATGAAACAGGTGAACAAATCCGTAAGATC
GGTCGTGAATACGGAACAACGACAGGACGTCCTCGCCGTGTGGGCTGGTTTGATACCGTCGTGATGCGCCATTCA
AAACGTGTTTCAGGGATTACAAACCTATCCCTTAACTCGATCGATGTCTTGAGCGGCTTAGAAACCGTGAAGATC
TGTACGGCTTATGAACTAGACGGCGAATTGATCTATCATTACCCAGCAAGCTTGAAAGAGTTGAACCGCTGCAAA
CCAGTCTACGAAGAACTTCCTGGCTGGTCTGAAGACATTACTGGCTGCAAAACATTAGCAGATCTGCCAGAAAAT
GCACGCAATTACGTTACCCGCATCTCTGAATTAGTCGGTGTCCGCATTTTCGACCTTCTCAGTAGGGCCNGACC

329 *Streptococcus agalactiae* (SEQ ID NO. 329)

CTCTTTGAAGGGCGCAAGGAGTTATGCTCGACATTGATCAAGGAACATACCCATTTGTAACATCTTCCAATCCAG
TAGCAGGTGGTGTCACAATTGGTTCGGGAGTTGGACCAAGTAAATTAATAAAGTAGTAGGTGTATGTAAAGCTT
ACACTAGCCGTGTTGGTGTGATGGACCATTCCTCAACAGAAGTGTGTTGATGAGGTTGGTGACCGTATTCGTGAGATTG
GTAAAGAGTATGGTACAACGACCGGTCGTCTCGTCGCGTTGGATGGTTTGATTCTGTTGTTATGCGTCACAGCC
GTCGAGTATCAGGTATTACTAACCTCTCTCTGAATTCAATTGATGTTCTTTTCAGGGCTTGATACGGTGAAAATTT
GTGTGGCTTATGACCTTGATGGGAAACGTATTGACTATTACCCAGCAAGCCTTGAACAGCTAAAACGTTGTAAAC

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CAATCTATGAAGAATTACCGGGCTGGTCTGAAGATATTACAGCTTGTCGTAGCTTAGATGATCTTCCAGAAAATG
CACGTAATTACGTTCCCGTGTTGGCGAATTGGTTGGTGTTCGTATTTCTACTTTNCTCAGTAGGNCCAGGTC

330 *Streptococcus sanguis* (SEQ ID NO. 330)

CTTTTTGAAGGGGCTCAAGGAGTTATGCTCGACATTGATCAAGGAACATACCCATTTGTAACATCTTCCAATCCA
GTAGCAGGTGGTGTCAACAATTGGTTCCGGGAGTTGGACCAAGTAAAATTAATAAAGTAGTAGGTGTATGTAAAGCT
TACACTAGCCGTGTTGGTGATGGACCATTCCCAACAGAACTTTTTGATGAGGTTGGTGACCGTATTCGTGAGATT
GGTAAAGAGTATGGTACAACGACCGGTCTCTCGTCGCGTTGGATGGTTTGATTCTGTTGTTATGCGTCACAGC
CGTCGAGTATCAGGTATTACTAACCTCTCTCTGAATTCAATTGATGTTCTTTCAGGGCTTGATACGGTGAAAATT
TGTGTGGCTTATGACCTTGATGGGAAACGTATTGACTATTACCCAGCAAGCCTTGAACAGCTAAAACGTTGTAAA
CCAATCTATGAAGAATTACCGGGCTGGTCTGAAGATATTACAGCTTGTCGTAGCTTAGATGATCTTCCAGAAAAT
GCACGTAATTACGTTCCCGTGTTGGCGAATTGGTTGGTGTTCGTATTTCTACTTTCTCAGTTGGGTCCAGACC

331 *Enterococcus faecium* (SEQ ID NO. 331)

TTCTTCGAAGGGGCGCAAGGGGTTATGCTGGATATTGACCAAGGGACTTATCCATTTGTAACCTCTTCTAATCCA
GTTGCAGGGGAGTCACCATCGGTTCCGGTGTTGGTCCGAGCAAAATTGACAAGGTAGTTGGTGTCTGCAAGGCCT
ACACCAGTCGGGTCGGAGATGGACCATTCCCAACAGAGCTTTTTGATGAAGTTGGTGACCGCATTCGTGATATCG
GCCACGAATATGGCACTACCACTGGTCGCCCCACGTCGGGTAGGTTGGTTTGAATCGGTTGTTATGCGCCATAGCC
GCCGTGTATCAGGGATTACCAATCTTTCGCTTAACTCCATCGATGTCTTGAGTGGTCTGGATACAGTGAAAATCT
GTGTAGCTTATGACTTGGATGGCCAAAGAATCGACCACTACCCAGCTAGTCTGGAACAGCTCAAGCGCTGCAAGC
CGATTTACGAAGAGCTGCCAGGCTGGTCAGAGGACATCACTGGAGTCCGCAGTCTGGAAGACTTGCCAGAAAATG
CCCCTAACTATGTTCCCGGAGTGAGTGAGCTGGTTGGCGTTTCGCATTTCTACCTTCTCAGTAGGGCCAGACC

332 *Enterococcus durans* (SEQ ID NO. 332)

CTCTTTGAAGGGGCACAAGGTGTGATGTTGGATATCGATCAAGGAACGTATCCATTTGTGACTTCTTCTAATCCG
GTAGCTGGTGGTGTAAACGATCGGTAGTGGCGTTGGCCCTTCAAAGATCAATAAAGTCGTTGGTGTATGTAAAGCT
TATACTTCTCGTGTAGGAGATGGCCCATTCCCAACAGAACTATTTGACGAAACAGGTCAACAAATCCGTGAAGTC
GGTCGTGAATATGGTACGACAACAGGTGACCTCGTCGTGTCGGTTGGTTTGATACAGTCGTGGTGCGCCATTCA
AAACGTGTATCAGGAATCACTAACCTATCATTGAATTCAATCGATGTATTAAGCGGACTAGAAACAGTAAAAATC
TGTACAGCGTATGAATTAGATGGAGAATTGATCTATCATTACCCAGCAAGCCTGAAAGAATTGAAACGTTGCAAA
CCAGTATACGAAGAACTTCCTGGTTGGTCTGAAGATATTACAGCATGTAAAACACTTGCTGAACTACCAGAAAAC
GCCCGTAACTATGTTAGACGTATCTCAGAGCCTGTAGGAGTCCGTATTTCAACATTCTCAGTAGGTCCAGACC

333 *Streptococcus pyogenes* (SEQ ID NO. 333)

CTATTTGAAGGGGCGCAAGGGGTTATGCTTGATATTGACCAGGAACGTACCCATTTGTAACGTCTTCAAACCCAG
TTGCTGGTGGTGTAAACATTGGTTCTGGTGTGGCCCAAATAAAATCAACAAAGTAGTTGGTGTCTGTAAAGCCT
ACACAAGCCGTGTCGGTGATGGGCCATTCCCTACAGAACTCTTTGATGAAGTGGGTGAGCGCATTCGTGAAGTGG
GTCATGAGTACGGGACAACGACCGGCCGTCCACGTCGTGTCGGTTGGTTTGATTGGTTGTCATGCGCCACAGTC
GTCGTGTATCAGGTATTACTAACCTCTCTCTGAATTCAATTGATGTTCTTTCAGGGCTTGATACGGTTAAGATTT
GTGTGGCTTATGACCTTGATGGGAAACGTATTGACTATTACCCAGCAAAACCTTGAACAACCTCAAACGTTGCAAAAC

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CAATCTATGAAGAATTACCAGGCTGGCAAGAGGACATCACAGGTGTTCTGTAGCCTTGATGAGCTTCCTGAAAATG
CCCGCAACTACGTTCTGTCTGTGGAGAATTGGTTGGCGTTCGCATTTCAACCTTCTCAGTTGGGCCAGACC

334 *Streptococcus pneumoniae* (SEQ ID NO. 334)

CTATTTGAAGGGGCTCAAGGTGTTATGCTAGATATCGACCAAGGTACTTATCCATTTGTTACGTCATCAAACCCCT
GTAGCTGGTGGTGTGACAATTGGTTCTGGTGTCCGTCCAAGCAAGATTGACAAGGTTGTAGGTGTATGTAAAGCT
TATACGAGTCGTGTAGGAGATGGTCCTTTCCCAACTGAGTTGTTTGATGAAGTGGGAGAACGTATCCGTGAAGTG
GGTCATGAATATGGTACAACAACCTGGTCGTCCACGTCGTGTAGGTTGGTTTGACTCAGTTGTGATGCGTCATAGC
CGTCGTGTTTCTGGTATTACTAACCTTTCTTTGAACTCTATTGATGTTTTGAGCGGTTTGGATACTGTGAAAATC
TGTGTGGCCTATGATCTTGACGGTCAACGTATTGACTACTATCCAGCTAGTCTTGAGCAATTGAAACGTTGCAAG
CCTATCTATGAAGAGTTGCCAGGTTGGTCAGAAGATATTACCGGAGTTGCAATTTGGAAGATCTTCCTGAGAAT
GCGCGTAACTATGTTTCGTCTGTGAGTGAATTGGTTGGCGTTCGTATTTCTACTTTTCTCAGTAGGTCCAGGCC

335 *Streptococcus oralis* (SEQ ID NO. 335)

CTTTTCGAAGGTGCGCAAGGTGTCATGTTGGACATTGATCAAGGGACTTATCCATTTGTTACTTCTTCAAACCCCT
GTCGCTGGTGGTGTGACGATTGGGTCTGGTGTGGTCCAAGTAAGATTGACAAGGTTGTAGGTGTCTGTAAAGCC
TACACAAGTCGTGTAGGAGATGGACCGTTCCCAACTGAATTATTTGATGAAGTGGGAGATCGCATCCGTGAAGTA
GGTCATGAATATGGTACAACAACCTGGTCGTCCACGTCGTGTGGGTTGGTTTGACTCAGTTGTGATGCGTCACAGC
CGCCGTGTATCTGGGATTACCAATCTTTCATTGAACTCTATAGATGTTTTGAGTGGTTTGGATACTGTGAAAATC
TGTGTGCGCTATGATCTTGATGGTCAACGTATTGATTACTATCCTGCTAGTCTTGAGCAGTTGAAACGTTGTAAG
CCAATCTACGAGGAATTGCCAGGTTGGTCAGAAGACATCACTGGAGTCCGTAATTTGGAAGACCTTCCTGAGAAT
GCACGCAACTATGTTTCGTCTGTAAAGCGAGTTGGTTGGTGTTCGTATCTCAACTTTCTCAGTTGGGCCAGATC

336 *Staphylococcus hominis* (SEQ ID NO. 336)

CTCTTTGAAGGAGCGCAAGGAGTTATGTTAGATATCGACCATGGTACATATCCTTTTGTAACGTCAAGTAATCCT
GTGGCAGGTAATGTGACAGTAGGAAGTGGCGTGGGTCCAACCTTCGTATCTAAAGTGATTGGGGTATGTAAATCC
TATACATCTCGTGTAGGTGACGGCCCATTCCCTACTGAATTATTCGACGAAGATGGTCATCATATTAGAGAAGTA
GGTCGTGAATATGGAACGACAACAGGACGTCTCTCGTGTAGGTTGGTTCGACTCAGTTGTATTACGTCACTCT
CGTCGTGTAAGTGGTATTACAGACTTATCTATTAACCTCAATTGACGTTTTAACAGGTTTAGATACGGTTAAATTT
TGTACAGCTTATGAGTTAGATGGTGAAACAATCACAGAATATCCAGCAAACCTTAGACCAATTACGTCGTTGTAAA
CCAATTTTCGAAGAGTTACCTGGTTGGACGGAAGACATTACAGGTTGTCGTACATTAGAAGAATTACCTGAAAAC
GCACGTAAATACTTAGAACGTATTTCTGAATTATGTGGCGTTCATATTTCAATCTTCTCAGTAGGTCCAGGCC

337 *Bacillus anthracis* (SEQ ID NO. 337)

CTATTTGAAGGTGCTCAAGGTGTTATGCTTGATATCGACCACGGTACGTACCCGTTGTTACATCTTCTAACCCA
ATTGCTGGTGGTGTAAACAGTTGGAACCTGGAGTTGGTCCTGCGAAAGTTACTCGCGTTGTAGGTGTATGTAAAGCA
TATACAAGCCGCGTTGGTGATGGTCCATTCCCTACTGAGCTTCATGACGAAATTGGTCATCAAATTCGTGAAGTT
GGTCGTGAGTATGGAACGACAACCTGGTCGTCCACGCCGCGTAGGTTGGTTCGATAGCGTTGTTGTAAGACATGCA
CGTCGTGTTAGTGGTTTAAACAGATTTATCATTAACCTCTATCGACGTTCTAACTGGTATTCCAACACTTAAATTT
TGTGTTGCTTACAAATGCGATGGGAAAGTTATCGATGAAGTTCAGCAAACCTTAAACATTTTAGCGAAATGTGAG

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CCTGTATACGAAGAGCTTCCAGGTTGGACAGAAGATATTACTGGTGTAAAGATCATTAGATGAGCTTCCTGAAAAT
GCTCGAAAATACGTAGAACGTGTTTCTGAGTTAACAGGAGTTCAATTATCTATGTTCTCAGTAGGGCCAGACC

338 *Bacillus cereus* (SEQ ID NO. 338)

GACNCGGTACGTACCCGTTTCGTTACATCTTCTAACCCAATTGCTGGTGGTGTAAACAGTTGGAAGTGGAGTTGGTC
CTGCGAAAGTTACTCGCGTTGTAGGTGTATGTAAAGCATATACAAGCCGCGTTGGTGATGGTCCATTCCCTACTG
AGCTTCATGATGAAATTGGTCATCAAATTCGTGAAGTTGGTCGCGAGTATGGAACGACAAGTGGTCGTCCACGCC
GCGTAGGTTGGTTTCGATAGCGTTGTTGTAAGACATGCACGTCGTGTTAGTGGTTTAACGGATCTATCATTTAAATT
CTATCGACGTTTTAACAGGTATTCCAACCTTAAATTTGTGTAGCTTACAAATACAATGGCGAAGTTATTGATG
AAGTTCCAGCTAACTTAAACATTTTAGCGAAATGTGAGCCTGTATATGAAGAGCTTCCAGGTTGGGAAGAAGATA
TTACTGGTGTAAATCATTAGATGAACTTCCTGAAAATGCACGAAAATACGTAGAACGTGTTTCTGAGTTAACAG
GAATTCAAATATCTATGTTCTCAGTAGGTCCCCACCA

339 *Bacillus megatherium* (SEQ ID NO. 339)

CTATTCGAAGGGGCACAAGGTGTTATGTTAGATATCGATCAAGGAACATATCCATTTGTTACATCTTCAAACCCA
GTAGCGGGTGGAGTAACAATTGGTTCTGGGGTAGGTCCATCTAAAATCAAACACGTTGTAGGTGTATCAAAGCG
TATACAACCTCGTGTTGGTGACGGCCCTTTCCCAACTGAATTAACAAACGAAATCGGTGATCAAATCCGTGAAGTA
GGACGTGAATATGGTACAACAACCTGGTCGTCTCGCCGTGTAGGTTGGTTCGACAGTGTAGTTGTACGTCATGCT
CGTCGCGTTAGTGGAATCACAGATCTATCTTTAACTCAATTGATGTATTAACGGGAATTGAGACATTAAAGATT
TGCGTAGCTTATCGTTATAAAGGGGAAGTTATGGAAGAATTCCTGCTAGCTTAAAAACACTTGCAGAGTGCGAA
CCTGTATATGAAGAGCTTCCAGGTTGGACAGAAGATATTACGGGTGTGAAAACATTAGATGAGTTACCTGATAAC
GCTCGCCACTACTTAGAGCGCGTGTCTCAATTAACAGGTATTCTTTTATCTATTTTCTCAGTAGGTCCAGGCC

340 *Enterococcus casseliflavus* (SEQ ID NO. 340)

TATTCGAAGGNAGCTCAAGGCGTGATGCTGGATATCGACCAAGGAACCTATCCTTTTCGTGACATCATCCAACCCC
GTTGCTGGAGGTGTACCATCGGTAGTGGTGTGGGTCTTCAAAAATCAACAAAGTCGTTGGTGTCTGCAAAGCT
TACACCTCTCGGGTAGGAGATGGTCCTTTCCCAACGGAAGTGTGATGAAACAGGTGAACAAATTCGTAAGATC
GGTCGTGAATACGGAACAACGACAGGACGTCTCGCCGTGTGGGCTGGTTTGATACCGTCGTGATGCGCCATTCA
AAACGGGTCTCAGGGATCACGAATCTATCCCTTAACTCGATCGATGCTTTGAGCGGCTTAGAAACCGTGAAGATC
TGTACGGCTTATGAACTAGACGGCGAATTGATCTATCATTACCCAGCAAGCTTGAAAGAGTTGAACCGCTGCAAA
CCAGTCTACGAAGAACTTCCTGGCTGGTCTGAAGACATTACTGGCTGCAAAACATTAGCAGATCTGCCAGAAAAT
GCACGCAATTACGTTACCGCATCTCTGAATTAGTCGGTGTCCGCATTTTCGACCTTCTCAGTAGGTCCAGACC

341 *Enterococcus raffinosus* (SEQ ID NO. 341)

CTATTTGAAGGTGCTCAAGGCGTTATGCTGGATATTGATCAAGGAACCTATCCATTTGTTACTTCTTCGAACCCA
GTTGCCGGTGGGGTAACTATCGGTAGTGGTGTAGGACCTGCTAAAATCGACAAAGTTGTCGGTGTGTTGTAAAGCC
TATACTTCACGCGTAGGTGATGGACCTTTCCCAACTGAATTGTTTGATGAAGTTGGAGATCAGATTTCGTGAAGTC
GGTCGTGAATATGGAACGACTACTGGTCGTCCACGTCGTGTGGGCTGGTTTGACTCGGTTGTGATGCGTCATTCA
AAACGTGTTTCTGGGATTACGAATCTTTCTTTAACTCGATTGATGTCTTGAGCGGTCTGGATACAGTGAAAATT
TGTACAGCGTATGAGCTGGACGGAGAATAATTTACCATTATCCAGCAAGCCTAAAAGAATTAAATCGTTGTAAG

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CCCGTTTATGAAGAACTACCTGGTTGGAGCGAAGATATTACAGGCTGCCGTGATTTAGCTGATCTACCGGAAAAT
GCGCGTAATTATGTACGTCGCGTTTCTGAACTTGTGGGTGTGCGTATCTCGACCTTCTCAGTTGGTCCTGGTC

342 *Staphylococcus aureus* (SEQ ID NO. 342)

CTATTTGAAGGGGCACAAGGTGTAATGTTAGATATCGACCATGGTACATATCCATTTCGTTACATCAAGTAATCCA
ATTGCAGGTAACGTTACTGTTGGTACAGGTGTAGGTCCTACATTTCGTTTCAAAGGTAATTGGTGTATGTAAAGCT
TATACATCACGTGTTGGTGATGGTCCATTCCCTACTGAATTATTCGATGAAGATGGACATCATATTAGAGAAGTT
GGTCGTGAATATGGTACAACAACAGGACGTCCACGTCGTGTAGGTTGGTTTGATTTCAGTTGTATTACGTCACTCT
CGTCGTGTAAGTGGTATTACAGATTTATCTATTAAGTCAATCGATGTTTTAACAGGCCTAGACACAGTGAAAATC
TGTACAGCTTATGAATTAGACGGTAAAGAAATTACTGAGTACCCAGCAAACCTTAGATCAATTTAAACGTTGTAAA
CCAATCTTTGAAGAGTTACCAGGTTGGACAGAAGACGTAACAAGTGTGCGTACTTTAGAAGAATTACCTGAAAAT
GCACGTAAATATTTAGAGCGTATTTTCAAGATTATGTAATGTACAAATTTCTATCTTCTCAGTAGGTCCAGGCC

343 *Staphylococcus epidermidis* (SEQ ID NO. 343)

CTCTTCGAAGGTGCTCAAGGTGTCATGTTAGATATCGACCATGGTACATATCCATTTCGTTACATCTAGTAATCCA
GTTGCAGGTAACGTTACAGTAGGTACAGGTGTTGGCCCTACATCAGTGTCTAAAGTGATTGGTGTATGTAAATCA
TATACATCTCGTGTAGGTGACGGTCCATTCCCACTGAACCTTTTGTATGAAGATGGCCACCATATTAGAGAAGTG
GGTCGTGAATATGGTACAACACTACTGGACGTCCACGTCGTGTAGGTTGGTTCGACTCAGTTGTATTACGTCATTCA
CGTCGTGTAAGTGGTATCACAGATCTTTCAATTAAGTCAATCGACGTTTTAACAGGATTAGACACAGTTAAAATT
TGTACTGCTTACGAATTAGATGGTGAAAAAATTACTGAATACCCAGCAAACCTTAGATCAATTAAGACGTTGTAAA
CCTATCTTCGAAGAGCTTCCAGGTTGGACTGAAGACATTACAGGTTGTCGTAGTTTAGATGAACTTCCTGAGAAT
GCACGTAATTACTTAGAGCGTATTTTCAAGATTATGCGGTGTCCATATTTCAATCTTCTCAGTAGGTCCCTGGTC

344 *Streptococcus mitis* (SEQ ID NO. 344)

TATGGCTAGCNATAGACCAAGGTACGTATCCATTTGTTACGTCATCAAACCCTGTGGCTGGTGGTGTACGATTG
GTTCTGGTGTGGTCCAAGTAAGATTGACAAGGTTGTAGGTTTATGTAAAGCCTATACGAGTCGAGTAGGAGACG
GTCCTTTCCCACTGAATTGTTTGATGAAGTGGGAGAACGTATCCGTGAAGTTGGTCATGAATATGGTACAACAA
CTGGTCGTCCACGTCGTGTGGGTTGGTTTGACTCAGTTGTGATGCGTCATAGTCGTGTTTCTGGTATTACTA
ATCTTTTCATTGAACCTCTATCGATGTTTTGAGTGGTTTAGATACAGTGAAAATCTGTGTGGCCTATGATCTTGATG
GTCAACGTATTGACTACTATCCAGCTAGTCTTGAGCAATTGAAACGTTGCAAGCCTATCTATGAAGAGTTGCCAG
GTTGGTCAGAAGATATTACTGGAGTTCGTAATTTGGAAGATCTTCCTGAGAATGCGCGTAACCTATGTTTCGTGCTG
TGAGTGAATTGGTTGGCGTTCGTATTTCTACTTTCTCAGTAG

345 *Streptococcus species* (SEQ ID NO. 345)

ATGGCTTGCTATTGACCAAGGGTACATACCCATTTGTAACATCATCTAACCCAGTCGCTGGTGGTGTAAACAATCG
GTTCTGGTGTGGTCCAAGTAAATCAACAAAGTTGTCGGTGTATGTAAAGCCTACACAAGCCGTGTTGGTGACG
GACCATTCCCACTGAACCTTTTAGACGAAGTTGGTGACCGCATCCGTGAAGTGGGTACGAATATGGGACAACAA
CTGGACGTCCACGTCGTGTTGGTTGGTTTGACTCAGTTGTTATGCGTCACAGCCGCCGCGTATCAGGTATCACAA
ACTTGTCACTTAACTCAATTGACGTTCTTTCAGGTCTTGATACGGTCAAAATCTGTGTGGCATAACGACCTTGACG
GTCAACGTATCGACCACTACCCAGCAAGCCTTGAAACATTGAAACGTTGTAAACCAATCTACGAAGAATTGCCAG

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GTTGGTCAGAAGACATCACAGGTTGCCGTAGCCTAGATGAACTTCCCGAAAATGCTCGTGACTACGTTGCGCCGTG
TTGGTGAACTCGTTGGTGTTTCGCATTTCAACATTCTCAGTTGGCCCC

346 *Streptococcus canis* (SEQ ID NO. 346)

TGGCTTGCNATCGACCAAGGTAACCTTACCCATTTGTTACTTCTTCAAACCCAGTTGCTGGTGGGGTAACAATCGG
TTCAGGTGTTGGTCCAAGCAAGATCAATAAAGTTGTCCGTGTATGTAAAGCTTACACAAGCCGTGTTGGTGACGG
TCCGTTCCCAACAGAACTTCTAGATGAAGTTGGAGATCGTATCCGTGAAATTGGTCACGAATATGGTACAACAAC
TGGACGTCCACGTCTGTGTTGGTTGGTTTGAAGTCTGTTATGCGTCACAGCCGCCGTATCAGGTATCACAAA
CTTGTCACTTAACTCAATCGATGTTCTTTTCAGGACTTGATACTGTTAAAATCTGTGTGGCATACGACCTTGACGG
TCAACGTATCGACCACTACCCAGCAAGTCTTGAACAATTGAAACGTTGTAAACCAATCTACGAAGAATTGCCAGG
TTGGTCAGAAGACATCACAGGTTGCCGTAGCCTAGATGAACTTCCCGAAAATGCTCGTGACTACGTTGCGCCGTG
TGGTGAACTCGTTGGTGTTTCGCATTTCAACATTCTCAGTTGGCCCC

347 *Streptococcus mutans* (SEQ ID NO. 347)

TATGGCTTGCNATTGACCAAGGTAACCTATCCATTTGTAACCTCATCAAATCCAGTTGCAGGTGGCGTTACCATC
GGATCTGGTGTTGGACCAAGTAAAATCAATAAGGTTGTTGGTGTCTGCAAAGCCTATACCAGCCGTGTAGGTGAT
GGTCCTTTCCCAACAGAACTTTTGGACCAACGGGAGAGCGCATTCGTGAAGTTGGGCATGAATACGGGACAACA
ACAGGGCGTCCGCGTCGAGTTGGTTGGTTTGAAGTCTGTTATGCGTCACAGCCGCCGTGTATCAGGCATTACC
AATTTATCTCTTAACTGTATTGATGTACTTTTCAGGTCTTGATATCGTAAAATCTGTGTAGCCTATGATTTGGAT
GGAAACGGATTGATCACTACCCTGCCAGTCTCGAACAACCTCAAACGCTGTAAACCTATTTATGAAGAATTGCCG
GGCTGGTCTGAAGATATTACAGGGGTTTCGCAGTTTAGAAGATCTTCTGAAAATGCTCGTAATTATGTCCGCCGT
GTAAGTGAATTAGTTGGTGTTTCGTATTTCTACTTTCTCAGTNGTCCCC

348 *Streptococcus gordonii* (SEQ ID NO. 348)

TAATGCTAGCAATTGACCAAGGTACCTATCCATTTGTAACCTCATCTAATCCAGTTGCTGGTGGTGTAAACGATCG
GTTCTGGTGTGGGTCTAGCAAGATTGACAAAGTAGTGGGTGTTTGTAAAGCCTATACAAGTCGTGTTGGTGATG
GTCCTTTCCCAACAGAGCTTTTCGATGAAGTAGGTGACCGCATTCGTGAGGTTGGTCATGAGTATGGTACAACAA
CAGGACGTCCGCGTCGAGTTGGTTGGTTTGAAGTCTGTTGTTATGCGCCATAGCCGCCGTGTATCTGGGATTACCA
ATCTTTTCGCTTAACTCTATCGATGTTTTGAGCGGTCTGGATACAGTCAAGATCTGTGTAGCCTATGATTTGGATG
GCCAAAGAATCGACCACTATCCAGCTAGTTTGAACAGCTTAAACGTTGTAAAGCCGATTTACGAAGAGCTTCCTG
GATGGTCTGAAGATATTACTGGCGTTTCGTAAGTTAGAAGATCTTCCAGAAAATGCTCGCAACTATGTTCCGGCGAG
TAAGCGAGTTGGTTGGTGACGTATTTCCACCTTCTCAGTTGGCCCC

349 *Bacillus species* (SEQ ID NO. 349)

TATGGCTTGCAATTGACNCGGTACGTACCCATTCGTTACATCTTCTAACCCGATTGCGGGTGGTGTAAACAGTTGG
AACTGGAGTTGGTCTGCGAAAGTTACTCGCGTTGTAGGTGTATGTAAAGCATATACAAGCCGTGTTGGTGACGG
TCCATTCCCTACTGAACTTAATGATGAAATTGGTCATCAAATTCGTGAAGTTGGTCGTGAGTACGGAACAACAAC
TGGTCGTCCGCGCCGCGTAGGTTGGTTTCGATAGCGTTGTTGTAAAGACATGCGCGTCGTGTAGTGGTTTAAACGGA
TCTATCATTAAATTCTATCGACGTTTTAACAGATATTCGACTCTTAAAATTTGTGTTGCTTACAAATACAATGG
CGAAGTTATCGATGAAGTTCCAGCAAACTTAAACATTTTAGCAAAATGTGAGCCTGTATATGAAGAGCTTCAGG

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TTGGACAGAAGATATTACTGGTGTAAAATCATTAGACGAGCTTCCTGAAAATGCACGAAAATACGTAGAACGTGT
TTCGTGAGTTAACAGGAATTCATTATCTATGTTCTCAGTNGTCCCC

350 *Bacillus pumilus* (SEQ ID NO. 350)

GTTATGGCTTGCTATTGATCAAGGGACATATCCATTTGTCACGTCATCTAACCCAGTAGCTGGAGGAGTGACGAT
TGGTTCTGGCGTAGGACCAACAAAAATTCACATGTGGTTCGGCGTGTCAAAGCGTACACAACACGTGTTGGAGA
TGGCCCATTTCCCGACAGAACTCCATGATGAAATTGGCGATCAAATCCGTGAGGTTGGCCGTGAATACGGTACAAC
AACTGGACGTCCGCGCCGTGTTGGCTGGTTTGACAGTGTCTGTTGTCCGTCATGCTCGACGTGTGAGCGGGATTAC
AGATCTATCTCTTAACCAATTGATGTACTGACAGGGATTGAAACATTGAAAATCTGTGTGCGCTTATAAATTGAA
CGGAGAAATCACAGAGGAATTCCCAGCAAGTCTAAATGAACTAGCGAAATGTGAGCCTGTCTACGAAGAAATGCC
AGGATGGACAGAGGATATTACAGGCGTGAAGAATTTAAGCGAACTGCCTGAAAATGCCCGTCATTATTTAGAGCG
CATTTACAATTAACAGGTATTCCACTTTCCATTTTCTCAGTTGNCCCC

351 *Enterococcus villorum* (SEQ ID NO. 351)

TATCGACCAGGGACATATCCATTTGTTACTTCTCCATCCAGTAGCAGGTGGTGTAAACAATTGGTAGTGGCGTTG
GTCCATCTAAAATTAATAAAGTCGTGCGAGTATGTAAAGCTTATACTTCTCGTGTGGAGATGGCCCGTTCCCTA
CAGAATTATTTGATGAAACAGGGCAACAAATACGTGAAGTAGGTCGTGAATATGGCACAACAACAGGTCGTCCAC
GACGAGTTGGATGGTTTGATACGGTTGTTATGCGCCATTCAAAACGTGTATCAGGTATTACAAATTTATCTCTTA
ATTCGATTGATGTATTAAGCGGATTAGAAACAGTAAAAATTTGTACGGCCTATGAACTAGATGGTGAGCTGATTT
ATCATTACCCAGCAAGTTTGAAAGAATTGAAACGTTGTAAACCAGTATATGAAGAACTACCTGGATGGTCTGAAG
ATATTACGAAATGCAAGACACTTTCTGAATTGCCAGAAAATGCACGTAACCTATGTAAGACGTATTTCTGAGCTTG
TAGGTGTACGCATCTCCACATTTCTCAGTGGNCCC

352 *Bacillus thuringensis* (SEQ ID NO. 352)

CNCGGTACGTACCCGTTTCGTTACATCTTCTAACCCGATTGCGGGTGGTGTAAACAGTTGGAACCTGGAGTTGGCCCT
GCGAAAGTTACTCGCGTTGTAGGTGTATGTAAAGCATATACAAGCCGTGTTGGTGACGGTCCATTCCCTACTGAA
CTTAATGATGAAATTGGTCATCAAATTCGTGAAGTTGGTCGTGAGTACGGAACAACAACCTGGTCGTCCGCGCCGC
GTAGGTTGGTTGCATAGCGTTGTTGTAAGACATGCGCGTCGTGTTAGTGGTTTAACGGATCTATCATTAATTTCT
ATCGACGTTCTAACAGATATTCCAACCTCTTAAAAATTTGTGTTGCTTACAAATACAATGGCGAAGTTATCGATGAA
GTTCCAGCAAACCTTAAACATTTTAGCGAAATGTGAGCCTGTATATGAAGAGCTTCCAGGTTGGACAGAAGATATT
ACTGGTGTAAATCATTAGACGAGCTTCCTGAAAATGCAAGAAAATACGTAGAACGTGTTTCTGAGTTAACAGGA
ATTCAATTATCTATGTTCTCAGTGGCCCCNNGGGCCCCA

353 *Bacillus mycoides* (SEQ ID NO. 353)

GGTNCGTACCCATTTCGTTACATCTTCTAACCCGATTGCTGGTGGTGTAAACAGTTGGAACCTGGAGTTGGTCCCTGCG
AAAGTTACTCGCGTTGTAGGTGTATGTAAAGCATATACAAGCCGTGTAGGTGATGGTCCGTTCCCTACTGAGCTT
CATGATGAAATTGGTCATCAAATTCGTGAAGTTGGTCGTGAATACGGAACAACAACCTGGTCGTCCACGCCGCGTA
GGTTGGTTGCATAGCGTTGTTGTAAGACATGCACGTCGTGTTAGTGGTTTAACAGATCTATCATTAATTTCTATC
GACGTTCTAACAGGTATTCCAACCTCTTAAAAATTTGTGTTGCTTACAAATACAATGGCGAAGTTATCGATGAAGTT
CCAGCAAACCTTAAACATTTTAGCGAAATGTGAGCCTGTATATGAAGAGCTTCCAGGTTGGACAGAAGATATTACT

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GGTGTAAGAGCATTAGACGAGCTTCCTGAAAATGCACGAAAATACGTAGAACGTGTTTCTGAGTTAACAGGAATT
CAATTATCTATGTTCTCAGTGGNCCCCCGG

354 *Bacillus weihennstephanensis* (SEQ ID NO. 354)

TTTTTTTNGGAAGNGCGCAAGGTGTTATGCTTGATATCGACCACGGTACGTACCCGTTTCGTTACATCTTCTAACC
CAATTGCTGGTGGTGTAAACAGTTGGAAGTGGGCTGCGAAAGTTACTCGCGTTGTAGGTGTATGTAAAG
CATATACAAGCCGTGTTGGTGATGGTCCATTCCCTACTGAACTTAATGATGAAATCGGTACCAAATTCGTGAAG
TTGGTCGTGAATACGGAACAACAACGGGTCGTCCACGCCGTGTAGGTTGGTTCGATAGCGTTGTTGTAAGACATG
CACGTCGTGTTAGTGGTTTAAACAGATTTATCATTAACTCTATCGATGTATTAACAGGTATTCCAACGTGTTAAAA
TTTGTGTTGCTTACAAATGCAATGGCGAAGTTATCGATGAAGTTCCAGCTAACTTAAACATTTTAGCGAAATGTG
AGCCTGTATATGAAGAGCTTCCNGGTTGGACAGAAGATGTTACTGCTGTGAAATCATTGGATGAGCTTCCTGAAA
ATGCAAGAAAATACGTAGAGCGTGTTCCTGAATTAACNGGAAGCCAATTNNCAAG

355 *Staphylococcus haemolyticus* (SEQ ID NO. 355)

CAAGGTGTCATGTTAGATATCGACCATGGTACATATCCTTTCGTAACCTCAAGTAACCCTGTTGCAGGTAATGTA
ACAGTTGGTACAGGTGTAGGCCCAACTTTCGTATCTAAAGTGATTGGTGTATGTAAAGCATATACATCTCGTGTA
GGCGATGGTCCATTCCCTACAGAATTATTTGATGAAAATGGACATCATATTAGAGAAGTTGGTCGTGAATACGGT
ACAACAACAGGACGTCCACGTGCTGTAGGTTGGTTTGACTCAGTTGTATTACGTCACTCTCGTCGTGTTAGTGGT
ATTACAGACTTATCTATTAACCTCTATCGACGTACTTACAGGTCTTGATACAGTGAAGATTTGTACTGCTTACGAA
TTAGATGGAGAAGAAATTACAGAATATCCTGCTAACTTAGATCAATTACGTCGTTGTAAACCAATCTTTGAAGAG
TTACCAGGATGGGAAGAAGATATCACTGGTTGCCGTACATTAGAAGAATTACCAGATAACGCACGTAAATACTTA
GAACGCATTTCTGAATTATGTAATGTACGTATTTCAATCTTCTCAGT

356 *Staphylococcus saprophyticus* (SEQ ID NO. 356)

GCAAGGTGTGATGTTAGATATCGACCATGGTACATATCCATTTCGTTTCATCAAGTAACCCAGTTGCAGGTAATGTG
ACTGTCGGTGGCGGTGTAGGTCCAACATTTCGTCTCTAAAGTTATCGGTGTGTGTAAAGCCTATACATCACGTGTC
GGCGATGGTCCATTCCCAACAGAACTATTTGACGAAGATGGGCACCACATCCGTGAAGTAGGTTCGTGAATACGGT
ACAACAACAGGACGTCCACGTGCTGTAGGTTGGTTCGACTCAGTTGTATTACGTCACTTCTCGTCGTGCAAGTGGT
ATTACAGATTTATCTATTAACCTCAATTGATGTATTAACAGGCCTTAAAGAAGTTAAAATCTGTACTGCTTATGAG
TTAGACGGTAAAGAAATTACGGAATACCCAGCTAACTTGAAAGACTTACAACGTTGTAAGCCAATTTTTGAAACA
TTACCAGGTTGGACAGAAGATGTGACAGGTTGTCGTTTCATTAGAAGAATTACCTAATAATGCGCGTAGATACTTA
GAACGTATTTCTGAATTATGTGACGTGAAGATTTCAATCTTCTCAGTTGGCCC

357 *Bacillus subtilis* (SEQ ID NO. 357)

CTCAAGGGGTATGCTTGATATTGACCAAGGGACATACCCGTTTGTCACTTCATCCAACCCGGTCGCCGGAGGGG
TGACGATCGGTTTCAGGCGTAGGCCCGACAAAAATCCAGCACGTTCGTCCGTGTATCTAAAGCGTACACAACCCGTG
TCGGTGACGGTCTTTCCCGACTGAGCTGAAAGATGAAACCGGGGATCAAATCCGTGAAGTCGGACGCGAATACG
GCACAACGACAGGCCGTCCGCGCCGTGTCGGCTGGTTTGACAGCGTTGTTGTCCGCCATGCCCGCCGCGTCAGCG
GAATCACAGATCTTTCTCTGAACTCAATCGATGTGCTGACTGGCATTGAAACATTGAAAATCTGTGTGCTTACC
GCTACAAAGGTGAAGTGATTGAAGAATTCGCCGCAAGTCTGAAAGCTCTCGCAGAGTGTGAACCGGTATATGAAG

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AAATGCCTGGCTGGACGGAAGATATCACAGGCGCAAAAACATTAAGCGATCTTCCTGAAAATGCGCGCCATTATC
TGGAACGCGTGTCTCANCTGACAGGTATTCCGCTTTCTATTTTCTCAGTAGGTCCAGA

358 *Listeria monocytogenes* (SEQ ID NO. 358)

TTTGGAAGGGGCGCAAGGGGTATGCTTGATATTGATCAAGGAACATATCCATTTGTAACCTCAAGTAACCCGAT
TGCTGGTGGCGTAACTATCGGTAGTGGTGTGGTCCTTCAAAAATCAATCATGTTGTTGGTGTGGCGAAAGCTTA
TACAACACGTGTTGGTGATGGTCCTTTCCCAACAGAATTATTTGATTCTATTGGTGACACTATTCGTGAAGTCGG
TCATGAATATGGTACAACGACTGGTCGTCGCGTCGTGTAGGTTGGTTTGATAGCGTAGTGGTTCGTCATGCGCG
TCGTGTTAGTGGATTAACAGATTTATCGTTAACACTACTTGATGTTTTGACAGGAATTGAGACACTTAAAATCTG
TGTAGCTTACAAATTAGACGGAAAAACAATTACAGAGTTCCAGCAAGTTTGAAAGATTTAGCTCGTTGCGAACC
TGTTTATGAAGAACTTCCAGGCTGGACGGAAGATATTACTGGAGTTACATCACTAGATGATCTTCCAGTGAAGTG
CCGCCATTACATGGAGCGTATCGCCCAACTTACGGGAGTGCAAGTTTCTATGTTCTCAGTAGGTCCCAGACCA

359 *Lactococcus lactis* (SEQ ID NO. 359)

TNATGCTTGATATTGACNAGGAACATACCCATTTGTAACCTCTCAAACCCAGTAGCTGGTGGGGTAACGATTGGC
TCTGGTGTGGGTCCATCAAAAATTTCAAAGTTGTTGGTGTGTTGTAAAGCCTATACTTCACGTGTGGGTGATGGT
CCATTCCCAACAGAACTTTTTGATGAAGTTGGACATCAAATTCGTGAAGTAGGACATGAATATGGAACAACAACA
GGACGTCCACGTCGTGTTGGTTGGTTTGACTCAGTCGTAATGCGTCATGCAAAACGTGTTTCTGGCTTGACAAAT
CTTAGCTTGAATTCAATTGACGTTCTCTCAGGACTTGAAACAGTAAAAATTTGTGTTGCTTACGAACGTAGTAAT
GGTGAACAAATTACTCATTATCCAGCATCACTTAAGGAATTAGCAGATTGCAAACCAATCTATGAAGAAATTGCCA
GGATGGTCTGAAGATATTACTTCATGCCGAACTTTAGAAGAGTTACCAGAAGCTGCTCGTAACTATGTTTCGTCGG
GTTGGTGAAGTAGTTGGCGTACGTATCTCGACTTTCTCAGTNGTCCCC

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Figure 15 represents marker II (pstI) sequences amplified from Gram-positive bacteria (SEQ ID NOs: 360-395; SEQ ID NOs: 397-399), and some Gram-negative bacteria (SEQ ID NOs 396, 400-403).

SEQ ID NO. 360 *Bacillus anthracis*

ACCNNTTTTACAGACGTAAAATAGATAGGTTATATGGTTGGTATAAGTAAGATACTTGTTTCGTTTCATACGGTCTG
CAGCCATTGTGTATTGAATTAAGTCATTTGTTCCGATAGAGAAGAAATCAACTTCTTTGCGAATTGATCTGCTA
ATACTGCTGAAGCTGGGATTTCAACCATCATACCAACTTCAATAGAATCAGAAACAGTTGTACCCACTTCTACAA
GTTTCGCTTTTTCTTCTAATAAGATCGCTTTTGCTTGACGGAACATCAAGAGTTGCAATCATTGGGAACATAA
TTTTTAAGTTACCGTATACGCTAGCACGAAGTAATGCACGAAGTTGTGTACGGAACACATCTTGCTCATCAAGAC
ATAAGCGAATTGCACGGTAGCCCAAGAACGGNTTCATTCTCTTA

SEQ ID NO. 361 *Bacillus cereus*

GCCTTCTTTATGAGCAGCATCGATAACCATTTTTACAAGACGTAAAATAGATGGGTTATATGGTTGGTATAAGTA
TGATACTTGTTTCGTTTCATACGGTCTGCAGCCATTGTGTATTGGATTAAATCATTGTTCCGATAGAGAAGAAGTC
AACTTCTTTCGCGAATTGATCTGCTAATACTGCTGAAGCTGGGATTTCAACCATCATACCAACTTCAATAGAATC
AGAAACAGTTGTACCCGCTTCTACAAGTTTCGCTTTCTTCTAATAAAATCGCTTTTCGCTTGACGGAACATC
AAGAGTTGCAATCATTGGGAACATAATTTTTAAGTTACCGTATACGCTAGCACGAAGTAATGCACGAAGTTGTGT
ACGGAACACATCTTGCTCATCAAGACATAAGCGAATTGCACGGTATCCCAAGAACGGATCATTCTCGTTA

SEQ ID NO. 362 *Listeria monocytogenes*

GCCCTCTTTATGAGAAGCATCAATTACCATTTTTACTAAACGTAAGATGGATGGATTGTATGGTTGGTAAAGGTA
AGAAACCGGTTTCGTTTCATACGGTCCGCAGCCATTGTATACTGAATTAAGTCATTTGTTCCGATAGAGAAGAAATC
AACTTCTTTTGCAAATTGATCAGCAAGAACTGCAGCGGCAGGAATTTCAATCATAATTCCAAGTTTCGATGGAATC
AGATACTTCTGTTCCAGCAGCTTTTAGTTTTGCTTTCTCATCTAGTAAATATCACGTGCTTGACGGAATTCATT
TACTGTTGCAATCATCGGGAACATAATTTTTAAGTTACCATATACACTTGCGCGAAGTAAGGCGCGAAGTTGCGT
ACGGAATAATTCTTCATTTCGCAAAACAAAGACGAATTGCGCGGAATCCCAAGAACGGATCNTTCTCCTTA

SEQ ID NO. 363 *Streptococcus pneumoniae*

CGCGTGAGCTGCTTTGATCCATTGTTAATCAAGCGTAGGATTGATGGGTTGTATGGTTGGTAAAGGTATGAACT
TGTTTCGTTTCATACGGTCTGCTGCCATTGTATATTGGATCAAGTCATTTGTACCAATTGAGAAGAAGTCAACTTCT
TTAGCAAATTGGTCTGCAAGCATAGCCGCTGCAGGAATCTCGATCATGATACCAACTTGAATGTTATCCGCAACT
GCAACACCTTCAGCAAGAAGGTTTGCTTTTTCTTCATCAAAGACTGCTTTTCGCTGCACGGAATTCTTTCAAGAGC
GCAACCATTGGGAACATGATACGCAATTGACCGTGAACAGACGCACGAAGAAGAGCACGGATTTGTGTGCGGAAC
ATAGCATCTCCAGTCTCAGAGATAGAGATACGAAGAGCACGGAATCCNANGAACGGATCCTTTTTTCNTA

SEQ ID NO. 364 *Streptococcus pyogenes*

TGCGCTGCTTTGATACATTGTTGATCAAACGTAATATTGATGGGTTGTATGGTTGGTAAAGGTATGATACTTGTT
CGTTCATACGGTCTGCTGCCATAGTGATTGGATAAGGTCGTTTGTTCGAATTGAGAAGAAATCAACTTCCTTAG

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CAAATTGGTCTGCAAGCATAGCAGCTGCAGGAATCTCAATCATGATACCAACTTGGATGTCATCAGCAACCGCAA
CGCCTTCTGCAAGCAAGTTTGCTTTTTCTTCGTCAAAGACTGCTTTTGCAGCACGGAATTCTTTAAGAAGCGCAA
CCATTGGGAACATAATACGAAGTTGTCCGTGAACAGAGGCACGAAGAAGCGCACGCATTTGTGTGCGGAACATGG
CATCCCCAGTTTCAGAGATGGAATACGAAGAGCACGGAAACCNAAGAACGGATCNTTTTTNCCNTA

SEQ ID NO. 365 *Streptococcus agalactiae*

GAGCAGCTTTGATAACGTTGTTAATCAAACGAAGGATTGATGGATTGTATGGTTGATAGAGGTATGAACTTGCT
CATTCATACGGTCCGCAGCCATTGTGTATTGGATAAGATCATTAGTACCAATTGAGAAGAAATCAACTTCTTTTG
CAAATTGGTCTGCAAGCATAGCTGCCGCTGGGATTTCAATCATAATACCAACTTCAATGCCTTCAGCTACTGCTA
CACCGTCAGCTAACAAGTTGCTTTCTCTTCTTCAAATATAGCTTTAGCAGCACGGAATTCTTTAAGCAAAGCAA
CCATTGGGAACATGATGCGTAGCTGTCCATGAAGTGAAGCACGAAGAAGTGCTCGGATTTGTGTGCGGAACATTG
CATCACCAGTTTCAGAAATTGAAATACGCAATGCACGGAATCCCAAGAACGGATCNTTTTTTCNTA

SEQ ID NO. 366 *Streptococcus mutans*

TGAGCAGCCTTAACCCATGATCAACCAAGCGAAGAATGGATGGATTATAAGGTTGGTAGAGGTATGATACTTGTT
CATTCATACGGTCAGCAGCCATGGTGTATTGAATAAGGTCATTTGTACCGATTGAGAAGAAATCAACTTCCTTAG
CAAATTGGTCAGCCAACATTGCAGCTGCAGGAATTTCAATCATGATACCAACTTGGATATCATCTGAAACAGCAA
CGCCTTCAGCTTTAAGATTAGCCTTTTCTTCTTCCAGAATACCTTTAGCTTTACGGAACTCATTGAGCAAAGCTA
CCATTGGGAACATGATACGCAACTGACCATGAACAGAAGCACGCAAAAGGGCACGCAACTGTGTGCGGAACATCT
GATTGCCTGTTTCTGAGATTGAAATACGAAGTGCACGAAAACCAAAGAACGGATCATTCTCTTA

SEQ ID NO. 367 *Enterococcus flavescens*

CGTCGTGTGCTGCATCAATTACATTTTTAATTAAACGTAAGATTGATGGGTTGTATGGTTGGTATAAGTAAGAAA
CGCGTTCGTTCATACGGTCTGCCGCCATTGTGTATTGGATTAAGTCGTTGGTTCCAACACTAAAGAAGTCTACTT
CTTTGGCAAATTTATCAGCTAATACGGCAGCTGCTGGAATTTCAATCATAATACCTACTTGGATATCGTTTTGAAA
CTTCAACACCTTCGTTGACTAATTTTTGTTTTTCGTCTTCAAAGATTGCTTTTCGTGCTCTAAATTCTTTCAAAG
TAGCAACCATTTGGGAACATGATACGTAAGTTACCATGAACAGACGCACGTAATAATGCACGCATTTGTGTACGGA
ACATGCCGTCACCTAGTTCTGATAAGCTAATACGTAATGCACGGTAACCCAAGAACGGATNATTCTCGTA

SEQ ID NO. 368 *Staphylococcus aureus*

NNCCNTCTTATGTGACGCTTCAATAACTTGTTTAACTAAACGTAAGATTGAAGGGTTATATGGTTGGTATAGAT
ATGATACACGCTCTGACATACGGTCAGCAGCTAATGTGTATTGAATTAAATCATTTGTACCGATACTGAAGAAAT
CTACTTCTTTAGCAAAGACATCAGCTAATGCTGCTGTTGCAGGTATCTCTACCATGATTCTAATTCTATATCAT
CCGAAATGTCATGACCTTCATTTTTAAGGTTTTCTTTTTCTTCTAATAATATAGCTTTTGCTTCTCTAAATTTCGT
TAATTGTTGCAACCATTTGGGAACATGATATTTAACTTACCATAAACTGATGCACGTAATAATGCACGTAGCTGTG
GTCTGAAAATATCTTGTTGCGCAAGGCATAAACGAATCGCACGGTAACCCAAGAACGGATCCNTTNTCCTTAA

SEQ ID NO. 369 *Staphylococcus epidermidis*

CTTCTTTATGAGAAGCTTCAATAACTTGTTTAACTAATCGTAAAATTGAAGGATTATATGGTTGATATAAGTATG
AAACTCGTTTCAGACATACGGTCAGCAGCTAATGTGTATTGAATTAAGTCATTGTTTCTATACTAAAGAAATCTA

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CTTCTTTAGCAAATACATCAGCAAGTGCCGCGGTAGCTGGAATTTCAACCATAATACCTAATTCAATATCATCTG
AAACTTCGTAACCTTCGCGAAGAAGATTTTCTTTCTCTTCAAGAAGCATTGATTTAGCGTCACGGAATTCCTTAA
TTGTTGCTACCATTTGGGAACATAATATTCAATTTCCCATAGACTGAAGCACGTAGTAATGCACGTAATTGTGGTC
TAAAGATTTCCGGCTGTGCTAAACATAAACGTATCGCACGATAACCCAAGAACGGATCNTTCTNCGTA

SEQ ID NO. 370 *Bacillus thuringensis*

CTTTATGAGCAGCATCGATAACCATTTTTACAAGACGTAAAATAGATGGGTTATATGGTTGGTATAAGTATGATA
CTTGTTTCGTTTCATACGGTCTGCAGCCATTGTGTATTGGATTAAATCATTCGTTCCGATAGAGAAGAAATCAACTT
CTTTTCGCGAATTGATCTGCTAATACTGCTGAAGCTGGGATTTCAACCATCATACCAACTTCAATAGAATCAGAAA
CAGTTGTACCCGCTTCTACAAGTTTCGCTTTCTCTTCTAATAAAATCGCTTTTCGCTTGACGGAATCATCAAGAG
TTGCAATCATTTGGGAACATAATTTTTAAGTTGCCGTATACGCTAGCACGAAGTAATGCACGAAGTTGTGTACGGA
ACACATCTTGCTCATCAAGACATAAGCGAATTGCACGGTATCCCAAGAACGGATCATTCTCNTTA

SEQ ID NO. 371 *Staphylococcus hominis*

CNCCNNCCTTATGAGGAAGCTTCAATAACCTGTTTAACTAAACGTAAAATTGCTGGATTATATGGTTGATATAAA
TATGAAACACGTTTCAGACATACGATCAGCTGCCATAGTATATTGAATTAAGTCATTAGTTCCTATACTAAAGAAA
TCTACTTCTTTAGCAAAGATATCAGCTAACGCAGCAGTAGAAGGAATCTCTACCATGATACCTACTTCGATATCA
TCAGCAACTTCTTGTCCTTCGCTAGTTAATTTATCTTTTTCTTCTAAAAGAATAGCTTTAGCATCTCTAAACTCT
TTAATAGTAGCTACCATTTGGGAACATAATATTTAATTTACCATAAGCAGATGCGCGTAATAACGCACGTAATTGT
GTTCTGAAGATGTCTTGTTGATCTAAGCACAAACGAATTGCACGATAACCCANGAACGGATTCATNTCNTA

SEQ ID NO. 372 *Enterococcus faecium*

CGCGTGTGCTGCATCAATTACATTTTTGATCAAACGTAAAATTGATGGGTTATATGGTTGGTACAAGTAAGAAAC
GCGTTTCGTTTCATACGGTCTGCTGCCATTGTGTATTGAATCAAATCGTTTCGTACCTACAGAGAAGAAATCTACTTC
TTTTGCAAACCTTGCTGCTAAGACTGCTGCTGCTGGAATCTCGATCATGATGCCGACTTGGATCGTATCAGATAC
TTCCTTGCCCTTCACTGATCAATTTTTGTTTTTCTTCTTCAAAGATCGCTTTTGCTGCGCGGAATTCTTTGAGTGT
AGCTACCATAGGGAACATGATACGTAAGTTACCATGAACAGATGCACGAAGCAATGCACGCATTTGTGTACGGAA
CATTTTCGTCGCCCTTGTTTCAGATAAACTGATACGCAATGCACGATATCCCAAGAACGGATCATTCTCCTTA

SEQ ID NO. 373 *Clostridium perfringens*

CNTGTTTGTGAGCTCCATCTATTGTCATTTTGATTAAATCTTAATACAGCTGGATGCATTGGATTGTAAAGGTATG
ATACCTTTTCACTCATTCTGTCAGCAGCTAATGTATATTGTATTAAATCGTTAGTTCCTATTGAGAAGAAATCAA
CATGCTTAGCTAATTCATCAGCATAAACTGCTGCAGCTGGGATTTCAACCATGATACCCCATTTGAATTGAATCTG
AGTATGCTATACCTTCTGCTTTTAACTCAGCTTTGCATTCTTCAACAAATGCTTTAGCTTGTTGGAATTCCTCTA
ATCCTGAAATCATTGGGAACATTACTGCAAGATTTCCATAAACAGAAGCTCTTAATAAAGCTCTTATTTGAACTC
TAAAGATATCTTTTCTGTCTAAGCATAATCTTATAGCTCTGTATCCCAAGAACGGATCNNTNNTCNTTAA

SEQ ID NO. 374 *Bacillus mycoides*

CTTTATGAGCAGCATCGATCACCATTTTTACAAGACGTAAAATTGATGGGTTATATGGTTGGTATAAGTAAGATA
CACGTTTCGTTTCATACGGTCTGCAGCCATTGTGTATTGGATTAAATCATTTGTTCCGATAGAGAAGAAATCGACTT

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CTTTTGCGAATTGATCTGCTAATACTGCTGAAGCTGGAATTTCAACCATCATACCAACTTCAATAGAATCAGAAA
CAGTTGTACCCGCTTGGACAAGTCTTTCTTTCTTCTTAATAAAATCGCTTTCGCTTGACGGAATTCATCAAGAG
TTGCAATCATCGGGAACATAATTTTTAAGTTACCGTATACGCTAGCACGAAGTAATGCACGAAGTTGTGTACGGA
ACACATCTTGTCTTCAAGGCATAAGCGAATTGCACGGTATCCCAAGAACGGATCNTTCTCNTTA

SEQ ID NO. 375 *Streptococcus oralis*

CNNTTTCCTTCGCGTGAGCTGCTTTGATAACGTTGTTGATCAGCGTAGGATTGATGGGTTGTATGGTTGGTAAA
GGTATGAACTTGCTCGTTCATACGGTCTGCTGCCATTGTGTATTGGATCAAGTCGTTTGTACCAATTGAGAAGA
AGTCAACTTCTTTAGCAAATTGGTCTGCAAGCATTGCTGCTGCAGGAATTTTCGATCATGATACCAACTTGGATAT
TATCCGCAACTGCAACACCTTCAGCAAGAAGGTTTGCTTTTTCTTCGTCAAAGACTGCTTTCGCTGCACGGAATT
CTTTCAAGAGCGCAACCATTTGGGAACATGATACGTAATTGACCGTGAACAGACGCACGAAGAAGAGCACGGATTT
GTGTGCGGAACATAGCATCTCCAGTCTCAGAGATAGAGATACGAAGAGCACGGAATCCNAAGAACGGATCNTTTC
TCTTA

SEQ ID NO. 376 *Enterococcus hirae*

CNATTTACCTTCGCATGCGCTGCATCGATCACGTTTTTAATCAAACGTAGGATTGATGGGTTGTAAGGTTGATAC
AAGTATGAAACACGTTTCGTTTCATACGGTCAGCTGCCATAGTGTATTGGATCAAGTCATTCGTTCCCTACTGAGAAG
AAGTCAACTTCCTTAGCAAACCTTGTCAGCTAAGACAGCTGCTGCTGGAATTTTCGATCATGATGCCGACTTGGATC
GTATCAGATACTTCACGCCTTCATTCAATAATTTTTGTTTTCTTCGTTCAAAGATTGCTTTTGCAGCACGGAAT
TCTTTAAGAGTCGCTACCATTGGGAACATGATACGTAAGTTTCCATGAACAGATGCACGTAATAATGCGCGCATT
TGCGTACGGAACATTTTCGTCACCTTGTCTGACAAGCTGATTTCGTAATGCACGATAGCCCAAGAACGGATCNTTN
TCCTTA

SEQ ID NO. 377 *Enterococcus avium*

CNATTTNCCTTCGCGTGCGCTGCATCAATCACGTTTTTGATTAAGCGTAGAATTGATGGGTTATATGGTTGGTAA
AGGTAAGAAACGCGTTTCGTTTCATACGGTCAGCTGCCATCGTGTATTGAATTAAGTCATTTGTTCCGATACTGAAG
AAATCAACTTCTTTGGCAAACCTTGTCAGCTAGTACAGCTGCAGCTGGAATTTTCGATCATGATTCCGACTTGGATC
GTATCAGAACTTCACGCCTTCTTTAACCAATTTTTCTTTTTCTTCGTTGAACATTTTCTTCGCTGCACGGAAT
TCTTTTAATGTGCAACCATTTGGGAACATGATGCGTAAGTTACCATGAACAGAAGCGCGCAACAATGCACGTAAT
TGTGTACGGAACATGTCATCGCCTAGTTCGGATAGACTAATACGCAATGCACGATAACCCAAGAACGGATCNTTT
TTCTTAA

SEQ ID NO. 378 *Staphylococcus saprophyticus*

TCGTAAGAAGCTTCTATTACTTGTTTTACTAAACGTAATATTGAAGGATTATATGGTTGATACAAGTAAGAAACA
CGTTCTGACATTCTATCAGCAGCCATTGTATATTGAATTAATCATTCGTTCCCTATACTGAAGAAATCAACTTCT
TTAGCAAATACATCTGCCAACGCAGCAGTAGAAGGAATTTCTACCATAATACCAAGTTTCGATATCATCAGAACT
TCAATGCCTTCATTTGTTAAGTTATCTTTTTCTTCAAGTAACAATGCTTTAGCATCACGGAACCTTTGGATTGTA
GCTACCATAGGGAACATGATATTCAATTTACCAAAAAGCAGATGCACGTAATAATGCACGCAACTGTGGTCTGAAA
ATATCAGGTTGATCTAGGCATAAACGGATAGCACGGTAACCCAAGAACGGATCATTCTCTTA

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SEQ ID NO. 379 *Staphylococcus haemolyticus*

GAAGCTTCATGACTTGTTTAACCAAGCGTAAATAGCTGGGTATAAGGTTGGTATAAGTATGAAACGCGTTCTG
ACATACGGTCAGCTGCCATAGTATATTGAATTAAATCATTAGTACCAATACTGAAGAAATCCATTTCTTTAGCAA
AGATATCAGCTAAAGCAGCTGTAGATGGAATCTCAACCATGATACCTAACTCAATTTTCATCAGAAACGTCATGAC
CATCATTTTTTAAGATTTTCTTTTCTTCTAACAGAATGGCTTTAGCATCACGGAATTCATTGATTGTAGCTACCA
TTGGGAACATAATGTTTAATTTACCGTAAGCTGACGCGCGTAATAATGCACGTAATTGTGTTCTGAAAATATCTT
GTTGATCTAAGCATAGACGAATTGCTCTGTAACCCAAGAACGGNTCNTTCTCTTA

SEQ ID NO. 380 *Enterococcus flavescens*

NGCATGCGCTGAGTCGATCACGTTTTTGATCAAACGTAAATTTGATGGGTGTATGGTTGGTACAAGTAAGACAC
GCGCTCGTTTCATGCGGTCTGCAGCCATTGTGTATTGGATCAAGTCATTGGTACCAATACTGAAGAAGTCAACTTC
CTTCGCAAACCTTGCTCTGCTAAGACAGCAGCTGCTGGAATTTTCGATCATGATTCCGACTTGGATCTCGTTAGAAAC
CTCAACGCCTTCGTCAATCAATTTTTGACGCTCTTCTTCATACATTTTCTTCGCAGTACGGAACCTTTTCAATGT
TGCCACCATTGGGAACATGATACGTAAGTTGCCGTGAGCAGAAGCACGTAACAACGCACGAAGTTGGGTACGGAA
CATGTCATCCCCAAGTTCAGATAAGCTGATACGCAATGCACGATAGCCCAAGAACGGATATTNNTCNTA

SEQ ID NO. 381 *Enterococcus casseliflavus*

GCGCTGAGTCGATACGTTTTTTGATCAAACGTAAATTTGATGGGTGTATGGTTGGTACAAGTAAGACACGCGCTC
GTTTCATGCGGTCTGCAGCCATGGTGTATTGGATCAAGTCATTGGTACCAATACTGAAGAAGTCAACTTCCTTCGC
AACTTGTCTGCTAAGACAGCAGCTGCTGGAATTTTCGATCATGATTCCGACTTGGATCTCGTTAGAAACCTCAAC
GCCTTCGTCAATCAATTTTTGACGCTCTTCTTCATACATTTTCTTCGCAGTACGGAACCTTTTCAATGTTGCCAC
CATTGGGAACATGATACGTAAGTTGCCGTGAGCAGAAGCACGTAACAACGCACGAAGTTGGGTACGGAACATGTC
ATCCCCAAGTTCAGATAAGCTGATACGCAATGCACGATAGCCCAAGAACGGATNATTTNTCTTA

SEQ ID NO. 382 *Enterococcus gallinarum*

ACCTTNGCATGTGCTGAATCGATTACGTTTTTTGATCAACGTAGAAATAGATGGGTATATGGTTGGTAAAGATATG
AACTTGTTCATTACATACGGTCTGCAGCCATTGTGTATTGGATCAAGTCATTGGTACCAATACTGAAGAAGTCTA
CTTCCTTGGCAAATTTGTCTAGCTAAGACAGCTGCTGCAGGAATTTTCGATCATGATACCTACTTGAATATCTTCAG
AGACGGTTACGCCTTCATCGATCAATTTTTGACGTTCTTCTTCGTACATTTTTTTTCGCAGCACGGAACCTTTTCA
ATGTTGCCACCATTGGGAACATAATCCGCAAGTTCCGTGAGCAGAAGCACGTAACAGCGCACGAAGTTGTGTAC
GGAACATGCCGTACCCAACTCAGACAACTGATACGCAATGCACGATAGCCCAAGAACGGATCTTTNTCCNTTA

SEQ ID NO. 383 *Enterococcus raffinosus*

NTGTGCTGCATCAATGACGTTTTTAATCAAACGTAAAGATTGATGGGTATATGGTTGATACAGGTATGAAACGCG
TTCGTTTCATACGGTCAGCAGCCATTGTGTATTGAATCAAGTCGTTTGTTCGGATACTAAAGAAGTCAACTTCTTT
TGAAACTTGTCTAGCTAGAACAGCTGCGGCAGGGATCTCGATCATGATTCCGACTTGAATCGTATCAGAAACCTT
CACGCCTTCGTTAACAAGCTTTTCTTTTCTTCGTTGAACATTTTCTTCGCTGCACGGAACCTTTTTAATGTTGC
AACCATTGGGAACATGATGCGTAAATTGCCATGAACTGAAGCGCGTAACAATGCACGTAAGTGTGTACGGAACAT
ATCGTCGCCTAATTCAGATAAACTGATACGCAATGCACGATAACCCAAGAACGGATNNTTCTNCGTAA

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SEQ ID NO. 384 *Enterococcus villorum*

GGNCTCTCGTCGTNAGCTGCATCAATCACGTTTTTGGATTAAACGTAAAATTGATGGGTTATAAGGTTGGTATAAG
TATGAAACGCGTTCGTTTCATACGGTCAGCTGCCATAGTGTATTGAATCAAATCATTTGTTCCCTACTGAGAAGAAG
TCAACTTCCTTCGCAAACTTGTCTAGCTAAAACAGCAGCTGCAGGAATTTCAATCATAATGCCGACTTGGATCGTA
TCAGATACTTCCACGCCTTCATTCAATAACTTTTTGTTTTTCATCTTCAAAGATTGCTTTTGCCCCACGGAATTCT
TTAAGTGTGCGCCACCATTTGGGAACATGATACGTAAGTTACCGTGAACGGATGCACGCAATAACGCACGCATTTGT
GTACGGAACATTTTCGTCTCCTTGTTCAGAAAGACTGATACGTAATGCACGATATCCNANGAACGGNTTATTTTTC
NTA

SEQ ID NO. 385 *Clostridium difficile*

TTTNNGGANGGCNTCTNTCGTANGCATTGTCTATANCAGTCTTTATAAGTCTTAAACAGCTGGATNAAATTGAT
TGTAAGNTAACTTATCTTTTGATTCATTCTATCAACTGCACAAGTGTATTGAATTAAATCATTAGTTCCCTATAG
AGAAGAAATCTACGTGTTTAGCCAATACATCAGATATCACAGCAGCAGATGGAACCTTCTATCATCATACCAATTT
CTACATCTTTAGCATAAGCCACACCTTCAGAATCAAGTTCGTCTAAAACCTTCTTTTACAACCTTCTTTAGCTTGTA
ACAACCTCTTCTAAAGATGAAATCATTTGGGAACATGATTCTTAATCTTCCATGAACACTAGCTCTATATAAAGCTC
TCAATTGAGTCTTAAATATATCTTTTCTATCTAGGCAAAGTCTTATTGCTCTGTAACCCAAGAACGG

SEQ ID NO. 386 *Streptococcus mitis*

NGCGTGAGCTGCCTTGATAACGTTGTTGATCAAGCGAAGGATTGATGGGTTATATGGTTGGTAAAGGTATGAAAC
TTGCTCGTTTCATACGGTCTGCTGCCATTGAGTATTGGATCAAGTCGTTTGTTCGAATTGACATGAAGTCTACTTC
TTTTGCAAATTGGTCTGCAAGCATCGCTGCTGCAGGGATTTCAATCATGATACCAACTTGGATATCATCCGCAAC
TGCAACACCTTCAGCAAGAAGGTTTGCCTTTCTTCTCATAAACTGCTTTGGCTGCACGGAATTCCTTTCAAAAG
AGCAACCATTTGGGAACATGATACGCAATTGACCATGAACAGAAGCACGAAGAAGAGCACGGATTTGTGTACGGAA
CATTCATCTCCAGTTTCAGAAATAGAGATACGAAGGGCACGGAATCCNAAGAACGGATATTTTTTCNTA

SEQ ID NO. 387 *Bacillus halodurans*

NCCTTCGCTATGAGCTGCTTTAATAACCATATCGACGAGGCGTAAAATCGCAGGGTGGTATGGCTGATACAGGTA
GGAGACTCGCTCATTTCATGCGGTCTGAGCCATCGTATATTGAATTAAGTCGTTTCGTTCCGATACTGAAAAAGTC
TACTTCTTTTGCAAAAAGATTAGCCGCTACCGCCGTCGATGGGATTTCTACCATGATTCCCACTTCAATTGAATC
GGATACGTCCACTCCTTCACTAAGAAGCTTGTCTTTTCTCTTGCATGATCGCTTTTGCTTGGCGAAGCTCTTC
AAGGGTGGCGATCATTGGAAACATCACCTTTAAGTTACCGTATGTGCTTGCGCGAAGCAAGGCACGGAGTTGGGT
CCGGAAAATATCTTGTTTTTCAAGGCACAGACGAATCGCCCGGAAACCNAAGAACGGATNNTTNTTCNTAA

SEQ ID NO. 388 *Bacillus weihenstephanensis*

NTGAGCAGCATCGATAACCATTTTTACAAGACGTAAAATAGATGGGTTATATGGTTGGTATAAGTAAGCTACTTG
TTCGTTTCATACGGTCTGCAGCCATTGTGTATTGGATTAAGTCATTTGTTCCAATAGAGAAGAAATCAACTTCTTT
TGCGAACTGATCAGCTAATACTGCTGAAGCTGGAATTTCAACCATCATACCAACTTCAATAGAATCAGAAACAGT
TGTACCCGCTTTAACAAGTCTTTCTTTCTTCTAATAAGATTGCTTTCGCTTGACGGAACCTCATCAAGAGTTGC
AATCATTTGGGAACATAATTTTTAAGTTACCGTATACGCTAGCACGAAGTAATGCACGAAGTTGTGTACGGAACAC
ATCTTGCTCATCAAGACATAAGCGAATTGCACGGTATCCCAAGAACGGATCNTTCTCNTTA

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SEQ ID NO. 389 *Streptococcus species*

CNNANTTNCCTTCGCGTGAGCTGCTTTGATAACGTTGTTAATCAACGAAGGATTGATGGGTTGTATGGTTGGTAA
AGGTATGAAACTTGTTTCGTTTCATACGGTCAGCAGCCATTGTGTATTGGATAAGGTCGTTTGTTCGATTGAGAAG
AAGTCAACTTCTTTTCGCAAATTGGTCAGCAAGCATAGCTGCAGCTGGGATTTCAATCATGATACCAACTTGGATA
TCATCTGAAACGGCAACACCTTCAGCTTTAAGGTTTGCTTTTTCTTCATCAAAGATTGCTTTAGCAGCACGGAAT
TCTTTAAGAAGAGCAACCATTGGGAACATGATACGAAGTTGTCCGTGTACAGATGCACGAAGAAGTGCACGGATT
TGTGTACGGAACATTGCATTTCTGTTTCTGAGATAGAAATACGAAGTGCACGGAATCCNAAGAACGGATCCTTT
TTCCTTAA

SEQ ID NO. 390 *Streptococcus gordonii*

NTGCCTTCGCATGAGCCGCTTGATAACATTGTTGATCAAGCGAAGGATAGATGGGTTATAAGGTTGATAGAGGT
AAGAGACTTGTTTCATTTCATCCGGTCAGCTGCCATAGTGTACTGGATCAAGTCGTTGGTACCAATTGAGAAGAAGT
CAACTTCCTTGGCAAATTGATCCGCCAACATAGCTGCTGCTGGAATTTCAATCATGATACCCACTTGAATGTTAT
CCGCTACAGCAACACCTTCAGCTTGCAATTTTCGCTTTTTCTTCTTCGTAAACTGCTTTAGCCTTACGGAATTCTG
TTAGAAGGGCTACCATTGGGAACATGATACGTAATTGTCCATGTACAGACGCACGTAAGAGAGCGCGGATTGTG
TACGGAACATAGCATTACCAGTTTCAGAGATAGAGATACGCAAAGCACGGAAGCCNAAGAACGGTCNTTTTT

SEQ ID NO. 391 *Streptococcus canis*

CNCGTGAGCTGCTTTGATAACGTTGTTAATCAAACGAAGGATTGATGGGTTGTATGGTTGGTAAAGGTATGAAAC
TTGTTTCGTTTCATACGGTCAGCAGCCATTGTGTATTGGATAAGGTCGTTTGTTCGATTGAGAAGAAGTCAACTTC
TTTCGCAAATTGGTCAGCAAGCATAGCTGCAGCTGGGATTTCAATCATGATACCAACTTCGATATCATCTGAAAC
GGCAACACCTTCAGCTTTAAGGTTTGCTTTTTCTTCATCAAAGATTGCTTTAGCAGCACGGAATTCCTTTAAGAAG
AGCAACCATTGGGAACATGATACGAAGTTGTCCGTGTACAGATGCACGAAGAAGTGCACGGATTTGTGTACGGAA
CATTCGATTTCTGTTTCTGAGATAGAAATACGAAGTGCACGGAATCCNAAGAACGGTCNTTTTTCTCTAA

SEQ ID NO. 392 *Bacillus pumilus*

CNTACGCTGCTTCATAACAAGCGTAATCAAACGTAAATCGCTGGATTGTAAGGCTGGTAAAGATAAGACACTCG
TTCGTTTCATTTCGATCAGCAGCCATTGTGTATTGAATCAAATCATTTGTTCCAATACTGAAGAAATCAACTTCTTT
TGCGAATTGGTCTGCGATGACAGCGGTTGATGGAATTTCTACCATTATACCGATTTCAATGGAATCGGATACGTC
TGTACCAGCGGCAACCAATGCTTCTTTTTCTTCAAGTAAAATGGCTTTTGCTTCTCTAAATTCTGATAATGTGCG
GATCATAGGGAACATGATTTTCAAGTTTCCATATGTACTTGCACGAAGTAAGGCGCGTAGTTGTGTTCTGAAAAT
CTCCTGTTCTTCGAGGCAAAGGCGGATCGCTCTAAAGCCNAAGAACGGATNTTTTTCTNTAA

SEQ ID NO. 393 *Bacillus species*

TGAGCGCATCGATAACCATTTTTACAAGACGTAAATAGATGGGTTATATGGTTGGTATAAGTATGATACTTGTT
CGTTCATACGGTCTGCAGCCATTGTGTATTGGATTAAATCATTTGTTCCGATAGAGAAGAAGTCAACTTCTTTTCG
CGAATTGATCTGCTAATACTGCTGAAGCTGGGATTTCAACCATCATACCAACTTCAATAGAATCAGAAACAGTTG
TACCCGCTTCTACAAGTTTCGCTTCTCTTCTAATAAAAATTGCTTTTGCTTGACGGAACATCAAGAGTTGCAA

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TCATTGGGAACATAATTTTTAAGTTACCGTATACGCTAGCACGAAGTAATGCACGAAGTTGTGTACGGAACACAT
CTTGCTCATCAAGACATAAGCGAATTGCACGGTATCCCAAGAACGGATCCNTTNTNCTTTAA

SEQ ID NO. 394 *Lactococcus lactis*

GTGAGCTGCTTTGATNCATTGTTAATCAAACGAAGGATTGATGGATTGTAAGGTTGGTAAAGGTAAGAACTTGT
TCATTACATACGGTCTGCAGCCATTGTATATTGGATGAGGTCGTTTGTACCAATTGAGAAGAAATCAACTTCCTTA
GCAAATTGGTCTGCAAGCATTGCTGCTGCTGGAATTTCAATCATGATACCTACTTCGATACCATCTGCAACTGGA
ACACCTTCAGCAATCAATTTTGCTTTTTCTTCGTCATAAATCTTCTTAGCTGCACGGAACTCAGTTACGAGAGCA
ACCATTGGGAACATGATACGAAGTTGTCCGTGTACAGAAGCACGCAAGAGTGCACGCAATTGTGTACGGAACATT
CCGTCACCAGCTGTTGAAAGGCTGATACGAAGTGCACGCCATCCCANGAACGGTNNTTTTTNTTTTAA

SEQ ID NO. 395 *Bacillus firmus*

TCCAGGANGGGTTCTNTCNTANGCTGCGTCAATTACCATTTTAACTAAACGCAGGATTGCAGGATTATACGGCTG
GTAAAGGTAAGAAACACGCTCATTCATGCGGTCTGCAGCCATTGTGTACTGAATTAGATCATTAGTGCCAACT
GAAGAAATCGACTTCTTTAGCAAACCTGATCAGCCATAACAGCAGTTGAAGGAATTTCAACCATAATTCCAATTC
AATGTTGTGCGCAACCTCTGCTCCTTCGCTCACAAGCTTTTGTTTTTCTTCTTCAAGGATTGCTTTGCCCTGACG
GAATTCCTCAAGAGTGGCAATCATAGGGAACATGATTTTAAAGGTTTCCATAGGTGCTTGCTCTTAATAAAGCCCT
TAATTGCGTCCTGAACATATCCTGTTCTTCCAGACACAGACGAATCGCCCGGAAGCCCAAGAACGGATTTCATNT
CTTA

SEQ ID NO. 396 *Haemophilus influenzae*

TGAGAGGCATCAATCACTTGTTTAATTAAACCAAGCACAGAGGGGTGCATCGGATTATAAAGATGGGAAATAAAC
TCATTACCGCGATCTACAGCCAAAGTATATTGAGTTAAATCGTTAGTACCGATACTAAAGAAATCCACTTCTTTT
GCTAAAAATTTTGCATTTACTGCGGCAGAGGGGGTTTCGACCATTACACCAACTTGGATATTATTATCAAACAGT
CTCCCCCTCTTCACGTAATTCGCTTTTAAATGTTTCAATAACCGCTTTTAAATCCCGAATTTCTTCTACAGAAATA
ATCATCGGGAACATTACCGCCAATTTACCAAAAGCTGAAGCACGTAACACCGCGCGTAATTGTGCATTTAAATTT
TCACGACGATCTAATGCAATGCGAATCGCACGCCATCCCAAGAACGGATNNTTTTTTCTT

SEQ ID NO. 397 *Streptococcus bovis*

TGAGCTGCTTTGATAACGTTGTTAATCAAACGAAGGATTGATGGGTTATATGGTTGGTAAAGGTATGAACTTGT
TCATTACATACGGTCAGCAGCCATTGTGTATTGGATAAGGTCGTTTGTTCGATTGAGAAGAAGTCAACTTCTTTT
GCAAATTGGTCAGCAAGCATAGCTGCAGCTGGGATTTCAATCATGATACCAACTTGGATATCATCTGAAACGGCA
ACACCTTCAGCTTTAAGGTTAGCTTTTTCTTCATCAAAGATTGCTTTAGCAGCACGGAATTCTTTAAGAAGTGCA
ACCATTGGGAACATGATACGAAGTTGTCCGTGTACAGATGCACGAAGAAGTGCACGGATTTGTGTACGGAACATT
GCATTTCTGTTTCTGAGATAGAAATACGAAGTGCACGGAATCCNAAGAACGGTCCNTTTTTNCTTA

SEQ ID NO. 398 *Enterococcus durans*

TGTGCTGCATCAATCACGTTTTTGATCAAACGTAAAATTGAAGGGTTATAAGGTTGATACAAGTAAGATACACGT
TCGTTTCATGCGGTGAGCTGCCATTGTGTATTGAATCAAGTCATTCGTACCTACTGAGAAGAAGTCAACTTCCTTC
GCAAACCTTATCTGCTAAGACAGCTGCTGCAGGGATTTCAATCATGATGCCGACTTGGATCGTATCAGATACTTCC

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ACGCCTTCGCTCACTAATTTTTGTTTTCTTCTTCAAAGATTGCTTTCGCTGCACGGAATTCTTTAAGAGTCGCT
ACCATTGGGAACATGATGCGTAAGTTTCCATGAACAGATGCACGTAACAATGCGCGCATTGTGTACGGAACATT
TCGTACCTAATTCAGACAAGCTGATACGTAGCGCACGATAGCCCCAAGAACGGATNNTTTTCCCTTAA

SEQ ID NO. 399 *Streptococcus sanguis*

CGCATGAGCTGCCTTGATAACATTGTTAATCAAGCGAAGGATAGATGGATTGTAAGGTTGATAGAGGTAAGAGAC
TTGCTCATTTCATCCGGTCAGCCGCCATAGTGTAATCAAGTCGTTAGTACCAATTGAGAAGAAGTCTACTTC
CTTGGCAAATTGATCCGCCAACATAGCTGCTGCTGGGATTTCAATCATGATACCCACTTGGATATTATCTGCTAC
TGCAACGCCTTCAGCTTGCAGCTTAGCTTTTTCTTCGTCATAAACCGCTTTAGCTTTCGGAATTCTGTCAGAAG
GGCCACCATTGGGAACATGATACGCAATTGTCCATGTACAGAAGCACGCAAGAGAGCGCGGATTTGTGTACGGAA
CATAGCATCGCCAGTTTCAGAGATAGAGATACGCAAAGCACGGAAACCAAAGAACGGTNNTTTTTNTCTTTAAAA

SEQ ID NO. 400 *Escherichia coli*

TCCTTTACCTTCTGCATGAGAGCATCAATAACTTGCTTGATCAAGTTCAGTACGGACGGTGACATTGGCTGGTAG
AGATGTGAAATCATATCATTACCACGGTCAACTGCCAGGGTGTACTGCGTTAAATCATTGGTGCCGATACTAAAG
AAATCAACTTCTTTGGCTAAATGACGCGCAATGGTCGCGGCTGCTGGTGTTCACCATTACGCCGATCTCAATT
GACTCGTCAAATGCTTTACCTTCGTCACGCAATTCCTGTTTGTAGATCTCGATCTCTTCTTCAGTGCACGCACT
TCTTCAACAGAGATGATCATCGGGAACATAATGCGCAGCTTACCGAAAGCAGAGGCACGCAGAATCGCACGCACC
TGGTCACGCAGGATTTCTTTACGATCCATGGCGATACGCACTGCACGCCAGCCCAAGAACGGATNNTTTTTTCTT
TAA

SEQ ID NO. 401 *Serratia liquefaciens*

NTGNCTTCTGCATGAGNATGCATCAATAACCTGTTTGATCAGGCCAAGCACTGATGGGGACATCGGGTTATAGAG
ATGAGAAATCAGCTCATTGCCCGCATCTACCGCCAGAGTATACTGGGTTAGATCGTTTGTCCCAATACTAAAGAA
GTGCACTTCTTTGCCAGGTGATGAGCAATCACTGCCGCGGCGGCTGTTTCCACCATTACGCCCACTTCAATGGT
CTCGTCAAAGGCCTTGGATTCTTCACGCAGCTGCGCCTTCAGCGTCTCGATTTACCTTTCAGATCGCGGACTTC
TTCCACGGAAATGATCATCGGGAACATGATGCGCAGTTTGCCGAACGCGGAAGCGCGCAGGATGGCGCGCAGTTG
CGCGTGCAGGATTTCTCTGCGGTCCATGGCGATACGAATCGCGCGCCAGCCNAAGAACGNTTNTTTTTANTTTA

SEQ ID NO. 402 *Proteus mirabilis*

GTGTGATGCATCAATCACCTGTTAATCAGATTAAGTACAGCAGGTGACATTGGATTATATAGATGAGATATCAG
CTCATTTCCACGGTCTACAGCCAGAGTATATTGTGTTAGATCGTTAGTCCCAATACTGAAAAAGTCAACTTCTTT
TGCCATATGGCGAGCCATAACAGCCGCTGCTGGCGTTTCAACCATAACACCGACTTCGATAGATTTCATCAAAAGG
CTTATTTTCTTCACGAAGCTGGCTTTTTCAGTATTTCAAGTTCCGCTTTCAATGCTCGGATCTCTTCAACAGAGAT
AATCATTGGAAACATAATACGTAGTTTACCAAAGCAGACGCTCTTAAGATAGCACGTAATTGTGGATGAAGGAT
CTCTTTGCGGTCAAGACAAATACGAATTGCACGCCAACCAAGAACGGAT

SEQ ID NO. 403 *Proteus vulgaris*

CCTTCTGCATGTGATGCATCAATAACCTGTTTTATCAGGTTAAGTACTGCTGGTGACATTGGATTATACAGATGA
GATATCAGCTCATTTCCACGGTCTACAGCCAGAGTATATTGTGTTAGATCGTTAGTCCCAATACTGAAAAAGTCA

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ACTTCTTTTGCCATGAGACGTGCCATTACGGCCGCCGCAGGGGTTTCAACCATGACACCGACTTCGATAGACTCA
TCGAAAGTTTTGTTTTCTGCACGAAGCTGGCTTTTCAGTATTTCAAGTTCTGCTTTCAATGCGCGAATCTCTTCA
ATAGAGATAATCATTGGAAACATAATGCGTAGTTTACCAAAAGCAGATGCTCTTAAGATAGCACGTAATTGCGAA
TGAAGGATCTCTTTACGGTCAAGACAAATACGAATTGCTCTCCAACCCAAGAACGGTC

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Figure 16 represents marker III (SpyM_0902 & SpyM_0903) sequences amplified from Gram-positive bacteria (SEQ ID NOs 404-412).

SEQ ID NO. 404 *Streptococcus pyogenes*

TTATTAGGCGCCGAAGGGGCAAGGCATACTGCTCAATCTCTCAGGCAAAGGACAGAAGGTAAAATACAAACACC
ATTAAGAACAGTCTTAGTCTTTTTTGTGTTTGCTGTTTTATCATTGCTTCAGAAGTTGTCTCAAAGAAAGAGATA
GCTTTTTTCTTTTGGCGTCTTCGATGACTTTTAGGAGAGAAAGATGATAGCACTCGTTAAATTAATTGATAACCT
TGTTTGGGGACCGCCCTCTTAATTTTATTGGTTGGGACGGGGATTACCTTACCAGTCATTTAGGATTAATTCA
AATCTTAAACTACCAAGAGCCTTTAAACTCATTTTTTCAGATGACGAAGGACATGGAGATATTTATCCTTTGC
TGCTCTTGCAACTGCCCTTGCCGCTACTGTGGAACCTGGTAACATTGTTGGGGTTGCCACTGCTATCAAGTCTGG
TGGTCCTGGAGCGCTCTTTTGGATGTGGGTTGCCGCTTTTTTTGGAATGGCCC

SEQ ID NO. 405 *Streptococcus oralis*

CCGTAAAGGCACCGAAGGGGCAAGGCAGGTAAGTCTCAAACTCTCAGGTAAAAGGACAGAGCTAGGATAGACCG
CTTTTTGGCATTATCTAAGCATTCCAGAGTACATGTATCTTGCACTGACTCTTTCTTTTGGGGTTGAAAGATAG
GAGAAGGACATGTTAGAATTGCTTAAAGCGCTTGATGCTTTTGCTTGGGGGCCTCCCCTCTTGATCTTATTGGTC
GGAACGGGTATCTATTTGACCATCCGACTGGGCCTTTTGCAGGTTACTCGTCTCCCTAAGGCCTTTCAGTTGATC
TTTACCAAGGACAAGGGGCACGGCGATGTGTGAGCTTTGCTGCTCTCTGTACGGCTCTAGCAGCCACAGTTGGT
ACGGGAAATATCATCGGGGTAGCGACAGCCATTAAGGTTGGAGGACCAGGGGCCCTCTTTTGGATGTGGATGGCG
GCCTTCTTTGGAATGGCCC

SEQ ID NO. 406 *Streptococcus faecalis*

GTAAAGGCACCGAAGGGGCAAGGCAGGTAAGTCTCAAACTCTCAGGTAAAAGGACAGAGCTAGGATAGACCGCT
TTTTGGCATTATCTAAGCATTCCAGAGTACATGTATCTTGCACTGACTCTTTCTTTTGGGGTTGAAAGATAGGA
GAAGGACATGTTAGAATTGCTTAAAGCGCTTGATGCTTTTGCTTGGGGGCCTCCCCTCTTGATCTTATTGGTCGG
AACGGGTATCTATTTGACCATCCGACTGGGCCTTTTGCAGGTTACTCGTCTCCCTAAGGCCTTTCAGTTGATCTT
TACCAAGGACAAGGGGCACGGCGATGTGTGAGCTTTGCTGCTCTCTGTACGGCTCTAGCAGCCACAGTTGGTAC
GGGAAATATCATCGGGGTAGCGACAGCCATTAAGGTTGGAGGACCAGGGGCCCTCTTTTGGATGTGGATGGCGGC
CTTCTTTGGAATGGCCC

SEQ ID NO. 407 *Streptococcus agalactiae*

TATAAGTAGCAACATCTTTGTATTGACACCAAGATGTGCTCTAGGCGCCGAAGGGGCAAGAAGAGTAAAACAACT
CCTCCAATCTCTCAGGCAAAGGACAGAAGCTAAAAGCCAATATTAATAATGAGTAGTAAGCTTATTAAGTTTAC
TACTACCTTTATTTGTGCGCTTTTTAGCTAGCATCTTTCAGAAGTTATCTCTTTTAGAGATAACTTTTTTCGTTT
CATTACAGAATCCATAGGTATGTCATGTATCAAAGGAGAACATATGCTAACACTTTTTACTCATATCAATAGCTT
CGTTTGGGGTCCACCTTTACTTGCTTTATTAGTCGGAACAGGTATTTACCTATCATTTGCTTAGGTTTTGTTC
ATTGAGACAACCTTTCTAGAGCTTTCAAATTGATTTTCCGAGAAGATAACGGACAAGGGGATATTTCAAGTTATGC
TGCTCTTGCAACTGCTCTTGCTGCAACGGTAGGGACAGGTAATATCGTTGGTGTGGCTACGGCTATTAATCTGG
AGGACCAGGAGCTTTGTTTTGGATGTGGGTAGCCGCCTTTTTTTGGAATGGCCC

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SEQ ID NO. 408 *Streptococcus pneumoniae*

GTAAAGGCACCGAAGGGGCAAGGCAGGCAACTGCTCAAACCTCTCAGGTAAAAGGACAGAGCTAGGATAGACCGCT
TTTTAGCATTTATCTAAGCATTCCAGAGTACATGTATCTTGCATGTGCTCTTTCTTTTGGGGTTGAAACGATAGG
AGAAGGAAATGTTAGAATTGCTTAAATCAATCGATGCTTTTGCTTGGGGACCGCCCTCTTGATTTTATTGGTTCG
GAACAGGGATTTACCTAACCATGCGGCTAGGACTCTTGCAAGTTTTGCGTCTGCCCAAGGCCTTTCAGCTTATTT
TTATCCAGGATAAGGGACATGGTGATGTATCCAGTTTTACAGCTCTGTGTACAGCCTTGGCATCAACTGTTGGAA
CAGGAAATATCATAGGAGTTGCGACGGCTATCAAGGTTGGTGGACCAGGAGCTCTATTTTGGATGTGGATGGCGG
TTTTCTTTGGAATGGCCC

SEQ ID NO. 409 *Enterococcus durans*

NGNCCGAGGGGCAAGGTCAGNACAACCTGCTCAAACCTCTCAGGTAAAAGGACAGAGCTAGGATAGACCGCTTTT
GCATTTATCTAAGCATTCCAGAGTACATGTATCTTGCATGTGCTCTTTCTTTTGGGGTTGAAACGATAGGAGAAG
GAAATGTTAGAATTGCTTAAATCAATCGATGCTTTTGCTTGGGGACCGCCCTCTTGATTTTATTGGTCGGAACA
GGGATTTACCTAACCATGCGGCTAGGACTCTTGCAAGTTTTGCGTCTGCCCAAGGCCTTTCAGCTTATTTTTATC
CAGGATAAGGGACATGGTGATGTATCCAGTTTTACAGCTCTGTGTACAGCCTTGGCATCAACTGTTGGAACAGGA
AATATCATAGGAGTTGCGACGGCTATCAAGGTTGGTGGACCAGGAGCTCTATTTTGGATGTGGATGGCGGTTTTC
TTTGGAATGGCCC

SEQ ID NO. 410 *Streptococcus anthracis*

CCCCCTCTCGCTTTAAATAGCGTAGAGGAAAACGAGCACC GAAGGAGCAAATCCGCTACTATAGCGGATAATCTC
TCAGGTAAAAGGACAGAGACAAGCGAAAGAAAATGCCGATTTGTATCGGTTTATTTTTCTATCCCTTGTTTCTCC
AGAGACCATTTTCATTTACTTGAAGTGGTTTTTATTTTTTCTAAAAAAGGAGAATAAAGATGGAGACAGTAAGTAA
AGTATTAGAACAAATCAATCACTATGTGTGGGGATTACCAACGTTATTGTTACTCGTTGGTACTGGTATTATTCT
CACAGTGCGTTTTAAAGGTTTACAGTTTAGTAACTATTATACGCTCACAACTAGCTTTTAAAAAATCAGAAGA
TACATCTTCTCTGGAGATATTAGCCACTTCCAAGCGCTTATGACAGCTATGGCGGCAACGATTGGTATGGGAAA
TATAGCTGGTGTTGCAACTGCTGTGACGATCGGTGGACCTGGTGCAATCTTTTGGATGTGGATTACTGCTTTGTT
TGGAATGGCCC

SEQ ID NO. 411 *Bacillus cereus*

CCCCCTCACGCCTATCATATAGTGCAGAGGAAACAGAGCACC GAAGGAGCAAATCCGCTGTATTAGCGGATAATC
TCTCAGGTAAAAGGACAGAGACAAGCGAAAGAAAACGCCGATTTGTATCGGTTTATTTTTCTATTCCCTTGTTTCT
CCAGAGACCATTTTCATTTATGTGAAGTGGTTTTTATTTTTTCTAAAAGGAGAATAAAGATGGAGACAGTAAGTA
AAGTATTAGAACAAATCAATCACTACGTATGGGGATTACCAACCTTATTCCTTTTAGTCGGGACTGGAATCATTC
TCACAGTGCGTCTAAAAGGTTTGCAGTTTAGTAACTGTTATACGCTCACAACTAGCATTTTCGAAAATCAGAAG
ATACATCTTCTTTGGGAGATATTAGTCATTTCCAAGCACTCATGACAGCAATGGCCGCCACCATCGGGATGGGAA
ATATAGCTGGTGTCGCAACAGCTGTTACAATCGGTGGACCGGGGCAATATTTTGGATGTGGATCACTGCCTTGT
TTGGAATGGCCC

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SEQ ID NO. 412 *Streptococcus mutans*

ACTGATAATTGACGGACTTCTGGAGAGACCTACTAGGCGCCGAAGGGGCAAGGCTGTTTGCTCAAACCTCTCAGGC
AAAAGGACAGAAAAGAAAAAAGAATTTTAAATGTTGAAACAATTCTTATCTTCTAACTCTAGAGGTATCGTCAA
GTATTGACAACCTCTTTTTTGATTTCCATTTTCGGTTTATGAGGAGAAAAGTTTATATGTTAACATTTTTTAAAGC
TCTAGACAGCCTTGTCTGGGGTGCTCCCCTATTAGTTCTTTTAGTCGGTACTGGAATTTATTTGAGTACTCGCTT
AAGATTATTGCAGGTGTTGAAACTCCCTTTAGCCTTTAAACTCATCTTTGCCGAGGACAAAGGGGAAGGTGATAT
TTCGAGTTTTGCGGCTTTAGCTACCGCTCTTGCTGCCACTGTTGGAAGTGGAAATATCGTTGGTGTGCGCACTGC
AATCAAAGCTGGCGGTCCGGGAGCACTCTTTTGGATGTGGATAGCAGCTTTTTTTGGTATGGCAACTAAATATGC
CGAAGGTCTTCTGGCTATAAAATACCGTACTAAGGA

Figure 17 represents marker IV (Spy1527, a putative GTP-binding factor plus 160 nt downstream) sequences amplified from Gram-positive bacteria (SEQ ID NOs 413-425).

SEQ ID NO. 413 *Listeria monocytogenes*

GTTAGAAAAAGGAAGTTCTATTGTAGCATCGCCAAAAATCCATCAAACCTTATTAGATAACTACCTGCCTTAAAG
AAAGCGCTCAACATAAAAAAACTTGTTTTTCAGAAAAATAAAATCGTGCCAAATCGGCTCAGCTATGCTATAATAG
GTAAGTTGATTTAAACGAGACGATAGCGACGGAGGAAAAATAAATCTATTTTCCTCTTTCTTTTGGCTAATCTTCA
CGATAAATGTTTGGATTTTAAATTTAGGAGGAAACAAGATTGAATTTAAGAAATGATATTCGTAATGTAGCAATT
ATTGCCCACGTTGACCATGGTAAAACAACCTCTAGTAGACCAATTATTACGCCAGTCAGGCACATTCCGCGACAAT
GAAACAGTTGCAGAACGCGCAATGGACAACAATGATTTAGAAAGAGAACGCGGTATTACAATTTTAGCGAAAAAT
ACAGCGATTAAAGTATGAAGATACACGTGTAAACATCATGGATACACCTGGACACGCCGATTTCCGGTGGAGAAGTA
GAACGTATCATGAAAATGGTTGATGGTGTTCTTTTAGTAGTGGACGCGTATGAAGGTACGATGCCTCAAACACGT
TTTGTTACTAAAAAAGCACTAGAACAAAACCTAACTCCAATCGTAGTAGTAAACAAAATTGACCGTGACTTTGCT
CGCCCAGAAGAAGTTGTTGATGAAGTATTAGAATTATTCATCGAACTAGGCGCAAACGACGATCAATTAGAATTC
CCAGTTGTTTATGCTTCTGCAATCAACGGAACCTCAAGCTATGATTCCGATCCAGCAGAACAAAAAGAAACAATG
AAACCACTTTTAGACACAATTATCGAACATATCCCGGCTCCAGTTGATAATAGCGACGAACCATTACAATTCCAA
GTATCATTACTTGATTATAATGACTATGTTGGTCGTATCGGTATTGGCCGCGTATTCCGTGGAACAATGCACGTG
GGACAAACAGTTGCTTTAATTAACTTGATGGCACAGTAAACAATTCGCTGTAACGAAAATGTTCCGGTTTCTTC
GGACTAAAACGTGACGAAATTAAAGAAGCAAAAGCTGGTGATTTAGTAGCATTAGCAGGTATGGAAGACATCTTC
GTTGGTGAAACAGTAACACCATTTGACCACCAAGAAGCACTTCCGTTATTACGTATTGATGAGCCAACCTTGCAA
ATGACTTTCGTAACAAATAACAGTCCTTTTCGCTGGTCGTGAAGGTAAACACGTAACAAGCCGTAAATTTGAAGAA
CGTTTACTTGACAGAGCTTCAAACGGACGTATCTTTACGCGTAGAGCCAACAGCTTCCCCTGACGCTTGGGTAGTT
TCTGGTCGTGGTGAGCTTCATTTATCCATTTTGATCGAAACAATGCGTCGCGAAGGTTATGAATTACAAGTTTCT
AAACCAGAAAGTAATCATCCGTGAAATTGATGGCGTGAAATGTGAACCAGTAGAAGATGTTCAAATTGATACTCCA
GAAGAATTCATGGGTTCCGTTATTGAATCTATCAGCCAACGTAAAGGCGAAATGAAAAACATGATTAACGATGGC
AACGGACAAGTTTCGTTTACAATTCATGGTTCCAGCTCGTGCTTAATCGGTTATACAACCTGATTTCTTTCAATG
ACTCGTGTTTATGGTATTATCAACCACACA

SEQ ID NO. 414 *Listeria innocua*

ATAAAAAAACTCATTTTCAGAAAATAAAAAATAGTGCTAAATCCGCTTAGCTATGCTATAATAGGTAAGTTGATTT
AAACGAGACGATAGCGACGGAGGAAAATAAATCTATTTTCCTCTTTCTTTTGGCTAATCTTCACGATAAATGTTT
GGATTTTAAATTTAGGAGGAAACAAGATTGAATTTAAGAAACGATATTCGTAATGTAGCAATTATTGCCCACGTT
GACCATGGTAAACTACACTAGTAGACCAATTACTACGCCAATCAGGTACTTCCGCGACAATGAAACAGTTGCA
GAACGTGCAATGGACAACAATGATTTAGAAAGAGAACGCGGTATTACAATTTTAGCGAAAAATACAGCAATTAAG
TATGAAGATACACGCGTAAACATCATGGATACACCTGGACACGCCGATTTTGGTGGAGAAGTAGAACGTATCATG
AAAATGGTTGATGGTGTTCTTTTAGTAGTGGACGCGTATGAAGGTACTATGCCTCAAACACGTTTTGTACTAAAA
AAAGCACTAGAACAAAACCTAACTCCAATCGTAGTAGTAAACAAAATTGACCGTGACTTTTGCTCGCCAGAAGAA
GTTGTTGATGAAGTACTAGAATTATTCATCGAACTAGGTGCGAACGACGATCAATTAGAATTCCCAGTTGTTTAT
GCTTCTGCAATTAACGGAACCTCAAGCTTTGAATCCGACCCAGCAGAACAAAAAGAAACAATGAAACCACTTTTA

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GACACTATTATTGAACATATTCCAGCTCCAGTTGATAACAGCGACGAGCCATTACAATTCCAAGTTTCTTTACTT
GATTATAATGACTATGTTGGTCGTATTGGTATTGGCCGCGTTTTCCGTGGAACAATGCACGTAGGACAAACAGTT
GCCTTAATTAAACTAGACGGCACAGTAAAACAATTCCGTGTAACGAAAATGTTTCGGTTTCTTCGGACTAAAACGT
GACGAAATTAAAGAAGCAAAAGCGGGTGACTTAGTAGCACTTGCAAGGAATGGAAGACATCTTCGTCCGTGAAACA
GTAACACCATTTGACCACCAAGAAGCACTTCCACTTTTACGTATTGATGAGCCAACCTTGCAAATGACTTTTGTGTA
ACAAATAACAGTCCTTTTCGCAGGCCGTGAAGGTAAACACGTAACAAGCCGTAAAATTGAAGAACGCTTACTTGCA
GAACTTCAAACGGATGTATCTTTACGCGTTGAACCAACAGCTTCTCCAGACGCATGGGTAGTATCTGGTCGTGGT
GAGCTTCACTTGTCTATCTTAATTGAAACGATGCGTCGTGAAGGTTATGAGTTACAAGTTTCTAAACCAGAAGTA
ATCATCCGTGAAATCGATGGCGTGAAATGTGAACAGTAGAAGACGTTCAAATTGATACTCCAGAAGAATTTCATG
GGTTCAGTTATTGAATCTATCAGCCAACGTAAAGGCGAAATGAAAAACATGATTAACGACGGCAATGGCCAAGTT
CGTTTACAATTCATGGTTCCAGCTCGTGGATTAATCGGTTATACAACGATTTCCTTTCAATGACACGTGGTTAT
GGTATTATCAACCATACATTCGATAGCTACCAACCAATCCAAAA

SEQ ID NO. 415 *Bacillus cereus*

TTACTTTTCAAAAAGTAAGAATACAACCTATATTTTCATTCTTGCTTTTATTTTAATTGCTATTGTATCCCCTTCG
CTCTTATAATAGAGAAGGATTAAAAAGACATTAGGAGTTGGACATGTTGAAAAACGACAAGATTTACGTAATAT
AGCAATTATTGCCCACGTTGACCATGGTAAAACAACACTTGTGACCAGTTATTACGTCAAGCGGGGACTTTCCG
TGCGAACGAACACGTTGAAGAACGCGCAATGGATTCAAATGATCTAGAAAGAGAACGCGGTATTACAATTTTAGC
GAAAAATACAGCGATTCACTATGAAGATAAAAGAATTAACATTTTAGATACACCTGGTCACGCTGACTTCGGTGG
AGAAGTAGAACGTATCATGAAAATGGTTGATGGTGTCTTACTTGTGTTGATGCATATGAAGGTTGTATGCCACA
AACACGATTTGTTTTAAAGAAAAGCTCTTGAGCAAACTTAACCTCAATCGTAGTTGTAAACAAAATTGACCGTGA
CTTCGCTCGTCCAGATGAAGTAGTTGATGAAGTAATCGACTTATTCATTGAGCTTGGTGCAAACGAAGATCAATT
AGAGTTCCAGTTGTATTTGCATCAGCAATGAACGGAACAGCAAGCTTAGATTCAAATCCAGCAAATCAAGAAGA
GAATATGAAATCATTATTCGATACAATTATCGAACATATTCCAGCACCAATTGATAACAGCGAAGAGCCACTTCA
ATTCCAAGTAGCACTTCTTGATTACAACGACTACGTTGGACGTATTGGAGTTGGTCGCGTATTCCGCGGTACAAT
GAAGGTTGGACAACAAGTTGCTTTAATGAAAGTAGACGGAAGCGTGAAGCAATTCCGCGTAACGAAATTATTCGG
TTACATGGGATTAAACGTCAAGAAAATTGAAGAAGCAAAAGCAGGGGACTTAGTAGCCGTTTCTGGTATGGAAGA
CATTACGTAGGTGAAACAGTATGTCCAGTTGAACATCAAGATGCGTTACCATTATTACGTATTGATGAGCCAAC
ACTACAAATGACGTTTCCTTGTAATAACAGCCCATTTCGAGGTCGTGAAGGTAAATACATTACATCTCGTAAAAT
TGAAGAGCGTCTTCGTTCACAATTAGAAACAGATGTAAGTTTACGTGTAGATAATACAGATTCTCCTGATGCGTG
GATCGTATCTGGACGTGGGGAACCTACATTTATCTATCTTAATTGAAAACATGCGTCGTGAAGGTTATGAATTACA
AGTATCTAAGCCAGAAGTAATCATTAAGAAGTTGATGGCGTAAGATGTGAGCCTGTAGAGCGGTACAAATCGA
TGTACCTGAAGAATACACTGGTTCTATTAT

SEQ ID NO. 416 *Bacillus anthracis*

CTATATTTTCATTCTTGATTTTATTTTAATTGCTATTGTATCCCCTTCGCTCTTATAATAGAGAAGGATTAAAAA
GACATTAGGAGTTGGACATGTTGAAAAAACGACAAGATTTACGTAATATAGCAATTATTGCCCACGTTGACCATG
GTAAAACAACACTTGTGACCAGTTATTACGTCAAGCGGGGACTTTCCGTGCGAACGAACACGTTGAAGAACGCG
CAATGGATTCAAATGATCTAGAAAAGAGAACGCGGTATTACAATTTTAGCGAAAAATACTGCGATTCACTATGAAG
ATAAAAGAATTAACATTTTAGATACACCAGGTCACGCTGACTTCGGTGGAGAAGTAGAACGTATTATGAAAATGG
TTGATGGTGTATTACTTGTGTTGATGCATATGAAGGTTGTATGCCACAAACACGATTTGTTTTAAAGAAAGCTC

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TTGAGCAAACTTAACTCCAATCGTAGTTGTAAATAAAATTGACCGTGACTTCGCTCGTCCTGATGAAGTAGTTG
ATGAAGTAATCGACTTATTCATCGAACTTGGTGCAAACGAAGATCAATTAGAGTTCCCAGTTGTATTTGCATCAG
CAATGAACGGAACAGCAAGCTTAGATTCAAACCCAGCAAATCAAGAAGAGAATATGAAATCATTATTTGATACAA
TTATTGAACATATTCCTGCACCAATTGATAACAGCGAAGAGCCACTTCAATTCCAAGTAGCACTTCTTGATTACA
ACGACTATGTTGGACGTATCGGGGTTGGACGCGTATTCCGCGGTACAATGAAGGTTGGACAACAAGTTGCTTTAA
TGAAAGTAGACGGAAGTGTAACAATTCCGCGTAACGAACTATTTGGTTATATGGGATTAACCGTCAAGAAA
TTGAAGAAGCAAAAGCTGGAGACTTAGTAGCTGTTTCTGGTATGGAAGACATTAACGTAGGTGAAACAGTATGTC
CAGTTGAACATCAAGATGCGTTACCATTATTACGTATTGATGAGCCAACACTACAAATGACATTCCTTGTAATA
ACAGCCCATTTCAGGTCGTGAAGGTAAATACATTACATCTCGTAAAATTGAAGAGCGTCTTCGTTCACAATTAG
AAACAGATGTAAGTTTACGCGTAGATAATACAGAATCTCCTGATGCGTGATCGTATCTGGACGTGGGGAACCTAC
ATTTATCTATCTTAATCGAAAACATGCGTCGTGAAGGTTATGAACTACAAGTATCTAAACCAGAAGTAATCATT
AAGAAGTTGATGGCGTAAGATGTGAGCCTGTAGAGCGTGTGCAAATTGATGTACCTGAAGAATACACTGGTTCTA
TTATGGAATCTATGGGTGCACGTAAAGGTGAAATGTTAGATATGGTGAATAACGGAAACGGTCAAGTTCGCCTTA
CTTTCATGGTTCAGCACGTGGTTTAATTGGTTACACAACAGAATTCTTAACATTAACTCGTGGTTACGGTATTT
TAAACCATACATTCGATTGCTACCAACCAGTACACGCTGGACAAGTTGGTGGACGTGTCAGGTGTTCTAGTTT
CACTTGAAACAGGAAAAGCATCACAATACGGTATTATGCAAGTTGAAGACCGTGGTGTAATCTTCGTTGAACCAG
GTACAGAAGTATATGCTGGTATGA
TTGTTG

SEQ ID NO. 417 *Staphylococcus aureus*

TCAATTATATGATATAATAAAAAAGTTGTAATTAAAAGTGGGATTTTACTTAAGAAAGAAGGAAACTATTTATAT
GACTAATAAAAGAGAAGATGTCCGCAATATAGCAATTATTGCTCACGTTGACCATGGTAAAACAACCTTTAGTAGA
TGAGTTGTTAAAACAATCTGGTATATTCAGAGAAAATGAACATGTCGATGAACGTGCAATGGACTCTAACGATAT
CGAAAGAGAGCGTGGAATTACGATTCTAGCCAAAAATACGGCTGTTGATTATAAAGGTACACGTATTAATATTTT
GGATACACCAGGACATGCAGACTTTGGTGGAGAAGTAGAACGTATTATGAAAATGGTTGATGGGGTTGTCTTAGT
AGTAGATGCGTATGAAGGTACAATGCCTCAAACACGTTTTGTACTTAAAAAAGCGCTAGAACAAAACCTGAAACC
TGTTGTTGTTGTTAATAAAATTGATAAACCATCAGCACGTCCAGAGGGTGTGTTAGATGAAGTTTTAGATTTATT
TATTGAATTAGAAGCAAACGATGAACAATTAGAATTCCTGTTGTTTATGCTTCAGCAGTAAATGGAACAGCTAG
CTTAGATCCTGAAAAACAAGATGATAATTTACAATCATTATATGAAACAATTATTGATTATGTACCAGCTCCAAT
TGATAACAGTGATGAGCCATTACAATTCGAAGTAGCATTGTTGGACTACAATGATTATGTTGGACGTATTGGTAT
TGGTCGTGTATTCAGAGGTAATGCGTGTGCGAGATAATGTATCACTAATTAAATTAGACGGTACAGTGAAAAA
CTTCCGTGTAACATAAATCTTTGGTTACTTTGGATTAAAACGTTTAGAAATTGAAGAAGCACAAGCTGGAGATTT
AATTGCTGTTTCAGGTATGGAAGACATTAATGTTGGTGAACTGTAACACCACATGACCATCAAGAAGCATTGCC
AGTTCTACGTATTGATGAGCCTACTCTTGAAATGACATTTAAAGTTAACAATTCTCCATTTGCTGGCCGTGAAGG
TGACTTTGTAACAGCACGTCAAATTCAGAACGTTTAAATCAACAATTAGAAACAGATGTATCTTTGAAAGTTTC
TAACACAGATTCTCCAGATACATGGGTAGTTGCTGGTCGCGGTGAATTGCATTTATCAATCCTTATTGAAAATAT
GCGTCGTGAAGGTTATGAATTACAAGTTTCAAACCAACAAGTAATTATTAAGAAATAGATGGTGTAATG

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SEQ ID NO. 418 *Staphylococcus epidermidis*

ACCCACCTTTTACTTATCTTTTCAATAATATATGATATAATAAACAGTTGCAATTAAAAGTGGGAGTATACAC
AAGAAAGGAATTTATAAAATGACTAATTTAAGAGAAGATGTTTCGTAATATAGCGATTATTGCGCATGTCGACCAT
GGTAAACAACATTAGTAGACCAGTTGCTTAAACAATCAGGTATATTTTCGTGAAAACGAACATGTCGACGAGCGT
GCAATGGACTCTAATGATTTAGAAAGAGAACGTGGTATTACGATTCTTGCTAAGAATACAGCGATAGATTATAAA
GGAACGCGTATCAATATATTAGACACACCTGGCCACGCCGATTTTGGTGGTGAAGTTGAACGTATCATGAAAATG
GTTGACGGTGTCTACTAGTGGTTGACGCATATGAAGGTACAATGCCTCAAACCTCGTTTTGTTCTTAAAAAAGCT
TTAGAACAAAACCTTAAAACCGGTTGTAGTTGTGAATAAAATTGATAAACAGCTGCTAGACCTGAGGGAGTTGTA
GATGAAGTATTAGACTTATTCATTGAATTGGAAGCGAATGATGAGCAATTAGACTTCCCAGTTGTTTATGCTTCA
GCTGTGAATGGAACAGCAAGTTTAGACTCTGAAAAGCAAGACGAAAATATGCAATCCCTATACGAGACGATTATT
GACTATGTACCGGCACCACTAGATAATTCAGATGAACCATTACAATTCCAAATTGCTTTACTAGATTATAATGAT
TATGTAGGTCGTATAGGCGTTGGACGTGTGTTTCAGAGGTAAAATGCGTGTAGGTGATAATGTATCACTAATTAAA
TTAGATGGTACAGTTAAGAAGTTTCGTGTGACGAAAATATTTGGTTACTTTGGTCTTAAACGTGAAGAAATTGAA
GAAGCACAAGCAGGAGACTTAATAGCTGTTTCAGGTATGGAAGATATTAACGTTGGTGAAACAGTTACACCACAT
GATCATCGTGACCCATTACCGGTGTTACGTATTGATGAACCAACCCTAGAAAATGACTTTTAAAGTAAATAACTCT
CCGTTTGGTGGACGTGAAGGTGATTATGTAACAGCTCGACAAATTCAGAAAGATTAGATCAACAACCTGAAACA
GATGTTTCTTTAAAGTTACACCTACTGATCAACCAGATTTCATGGGTTGTTGCTGGTGGTGAACCTACACTTG
TCTATTCTTATTGAAAACATGAGACGTGAAGGCTTTGAATTACAGGTTTCTAAACCTCAAGTTATTTTAAAGAGAA
ATCGATGGTGTGTTAAGTGAACCATTTGAGCGTGTACAATGTGAA

SEQ ID NO. 419 *Bacillus subtilis*

GAAAAACGTGACGCTTTTAAAGAGGATGTGTGATATAATATGAAAGTTATCTAATTTTTTTTAGGAGATGAAAAAG
TGAAACTTCGAAATGATCTTCGCAACATCGCGATTATTGCCACGTTGACCATGGGAAAACGACTCTAGTCGATC
AGCTTTTACATCAGGCTGGTACGTTCCGTGCCAACGAACAGGTTGCTGAACGCGCAATGGACTCTAATGATCTTG
AACGCGAACGCGGCATTACAATATTGGCGAAAAATACTGCGATTAACTATAAAGATACACGTATCAATATTTTGG
ACCCCCCTGGACATGCAGACTTTGGGGGAGAAGTAGAACGGATTATGAAAATGGTTGACGGCGTAGTGCTTGTCG
TTGACGCATATGAAGGCTGTATGCCTCAAACCTCGTTTTGTTCTGAAAAAAGCTCTTGAGCAAAACCTGAACCCTG
TTGTTGTTGTAAACAAAATTGACCGTGACTTTGCTCGTCCAGAGGAAGTTATCGATGAAGTTCTGGATCTGTTCA
TTGAGCTTGATGCCAATGAAGAGCAGCTCGAGTTCCCAGTGGTATATGCTTCCGCGATTAATGGAACAGCGAGTC
TTGATCCGAAACAACAGGATGAAAACATGGAAGCTTTATATGAAACCATTATTAAGCATGTTCCGGCACCTGTTG
ATAATGCAGAGGAGCCGCTTCAATTCCAAGTTGCCCTTCTTGACTACAACGACTATGTAGGCCGTATCGGAATCG
GACGCGTATTCCGCGGCACAATGAAAGTCGGACAGCAGGTTTCTCTTATGAAGCTTGACGGAACGGCAAAGTCAT
TCCGTGTTACAAAGATTTTTGGTTTCCAAGGCTTAAAGCGTGTGGAAATTGAAGAAGCAAAAGCGGGAGACCTCG
TTGCGGTTTCCGGGATGGAAGATATCAACGTTGGTGAAACGGTATGTCCTGTAGACCATCAAGATCCGCTTCCGG
TCCTTCGCATTGATGAGCCGACACTTCAAATGACATTTGTCTGTAATAACAGTCCGTTTGCAGGCCGTGAAGGCA
AATATGTAACGGCCCGCAAAATCGAAGAGCGTCTTCAATCACAGCTTCAGACGGATGTGAGCTTGCGTGTTGAGC
CAACAGCTTCTCCTGATGCTTGGGTTGTTTCAGGACGCGGTGAGCTGCACCTGTCAATTTTAATTGAAAATATGC
GTCGTGAGGGCTATGAGCTTCAAGTGTCAAACCTGAAGTTATTATCAAAGAAATCGACGGCGTACGCTGTGAGC
CTGTTGAACGTGTGCAAATTGATGTTTCTGAAGAGCATACTGGCT

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SEQ ID NO. 420 *Streptococcus mutans*

GGAATGGAAGTAAAGAGAAGAATTAGTTCTTTTTTGAGATAATGACAGGGATTAGTATGAGCTGTTGTCTTT
TGTTTTTGCAATACTGGTTGATTGAGGACTTATTTTATAAAATTTGGAGATACCAAGACTGCGACTTTGCTATCT
TGGTTTTCTTTTATATTTTAAAACATTTACATATCTCTCCTGAGTTTTTCCCTAATTTTTATGGTATAATAGAT
AAGTTGAAATAAATTAATGTAAATGTAAGAGGAATTATGACAAATTTTAGAGAAGATATTAGAAATGTTGCTAT
CATTGCCACGTTGACCATGGGAAAACAACCCTTGTTGATGAGCTCTTAAAACAATCGCATACACTTGATGAGCA
TAAAAAATTAGAAGAACGTGCGATGGACTCTAATGATCTTGAAAAAGAGCGTGGGATTACTATTCTTGCAAAAA
TACTGCTGTTGCCTACAATGGTGTACGTATTAACATTATGGACACACCAGGACATGCGGATTTTGGTGGAGAAGT
AGAGCGTATCATGAAATGGTTGATGGGGTGTCTTGTGTTGATGCTTATGAAGGTACCATGCCGCAACACG
TTTTGTTTTGAAAAAGCTTTGGAACAAAACCTGGTTCCAATCGTGGTGGTGAATAAGATTGACAAGCCATCAGC
TCGTCCGGCAGAAGTTGTTGATGAAGTTCTTGAACCTTTTCATTGAACCTTGGAGCAGATGATGACCAGTTAGAGTT
TCCAGTCGTTTACGCTTCGGCGATTAATGGAACCTTCTTCATTATCAGATGAACCAGCGGATCAAGAACATACAAT
GGCACCCGTTTTTGATAC TATTATTGAGCATATTCCAGCACCGATCGATAATTCAGATCAGCCACTTCAATTTCA
AGTGCTCTCCTTGATTATAACGACTTTGTTGGACGTATCGGTATTGGGCGAGTCTTCCGTGGTTCTGTTAAAGT
CGGGGATCAAGTGACACTTTCTAACTTGATGGTACAACAAAGAATTTTCGTGTTACAAACTTTTCGGTTTCTT
CGGTTTGGAACGTCGTGAGATTAAGGAAGCTAAGGCTGGCGATTTGATTGCTGTTTCAGGTATGGAAGATATCTT
TGTTGGTGAAACGATTACACCAACTGATGCTGTAGAACCCTTCTTATTCTTCACATTGATGAGCCAACCTCTGCA
AATGACCTTTTTAGCTAACAATTTCCCTTTTGCAGGCCGTGAAGGTAAATTTGTAACCTCGCGTAAGGTAGAAGA
GCGTTTGTGGCAGAATTGCAAACAGATGTTTCCCTTCGTGTAGAAGCCACTGACTCACCAGATAAATGGACGGT
TTCAGGTGCTGGGGAGTTACATCTGTCAATCCTTATTGAAACCATGCGCCGTGAAGGATATGAGCTGCAAGTATC
GCGTCCAGAAGTTATTATCAAAGAAATTGATGGCATCAAATGTGAGCCATTTGAACGCGTGCAAATTGACACACC
GGAAGAATACCAAGGTGCTGTTATCCAGTCCCTTTCAGAACGTAAAGGTGAAATGCTTGA

SEQ ID NO. 421 *Streptococcus pneumoniae*

AAGCGGAGTGAAAACATTTACACTTGCTTGAGTTATGTTATTTATTTGAAATTATGGTATAATCGTTTCAAGTTAGA
AAATAAATTTTGAATATTATAGAGGAAATCATGACAAAATTAAGAGAAGATATCCGTAACATTGCGATTATCGCC
CACGTTGACCACGGTAAAACAACCCTGGTTGACGAATTATTGAAACAATCAGAAACGCTTGATGCACGTAAGTAA
TTGGCAGAGCGTGCTATGGACTCAAACGATATCGAAAAAGAGCGTGGAATCACCATCCTTGCTAAAAATACTGCC
GTTGCTTACAACGGAACCTCGTATCAACATTATGGACACACCAGGACACGCGGACTTCGGTGGAGAAGTTGAGCGT
ATCATGAAAATGGTTGACGGTGTGTCTTGGTCGTAGATGCCTATGAAGGAACCATGCCACAACTCGTTTTCGTA
TTGAAAAAAGCCTTGGAACAAGACCTTGTCCCAATCGTGGTTGTTAACAAAATCGATAAGCCATCAGCTCGTCCA
GCAGAAGTAGTGGAATGAAGTCTTGGAACCTTTTCATCGAGCTTGGTGCAGATGACGACCAGCTTGATTTCCCAGTG
GTTTATGCTTCAGCGATCAACGGAACCTTCTTCATTGTGATGATCCAGCTGACCAAGAAGCGACTATGGCACCA
ATCTTTGACACGATTATCGACCATATCCCAGCTCCAGTAGATAACTCAGATGAGCCTTTGCAGTTCCAAGTGTCA
CTTTTGGACTACAATGACTTCGTTGGACGTATCGGTATCGGTGCTGTCTTCCGTGGTACAGTTAAGGTTGGGGAC
CAAGTTACCCCTTTCTAACTTGACGGTACAACATAAACTTCCGTGTTACAAAACCTTTCGGTTTTCTTTGGTTTG
GAACGTCGTGAAATCCAAGAAGCCAAAGCGGGTGACTTGATTGCCGTTTCAGGTATGGAAGACATCTTTGTGCGGT
GAAACCATCACTCCGACAGATGCAGTAGAAGCTCTTCCAATCTACACATCGATGAGCCAACCTTTCAAATGACT
TTCTTGGTCAACAACCTCACCATTGCTGGTAAAGAAGGTAAATGGGTAACCTTCTCGTAAGGTGGAAGAAGCCTTG

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CAGGCAGAATTGCAAACAGACGTTTCCCTTCGTGTTGACCCAAC TGATTACCAGATAAATGGACTGTTTCAGGA
CGTGGAGAATTGCACTTGTCAATCCTTATCGAAACAATGCGTCGTGAGGGCTATGAACT

SEQ ID NO. 422 *Streptococcus agalactiae*

AGAAATGAATTAAATTGAAAAAGTAGAAAAATAATGGCATAAATAATGAAATGATGAAAAGTTTCTTATCACA
AATAGGCAGTTAATATGAAAACATTTACACTTGTGTAAATTCTGTTTTTTAAGAAAAATTGTGTTATAATTCATA
AGTTAACAGAATTACATTATAAAATAGAGGAAAACATGACAAATTTAAGAACAGATATCCGTAACGTTGCGATCA
TTGCCACGTTGACCACGGTAAAACAACCTCTCGTTGATGAATTATTAAAACAATCACATACTCTTGATGAGCGTA
AAGAGCTTGAAGAACGTGCAATGGATTCAAATGATATCGAAAAAGAACGTGGTATCACCATTCTTGCAAAAAATA
CAGCCGTAGCATACAACGATGTTTCGTATCAATATTATGGACACACCTGGTCACGCGGACTTTGGTGGTGAAGTTG
AGCGTATTATGAAAATGGTTGATGGTGTGTTTTAGTCGTTGATGCCTACGAAGGAACAATGCCACAAACACGTT
TTGTTTTGAAGAAAGCTCTTGAACAAAACCTTAATCCAATCGTTGTTGTAAATAAAATTGATAAGCCGTCAGCTC
GTCCATCAGAGGTTGTTGATGAAGTTCTTGAACACTATTTATTGAGCTCGGTGCTGATGATGATCAACTAGATTTC
CTGTTGTTTATGCTTCAGCTATCAATGGAACATCTTCAATGTCAGATGATCCTTCAGATCAAGAAAAACAATGG
CACCGATTTTTGATACTATCATTGATCACATTCCAGCCCCAGTTGACAACCTCGGAAGAACCACTTCAATTCCAAG
TTTCTCTTCTTGATTACAATGATTTTGTAGGACGTATTGGTATTGGACGTGTTTTCCGCGGGACTGTCAAAGTTG
GAGATCAAGTTACTCTTTCAAACCTTGATGGTACAACATAAAACCTTCCGCGTAACAAAACCTTTTTGGTTTCTTTG
GACTTGAACGTAAAGAAATCCAAGAGGCTAAAGCGGGTGATTTAATCGCTGTTTCTGGTATGGAAGATATCTTCG
TTGGTGAGACAGTAACCTCCGACAGATGCTATTGAACCACTACCAGTTTTACGTATTGACGAGCCAACACTTCAAA
TGACTTTCTTGGTGAATAATTCACCATTTGCAGGTCGGAAGGTAAATGGATTACGTCACGTAAGGTTGAAGAAC
GTCTTTTAGCAGAATTACAAACAGACGTTTCTTTACGTGTTGACCCAACAGATTCGCCAGATAAATGGACGGTTT
CAGGGCGTGAGAAATTACATTTATCTATCCTTATTGAAACAATGCGTCGTGAGGGATATGAACTTCAAGTATCAC
GTCCAGAAGTTATCATCAAAGAAATTGATGGTGTTCATGCGAGCCGTTTGAGCGTGTTCAAATTGATACTCCAG
AAGAATATCAGGGTGCTATTATCCAAAGTTTGTGAGAGCGTAAAGGTGATATGCTTGATATGCAGATGGTTGGTA
ATGGTCAAACGCGTTTGATTTTCTTGATTCTTGCACGTGGTTTGATTGGTTATTCAACAGAGTTTCTTTCAATGA
CACGTGGATATGGTATCATGAATCATACTTTTGACCAGTATCTACCGGTTGTTCAAGGAGAAATTGGTGGTCGTC
ATCGTGGTGCCCTTGTTTCTATTGAAAATGGTAAAGCAACTACATATTCAATTATGCGTATTGAAGAACGTGGGA
CTATCTTTGTAAATCCAGGTATAGAAGTTTATGAAGGAATGATTGTTGGTGAGAATTCTCGTGATAATGACCTCG
GAGTCAATATTACAACCTGCTAAACAAATGACAAATGTCCGTTTCAGCAACTAAAGATCAAA

SEQ ID NO. 423 *Streptococcus pyogenes*

GTCTTAAAGACGGTATTGATTATTGGGATGGCAAAGTTAAACAAACAACCTAGTTAAGAGTAACGTGGAGTTAA
GGGAATAAAGGCAGTCACTGTCTCAAAAACCTTAATTCCTTTTTTTGCTGTATCCAGACTTGCTGAAAGTCTGA
AAATATTTACAATTGATTAAAACAGTTTTTTTAAACATTTTGTGTTATACTTATCTAGTTAAAATATATTTACT
TAGAGGAACAAATGACTAACTTAAGAAACGATATCCGTAACGTAGCGATTATTGCCACGTTGACCACGGAAAAA
CAACACTTGTAGATGAATTATTAAAACAATCCCATACTCTTGATGAGCGTAAAGAGCTTCAAGAGCGTGCCATGG
ATTCCAATGACCTTGAAAAAGAACGTGGGATTACAATCCTTGCGAAAAATACGGCAGTAGCCTATAACGATGTTT
GTATTAACATCATGGATACCCAGGACACGCGGACTTCGGTGGTGAAGTTGAACGTATCATGAAAATGGTTGACG
GGGTTGTTCTTGTTGTGGATGCCTACGAAGGAACAATGCCCCAGACGCGTTTCGTATTGAAAAAAGCACTTGAGC
AAAACCTTATCCCGATCGTTGTGGTGAACAAGATTGACAAACCTTCAGCTCGTCCAGCAGAAGTTGTAGATGAAG

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TGCTTGAATTATTTCATCGAACTTGGTGCCGATGATGAGCAATTGGAATTCCTCAGTTGTTTACGCATCAGCTATTA
ATGGAACATCATCATTATCAGATGACCCCTGCTGACCAAGAGCATACTATGGCACCGATCTTTGATACGATTATTG
ATCATATTCCAGCGCCAGTTGATAATTCAGATGAGCCTTTGCAATTCGAAGTGTCACTTTTGGACTACAACGATT
TCGTAGGTCGTATCGGTATCGGTTCGTGTTTCCGTGGTACTGTTAAAGTGGGTGACCAAGTAACTCTTTCAAAC
TTGATGGTACCCTAAAACTTCCGTGTTACAAAACTGTTTGGTTTCTTCGGTTTGGAACGTCGTGAAATTCAAG
AAGCTAAAGCAGGTGACTTGATTGCTGTTTCAGGTATGGAAGATATCTTTGTTGGAGAAACCATACACCAACTG
ACTGTGTGGAAGCTCTGCCAATTCTTCGTATTGATGAGCCAACACTTCAGATGACTTTCTTGGTCAATAACTCTC
CTTTTGCAGGTCGTGAAGGTAAATGGATCACGTCACGTAAGGTTGAAGAACGTCTTTTAGCAGAATTGCAAACAG
ACGTGTCACCTTCGTGTTGACCCAACAGATTCGCCAGATAAATGGACGGTTTCAGGGCGTGGAGAATTGCATTTAT
CTATCCTCATTGAAACCATGCGCCGTGAAGGCTATGAACTTCAAGTATCACGTCCAGAAGTTATCATCAAAGAAA
TTGATGGTGTCAAATGTGAACCGTTTGAGCGTGTTCAAATTGATACACCAGAAGAATATCAGGGTGCAATCATCC

SEQ ID NO. 424 *Enterococcus faecalis*

CATCACGCAACGGAAATCGGACAAGCAAGCATGGGCGTGCGTATTAGCGGTTGTGCAGGTTTGGAAATTATTGCT
ATGTTAAAAGGCAACCATCATGGCTATTTATCTAATCTAAGTCCTTGGGATTATGCAGCAGGCTTAGTACTTTG
GAAGAATTTGGGTTTAAATACTCTGGTATTACAGGAAAACCATTAACCTTTTGCGGGTCGTGAATACTTTATTGCA
GCAACTCCTGAAACCTATGATGAAGTATTTACCCGATATTTAAATGAATCGGAATAATCAAAGAAGAGCGTTGCT
GAAAGGTAAGGCTCTTCCTCTTTTAAAAGAGAAAAATTTGTAAAAAAATGTCCTTGTTTTTCAGAAAAAGCCGAAT
AATTTCTAAAACCTTTCATTATTTTTGCAGGCGAAAGCCTTTTTTTAATGAAAAAGTTTGCTATAATAAGCAGTC
GGCTTTTATGGACTTAAGTAACATAAGCGTATATAGATAAGGAGCAATTAAATTGAAATACAGAGATGATATTCG
TAACGTGGCAATTATCGCCACGTTGACCATGGTAAACAACCTTAGTAGATGAACTTTTAAAACAATCTGACAC
TTTAGATGGACACACACAATTACAAGAACGTGCAATGGATTCCAATGCACCTGAAAGTGAACGTGGAATTACTAT
CTTAGCAAAAAATACAGCCGTAGATTATAACGGTACACGTATCAACATTCCTAGATACACCAGGACACGCGGACTT
CGGTGGTGAAGTAGAACGTATCATGAAAATGGTAGACGGTGTTGTTTTAGTTGTTCGATGCGTATGAAGGAACAAT
GCCTCAAAACACGTTTCGTATTGAAAAAGCATTAGAACAAAAAGTAACACCAATCGTGGTTGTTAACAAAATTGA
CAAACCTTCTGCTCGTCCTGAACACGTAGTAGATGAAGTTTTAGAGTTATTCATCGAATTAGGTGCAGACGACGA
TCAATTAGATTTCCAGTTGTTTATGCTTCTGCTTTAAACGGAACTTCAAGTGAATCAGATGATCCAGCAGATCA
AGAGCCAACAATGGCCCCAATTTTTGATAAAATTATTGAACATGTGCCAGCTCCAGTTGACAATTCAGACGAACC
ACTTCAATTCCAAGTCTCATTACTAGACTACAACGATTACGTTGGACGTATTGGGATTGGCCGTGTGTTCCGTGG
CACAATGAAAGTCGCGGACCAAGTTGCGTTGATGAAATTAGATGGCAGCGTGAAAAATTTCCGTGTAACGAAAAT
TTTAGGTTTCTTTGGCTTACAACGTGTGGAATTGATGAAGCAAAAGCGGGCGATTAAATTGCCGTTTCTGGAAT
GGAAGACATTTTCGTTGGGGAACAGTTGTAGATGTTTACAATCAAGAAGCATTACCAATTCTACACATTGATGA
GCCAACCTTACAAATGACTTTCTTAGTTAACAATTCTCCATTTGCGGGACGTGAAGGAAAATACATCACCGCTCG
TAAATCGAAGAACGTTAATGGCTGAGTTACAAACAGACGTATCTTTACGTGTTGATCCAATTGGCCCAGATTC
TTGGACTGTATCAGGTCGTGGCGAATTGCATTTATCAATTTTAATTGAAAACATGCGTCGTGAAGGCTATGAATT
ACAAGTTTCTCGTCCAGAAGTTATTGAACGTGAAATTGATGGAGTTAAATGTGAACCATTGTAACGTGTTCAAAT
TGACACACCTGAAGA

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SEQ ID NO. 425 *Lactococcus lactis*

CGAAAAAGCAAGTTAAATATGTTGTAAATAATGGTGTTACATTAGATAAATACTAGTGGTGGGCCTAATTTGGCTG
CACCTGTGACGGTGGATAGTCAGGTAATTTGCAACGATAAAGGTACGATTATGGGTGTAAGGACCTATACAGCAG
ATTTAAGCCAAGCAGAAGTAGTTAAAAAAGTGGGTAATTTGAATGCAATGTCCTTTGGAGAATTTGGGGGTACAA
AAGTTTTTGCTGCCAGCCAAAATCAGACAAATTCAGATAAGACTTATTCTGTTACGTTTAAACTGAATATAAATT
GGATAGTATCTAATGGCTATGCTTCGCTAACAAAAGTAACAGGTGGCTATGGTTCTTGCAATTGACCATGTTTATG
TTGCTAATTCTAGTGTTACTACTGCAACGAATGGTCAGATTAAAGGTTCAAGTGGTTATACTCAACAAGTTGATG
ACAAATCAGAAGGGAATAGTTTATCGTGGTCAATTACGCGAAACTATAAACCTGTAAAAGTTCCAGCAAGTGGGG
CAAAATGTAGGAGCTACGTATTTTGCCACACTTAAACGGGGAAATAGTACATGGAAATTCCAAACAACAAATAGAG
CTTATTAAGTGGGAGGAAGTGAATGAATATAAAAGGCATAAAAAATTTGGCAAGTATTTCTTGCAATTCATCATTT
GGATAGGAACCATGTTTCTTCCTGCAACGGTAAATCAGGCTAAATTGAATACGAATTTTGACTATAAAAAAAGTC
GAGAAAAATTTCTTTTATTTTCTTTTTCATCAAGTCCCTTTTTATAGTTTCATTTTGGGATTGGTGTTGCTTATAT
CACTTTTTCTCATTTTATAGGAAAATAAATTTTAGTGTCTATTTTTCTTTTGCTAGTCTTATTTTTTACATTAGTT
TCTTAGTTATAGCTTTTCCGTCCTATGATTATTTTAATCATAGTTTATCTGGGAATACTTTTGGGGCTGAACTTT
CTATCTTTCTAACCTTTTATGGAGCTGGATATATTATGCTGTTCTATTTGGTTTAGTTGCTTTTCTTTTACTCT
TTCTCTACAGTTTAAGAATAAAAGAATGTTAACAACATAATCATTTTTACTGATTTTATTAATTATAAAAAAATA
AAGAACTCCTTAGAAATTTTCTTTGGGGTTTTCATTTTGAAGTAAAAAATCTTTGTTAGGCTTGTAACGTG
TGCATTTACAGCTTTTAGAAAAGTGTGCTATAATGGGTAGATATATACGAAAGTAAGGTATGATAAAATTGACT
AAATTACGCGAAGATATTAGAAACGTCGCTGTTATTGCCACGTTGACCATGGTAAAACCTACATTGGTTGACGAA
CTCTTAAAACAATCTCAAACGTTGGATGCTCGTAAAGAATTAGCTGAACGTGCGATGGACTCAAATGCACTTGAG
CAAGAACGTGGGATTACTATCCTTGCCAAAAATACAGCAGTTGAATATAACGGAACCTCGTATCAACATCTTGAC
ACACCAGGTCACGCGGACTTCGGTGGAGAAGTTGAACGTATTATGAAAATGGTTGATGGGGTTGTCCCTCGTTGTC
GATGCTTATGAAGGAACAATGCCTCAAACACGTTTTGTTTTGAAA

Figure 18 represents sequences amplified with molecular marker VI (pgi) from various Gram-negative bacteria (SEQ ID NOs 426-430).

SEQ ID NO. 426 *Citrobacter freundii*

ATCTGGTACAACAATTTCTTCGGTGCTGAAACCGAAGCGATTCTGCCGTACGACCAGTATATGCACCGTTTCGCG
GCCTACTTCCAGCAGGGCAATATGGAATCCAATGGTAAATACGTTGACCGTAACGGCAATGCGGTGGATTACCAG
ACAGGCCCAATCATCTGGGGTGAGCCGGGTACTAACGGTCAGCATGCGTTCTACCAACTGATTCATCAGGGTACC
AAAATGGTTCGCTGCGATTTTCATCGCTCCGGCAATCACCCACAACCCGCTGTGCGGATCACCATCCGAAACTGCTG
TCTAACTTCTTCGCTCAGACCGAAGCGCTGGCTTTTGGTAAATCCCGCGAAGTGGTTGAGCAGGAATACCGCGAC
CAGGGTAAAGATCCGGCAACGCTTGACCACGTTGTGCCGTTCAAAGTGTTTGAAGGTAACCGTCCAATAACTCC
ATCCTGCTGCGCGAAATCACACCGTTTACGCTGGGTGCGCTGATTGCGCTGTACGAGCACAAAATCTTCACTCAG
GGCGCGATCCTGAATATCTTCACCTTTGACCAGTGGGGCGTTGAGCTGGGCAAACAGCTGGCGAATCGCATTTCTG
CCAGAGCTGAATGATGATAAAGAAATCACCAGCCATGATTGCTCAACTAACGGTTTGATTAACCGCTATA

SEQ ID NO. 427 *Klebsiella pneumoniae*

ATCTGGTACAACAATTTCTTCGGTGCGGAAACCGAAGCGATTCTGCCGTACGACCAGTACATGCACCGCTTTGCC
GCTTACTTCCAGCAGGGCAACATGGAGTCCAACGGTAAGTATGTTGACCGTAACGGCCACGCGGTAGACTACCAG
ACTGGCCCAATCATCTGGGGTGAGCCGGGCACCAACGGTCAGCACGCGTTCTACCAGCTGATCCACCAGGGCACC
AAAATGGTACCGTGCGATTTTCATCGCTCCGGCTATCACCCACAACCCGCTGTCTGACCACCATCAGAACTGCTG
TCTAACTTCTTCGCCCAGACCGAGGCCCTGGCCTTTGGTAAATCCCGCGAAGTGGTTGAGCAGGAATATCGCGAT
CAGGGTAAAGACCCGGCGACCCTGGAGCACGTGGTGCCGTTCAAAGTGTTTGAAGGTAACCGCCCGACTAACTCC
ATCCTGCTGCGCGAGATTACCCCGTTTACGCTCGGGGCGCTGATTGCCCTGTACGAGCACAAAATCTTCACCCAG
GGCGCGATCCTCAACATCTTCACCTTTGACCAGTGGGGCGTTGAGCTGGGCAAACAGCTGGCTAACCGCATCCTG
CCGGAGCTGAAAGACGGCAGCGAAGTTAGCAGCCACGACAGCTCTACTAACGGCCTGATTAACCGCTATA

SEQ ID NO. 428 *Klebsiella oxytoca*

ATCTGGTACAACAATTTCTTCGGCGCTGAAACCGAAGCGATTCTGCCGTACGACCAGTATATGCACCGCTTTGCC
GCCTACTTCCAGCAGGGCAACATGGAATCCAACGGTAAATACGTTGACCGTAACGGCAACGCCGTGGATTACCAG
ACGGGCCCCGATCATCTGGGGCGAGCCGGGCACCAACGGTCAGCACGCGTTCTATCAGCTGATTCACCAGGGGACC
AAAATGGTGCCGTGCGATTTTATCGCTCCGGCGATTACGCATAACCCGCTGTCTGACCATCATCCGAAGCTGCTG
TCTAACTTCTTTGCGCAGACCGAAGCGCTGGCGTTTGGTAAATCCCGCGAAGTGGTTGAACAGGAATATCGCGAT
CAGGGTAAAGATCCCGCGACGCTGGAACACGTGGTGCCGTTCAAAGTGTTTGAAGGCAACCGCCCGACTAACTCC
ATCCTGCTGCGTGAAATCACGCCGTTTACGCTGGGGCGCTGATTGCCCTGTATGAACATAAGATTTTACCCAG
GGCGTGATTATGAACATCTTCACCTTCGACCAGTGGGGCGTTGAGCTGGGCAAACAGCTGGCGAACCGCATCCTG
CCGGAGCTGAAGGATGGTTCTGAAGTCAGCAGCCACGACAGCTCCACTAACGGCCTGATTAACCGCTATA

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SEQ ID NO. 429 *Escherichia coli*

ATCTGGTACAACAAC TTCTTCGGGGCTGAAACCGAAGCGATTCTGCCATACGACCAGTACATGCACCGTTTTGCG
GCCTACTTCCAGCAGGGCAACATGGAATCCAACGGTAAATACGTTGACCGTAACGGTAACGCTGTGGATTACCAG
ACTGGCCCAATCATCTGGGGCGAGCCAGGCACTAACGGCCAGCATGCGTTCTATCAGCTGATCCACCAGGGCACC
AAAATGGTTCCGTGCGATTTTCATCGCCCCGGCCATTACCCATAACCCGCTGTCAGACCACCATCCGAAGCTGCTG
TCTAACTTCTTCGCACAGACTGAAGCGCTGGCGTTTCGGTAAGTCTCGTGACGTGGTTGAGCAGGAATACCGCGAC
CAGGGTAAAGATCCGGCCACGCTGGACCACGTTGTGCCGTTCAAAGTGTTTGAAGGCAACCGTCCAACCAACTCC
ATCCTGCTGCGCGAAATTACGCCGTTTACGCTGGGTGCGCTGATTGCCCTGTACGAGCATAAGATCTTCACTCAG
GGCGCTATCCTGAACATCTTACCTTTGACCAGTGGGGCGTTGAGCTGGGTAAACAGCTGGCAAACCGTATCCTG
CCTGAACTGGGTGACGATAACGCGATTAACAGCCACGACAGCTCCACAAATGGTCTGATTAACCGCTATA

SEQ ID NO. 430 *Serratia marcescens*

AAGCACTTTGCCGAAACGCCGGCGGAGAAAAACCTGCCGGTGTTGCTGGCGCTGATCGGTATTTGGTACAACAAC
TTCTTTGGCGCCGAAACCGAAGCCATTCTGCCGTACGATCAGTACATGCACCGTTTTGCCGCTTACTTCCAGCAG
GGCAAGATGGAATCCAACGGCAAGTACGTGATCGCAACGGCAACCCGGTGGATTACCAGACCGGTCCCGTCATT
TGGGGCGAGCCGGGCACCAACGGCCAGCATGCGTTCTATCAGTTGATCCACCAGGGCACCAAGCTGGTGCCGTGC
GATTTTCATCGCGCCGGCCATCAGCCATAACCCGCTGGGCGATCATCACGCCAAACTGCTGTCCAACCTTCTTCGCT
CAGACCGAAGCGCTGGCGTTTCGGCAAGTCGCTGGAAGTGGTGAAGCCGAGTTCGCGGCGCAGGGCAAACTCCT
GAGCAGGTCAAGCACGTGGCGCCGTTCAAGGTGTTGAAGGCAACCGGCCG

Figure 19 represents sequences amplified with molecular marker V (carB) from various Gram-negative bacteria (SEQ ID NOs 431-442).

SEQ ID NO. 431 *Neisseria gonorrhoeae*

TTCGCCCTTCGACCTTATGACTGACCCTGAAATGGCGGATGTTACCTACATCGAACCGATTATGTGGCAGACGGT
GGAGAAGATTATCGCCAAGGAGCGGCCCGATGCGATTCTGCCCACGATGGGCGGTCTAGACCGCGCTGAACTGTGC
GCTGGATTTGGCGCGTAACGGCGTGCTGGCGAAATACAATGTGAGTTAATCGGCGCAACGGAAGACGCGATCGA
CAAGGCGGAAGACCGCGGCCGCTTTAAAGAAGCGATGGAAAAATCGGCCTCTCTTGCCCGAAATCTTTTGTCTG
CCACACCATGAACGAAGCCTTGGCGGCGCAAGAACAGGTCGGCTTTCCGACGCTGATTTCGTCCGTCTTTCACGAT
GGGCGGTTCTGGGCGGCGGCATTGCCTACAATAAGGATGAGTTTTTGGCGATTTGCGAACCGGTTTCGATGCGTC
GCCTACGCATGAGCTGCTGATTGAGCAGTCTGTGCTCGGCTGGAAAGAGTACGAGATGGAAGTGGTGCGCGATAA
GGCGGACAACATGCATCATCTGTTCGATTGAAAACCTTCGACCCGATGGGCGTTCATACGGGCGACTCGATTAC
GGTTGCGCCGGCGCAAACGCTGACGGACAAGGAATACCAAATCATGCGCAACGCTTCGTTGGCGGTATTGCGCGA
AATCGGCGTGGACACGGGCGGCTCGAACGTGCAGTTTGCGGTGAACCCTGAAAACGGCGAGATGATTGTGATCGA
GATGAACCCGCGCGTGAGCCGTTTCGTCCGCGCTGGCTTCAAAGCAACGGGCTTCCCGATTGCGAAGGTGGCGGC
GAAGCTGGCGGTTCGGCTTTACGCTGGACGAGTTGCGCAACGACATCACGGCGGCCGACGCCCCGCGTCGTTCGA
GCCTTCCATCGACTATGTGGTAACCAAAATCCCGCGTTTCGCGTTTGAAAAATTCCCCGCCGACGACCGCCCT
GACCACGCAGATGAAATCAGTAGGCGAAGTAAGGGCGAATTCCAGCACACTGGCGGCCGTTACTAGTGGATCCGA
GCTCGGTACCAAGCTTGATGCATAGCTTGAGTATTCTAACGCGTCACCTAAAT

SEQ ID NO. 432 *Serratia marcescens*

TTTNGNATTCGCCCTTCGACGATTATGACTGACCCGGCAAATGGCGGATGCAACCTACATCGAGCCAATTCCTG
GGAAGTGGTACGTAAAATCATCGAGAAAGAGCGTCCGGATGCGGTTCTGCCGACCATGGGTGGCCAGACTGCGCT
GAACTGTGCGCTGGAGCTGGAGCGTCAGGGCGTGCTGGAAGAGTTTCGGCGTGACCATGATTGGTGCGACCGCCGA
CGCGATTGATAAAGCAGAAGACCGTCGTCGCTTCGACGTGGCGATGAAAAAATCGGCCTCGACACCCGCGCGTT
CCGGTATCGCTCACAACATGGAAGAGGCGCTGGCCGTTGCGGCTGAAGTGGGTTATCCGTGCATCATCCGTCCTT
CCTTACCATTGGGCGGCACCGGCGGCGGTATCGCCTACAACCGCGAAGAGTTTGAAGAGATTTGCGAGCGCGGCC
TGGATCTCTCCCCAACCAAGAGCTGCTGATTGATGAATCGCTGATTGGCTGGAAAGAGTACGAGATGGAAGTGG
TGCGTGATAAAAACGACAACATGCATCATCTGCTCCATCGAAAACCTTCGATGCGATGGGTATCCACACCGGCG
ACTCCATTACCGTTGCGCCAGCGCAAACGCTGACCGACAAAGAGTACCAAATCATGCGTAACGCATCGATGGCGG
TACTGCGTGAAATCGGCGTCGAAACCGGTGGTTCTAACGTGCAGTTCTCGGTGAACCCGAAAACCGGCCGCTCTGA
TTGTTATCGAAATGAACCCGCGCGTGTCGCTCCTCCGCGCTGGCTTCTAAAGCGACCGGCTTCCCGATTGCGA
AGGTGGCGGCGAAACTGGCGGTTCGCTTACCCCTTGACGAGCTGATGAACGATATCACGGGGGCGCGACGCGCTG
CGTCCTTCGAACCGTCTATCGACTACGTTGTGACCAAAATTCACGCTTCAACTTCGAGAAATTCGCTGGCGCGA
ACGACCGTCTGACCACCCNGTTGAAATCCTGTAAAAAGAAGTAAGGGGTNACTCNAAAAA

SEQ ID NO. 433 *Citrobacter freundii*

TCGCCCTTCGACTATTATGACTGACCCGAAATGGCCGATGCCACCTACATCGAGCCGATTCACTGGGAAGTGGT
ACGCAAAATCATTGAGAAAGAGCGCCCGGATGCGGTGCTGCCAACCATGGGCGGTCTAGACGGCGCTGAACTGTGC

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GCTGGAGCTGGAACGCCAGGGCGTACTGGCTGAATTCGGCGTGACCATGATTGGCGCAACGGCGGATGCCATTGA
TAAAGCGGAAGACCGTCGTCGCTTTGATATCGCGATGAAGAAAATTGGTCTCGACACCGCGCGCTCTGGCATCGC
TCACACCATGGAAGAAGCGCTGGCGGTTGCTGCTGACGTGGGCTTCCCGTGCATCATCCGACCGAGCTTCACCAT
GGGCGGCACCGGCGGCGGTATCGCTTATAACCGTGAAGAGTTCGAAGAGATTGCGAACGCGGTCTGGACCTTTC
CCCAACCAACGAGCTGCTGATTGATGAATCGCTGATTGGCTGGAAAGAGTACGAGATGGAAGTGGTGCGTGATAA
AAACGACAACCTGCATCATCGTCTGCTCCATCGAAAACCTTCGACGCGATGGGCATCCATACCGGTGACTCCATCAC
CGTAGCACCTGCCCAGACGCTGACCGACAAAGAATATCAAATCATGCGTAACGCCTCGATGGCGGTACTGCGTGA
AATCGGCGTGGAAACCGGCGGTTCTAACGTCCAGTTTGCGGTAAACCCGAAAAACGGTCGCGCTGATTGTCATCGA
GATGAACCCGCGCGTATCCCGCTCCTCGGCGCTGGCGTCCAAAGCTACCGGCTTCCCGATTGCGAAAGTCGCCGC
CAAGCTGGCCGTAGGTTACACCTCGACGAACTGATGAACGACACCACCGCGGCCGTACTCCGGCCTCGTTTGA
GCCGTCCATCGACTACGTTGTGACGAAAAATTCCACGCTTCAACTTCGAGAAATTGCTTGGTGCTAATGACCGTCT
GACCACGCAGATGAAATCAGTAGGAGAAGTAAGGGCGAATTCCAGCACACTGGCGGCCGTTACTAGTGGATCCGA
GCTCGGTACCAAGCTTGATGCATAGCTTGAGTATTCTAACGCGTCACCTAAATAGCTGGCG

SEQ ID NO. 434 *Enterobacter aerogenes*

TTNCGNATTCGCCCTTCGACGATTATGACTGATCCGGAAATGGCCGATGCGACCTACATCGAGCCGATTCACTGG
GAAGTAGTACGCAAGATTATTGAAAAAGAGCGCCCGGACGCGGTGCTGCCAACGATGGGCGGTGACACGGCGCTG
AACTGCGCGCTGGAGCTGGAGCGTCAGGGCGTGTTGGAAGAGTTCGGCGTGACTATGATTGGTGCGACCGCCGAT
GCGATTGATAAAGCAGAAGACCGCCGTCGTTTCGACGTAGCGATGAAGAAAATTGGTCTGGAACCGCGCGTTCC
GGTATCGCACACAGATGGAAGAAGCGCTGGCGGTTGCCNGTACTGGGCTTCCCGTGCATTATTNGNCCCATCC
TTTACCATGGGCGGTAGCGGCGGCGGTATCGCTTATAACCGCGAAGAGTTGAAGAAATTTGCGCCCGCGGTCAGG
ATCTCTCCCCAACCAAGAGCTGCTGATTGATGAGTCGCTGATCGGCTGGAAAGAGTACGAGATGGAAGTGGTG
GTGATAAAAACGACAACCTGCATCATCGTCTGCTCTATCGAAAACCTTTGATGCGATGGGCATCCATACCGGTGACT
CCATCACTGTGCGGCCAGCCCAAACGCTGACCGACAAAGAATATCAAATCATGCGTAACGCCTCGATGGCGGTGC
TGCGTGAAATCGGCGTTGAAACCGGTGGTTCCAATGTCCAGTTTGCGGTGAACCCGAAAAACGGTCGCGCTGATTG
TTATCGAAATGAACCCACGCGTGTCGCTTCTTCGGCGCTGGCGTCGAAAGCGACCGGTTTCCCGATTGCTAAAG
TGGCGGCGAAACTGGCGGTGGGTTACATCCTCGACGAACTGATGAACGACATCACTGGCGGACGTACTCCGGCCT
CCTTCGAGCCGTCCATCGACTATGTGGTTACTAAAATTTCCTCGCTTCAACTTCGAAAAATTCGCTGGTGCTAACG
ACCGTCTGACCACTCAGATGAAATCCGTAGGTGAAGTAAGGGCGAATTCCAGCACACTGGCGGCCGTTACTAGTG
GATCCGAGCTCGGTACCAAGCTTGATGCATAGNCTTGAGTATTCTAACGCGTCACCTAAATAGGCTGGCGTAANC

SEQ ID NO. 435 *Enterobacter cloacae*

ATTCGCCCTTCGACGATTATGACTGATCCGGAAATGGCGGATGCAACCTACATCGAGCCAATTCCTGGGAAGTG
GTACGTAAAATCATCGAGAAAGAGCGTCCGGATGCGGTTCTGCCGACCATGGGTGGCCAGACTGCGCTGAACTGT
GCGCTGGAGCTGGAGCGTCAGGGCGTGCTGGAAGAGTTCGGCGTGACCATGATTGGTGCGACCGCCGACGCGATT
GATAAAGCAGAAGACCGTCGTCGCTTCGACGTGGCGATGAAAAAATCGGCCTCGACACCGCGCGTTCCGGTATC
GCTCACAACATGGAAGAGGCGCTGGCCGTTGCGGCTGAAGTGGGTTATCCGTGCATCATCCGTCTCTTCCTTACC
ATGGGCGGCACCGGCGGCGGTATCGCTACAACCGCGAAGAGTTTGAAGAGATTGCGAGCGCGGCGCTGGATCTC
TCCCCAACCAAGAGCTGCTGATTGATGAATCGCTGATTGGCTGGAAAGAGTACGAGATGGAAGTGGTGCGTGAT
AAAAACGACAACCTGCATCATCGTCTGCTCCATCGAAAACCTTCGATGCGATGGGTATCCACACCGGCGACTCCATT

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ACCGTTGCGCCAGCGCAAACGCTGACCGACAAAGAGTACCAAATCATGCGTAACGCATCGATGGCGGTACTGCGT
GAAATCGGCGTCGAAACCGGTGGTTCTAACGTGCAGTTCTCGGTGAACCCGAAAACCGGCCGTCTGATTGTTATC
GAAATGAACCCGCGCGTGTCCCGCTCCTCCGCGCTGGCTTCTAAAGCGACCGGCTTCCCGATTGCGAAGGTGGCG
GCGAAACTGGCGGTGCGTTACACCTTGACGAGCTGATGAACGATATCACCGGGGGCCGCACGCCTGCGTCCTTC
GAACCGTCTATCGACTACGTTGTGACCAAAATTCACGCTTCAACTTCGAGAAATTCGCTGGCGCGAACGACCGT
CTGACCACCCAGATGAAATCAGTCGGCGAAGTAAGGGCGAATTCCAGCACACTGGCGGCCGTTACTAGTGGATCC
GAGCTCGGTACCAAGCTTGATGCATAGNCTTGAGTATTNCTAACGCGTCACCTAAATNGTCTGGCGAA

SEQ ID NO. 436 *Morganella morganii*

TTGGAGTCGCCTCTTCGACGATTATGACTGATCCGGCAAATGGCGGATGCGACTTACATCGAGCCGATTCACTGG
GAAGTGGTGCGCAAATCATCGAAAAAGAGCGCCCGGATGCCGTTCTGCCGACCATGGGCGGACAAACCGCGCTG
AACTGTGCGCTGGATCTGGAACGTCACGGCGTGCTGGCAGAGTTCCGGCGTCGAAATGATTGGCGCGACAGCAGAT
GCGATTGATAAAGCCGAAGATCGCCGCCGTTTCGATATCGCGATGAAAAAATCGGTCTGGATACAGCGCGTTCC
GGTATCGCACACACCATGGAAGAAGCGTTTGCGGTGCTGAAGATGTCGGATTCCCTGCATCATTCGTCCTTCAT
TTACTATGGGCGGCACGGGGGGCGGTATCGCTTATAACCGTGAAGAATTTGAAGAAATTTGTAAGTGGATTAG
ATTTATCACCGACTAACGAGTTATTGATTGATGAATCACTTATTGGTTGGAAAGAGTATGAAATGGAGGTGGTGC
GCGATAAAAACGACAACGTCATTATTGTCTGCTCTATCGAAAACTTTGATGCGATGGGTATCCATACTGGAGATT
CGATTACGGTTGCACCAGCTCAAACGTTAACGGATAAAGAGTACCAAATTATGCGTAATGCCTCGATGGCAGTCT
TACGCGAAATTGGTGTGAAACAGGTGGCTCTAACGTTTCAGTTTGCTGTTGACCCAAAAACAGGACGCTTAATTG
TTATTGAGATGAATCCACGTGTTTCACGTTTCATCAGCGCTAGCGTCAAAAGCGACAGGATTTCCCTATCGCTAAAA
TAGCGGCAAAACTGGCTGTGGGTTATACCTTGATGAGTTAATGAATGATATCACTGGCGGTAGAACGCCTGCCT
CTTTTGAGCCTTCTATCGATTATGTGGTAACAAAAATTCCTCGATTTAATTTTGAAAAATTCGAGGTACTAATG
ACAGATTAACCACACAAATGAAATCCGTAGGCGAGTAAGGGCGAATTCCAGCACACTGGCGGCCGTTACTAGTGG
ATCCGAGCTCGGTACCAAGCTTGATGCATAGCTTGAGTATTCTAACGCGTCACCTAAATA

SEQ ID NO. 437 *Escherichia coli*

CACGACGCCGCGCCGTTGTTTCGACCACTTTATCGAGTTAATTGAGCAGTACCGTAAAACCGCTAAGTAATCAGGA
GTAAAAGAGCCATGCCAAAACGTACAGATATAAAAAGTATCCTGATTCTGGGTGCGGGCCCCGATTGTTATCGGTC
AGGCGTGTGAGTTTACTACTCTGGCGCGCAAGCGTGTAAGCCCTGCGTGAAGAGGGTTACCGCGTCATTCTGG
TGAATCCAACCCGGCGACCATCATGACCGACCCGAAATGGCTGATGCAACCTACATCGAGCCGATTCACTGGG
AAGTTGTACGCAAGATTATTGAAAAAGAGCGCCCGACGCGGTGCTGCCAACGATGGGCGGTGACACGGCGCTGA
ACTGCGCGCTGGAGCTGGAACGTCAGGGCGTGTTGGAAGAGTTCGGTGTCACCATGATTGGTGCCACTGCCGATG
CGATTGATAAAGCAGAAGACCGCCGTCGTTTCGACGTAGCGATGAAGAAAATTTGGTCTGGAAACCGCGCGTTCCG
GTATCGCACACACGATGGAAGAAGCGCTGGCGGTTGCCGCTGACGTGGGCTTCCCGTGCATTATTCGCCCATCCT
TTACCATGGGCGGTAGCGGCGGCGGTATCGCTTATAACCGTGAAGAGTTTGAAGAAATTTGCGCCCGCGGTCTGG
ATCTCTCTCCGACCAAAGAGTTGCTGATTGATGAGTCGCTGATCGGCTGGAAAGAGTACGAGATGGAAGTGGTGC
GTGATAAAAACGACAACGTCATCATCGTCTGCTCTATCGAAAACTTCGATGCGATGGGCATCCACACCGGTGACT
CCATCACTGTGCGCCAGCCCAAACGCTGACCGACAAAGAATATCAAATCATGCGTAACGCCTCGATGGCGGTGCG
TGCGTGAAATCGGCGTTGAAACCGGTGGTTCCAACGTTTCAGTTTGCGGTGAACCCGAAAAACGGTCGTCTGATTG
TTATCGAAATGAACCCACGCGTGTCCCGTTCTTCGGCGCTGGCGTCGAAAGCGACCGGTTTCCCGATTGCTAAAG

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TGGCGGCGAAACTGGCGGTGGGTTACACCCTCGACGAACTGATGAACGACATCACTGGCGGACGTACTCCGGCCT
CCTTCGAGCCGTCCATCGACTATGTGGTTACTAAAATTCTCGCTTCAACTTCGAAAAATTCGCCGGTGCTAACG
ACCGTCTGACCACTCAGATGAAATCGGTTGGCGAAGTGATGGCGATTGGTCGCACGCAGCAGGAATCCCTGCAA
AAGCGCTGCGCGGCCTGGAAGTCGGTGCGACTGGATTGACCCGAAAGTGAGCCTGGATGACCCGGAAGCGTTAA
CCAAAATCCGTGCGGAACTGAAAGACGCAG

SEQ ID NO. 438 *Proteus mirabilis*

TCTTTTCGNATTCGCCCTTCGACTATTATGACTGATCCTGAAATGGCAGATGCCACTTATATTGAGCCTATTCATT
GGCAAGTGGTCAGAAAGATTATTGAGAAAAGAGCGCCCTGATGCCATATTACCGACAATGGGCGGACAAACGGCAT
TAAACTGTGCCTTAGAATTAGAGCGTCAAGGGGTGTTAACTGAATTTGGCGTAACAATGATAGGTGCAACGGCTG
ATGCTATTGATAAAGCGGAAGATAGACAACGCTTTGATAAAGCGATGAAAAAATTGGTCTGGATACGGCTCGTT
CAGGCATCGCTCATACTATGGACGAAGCATTTGCAGTGGCTGAGCAAGTGGGTTTCCCTTGTATTATTCGCCCTT
CATTTACTATGGGGGGAACGGGAGGCGGGATCGCCTATAATCGTGAGGAATTTGAAGAAATTTGTACTCGAGGTT
TAGATTTATCACCGACAAATGAACTATTAATTGATGAATCATTAAATTGGCTGGAAAGAGTATGAAATGGAAGTGG
TGCGCGATAAAAATGATAACTGCATTATCGTTTGCTCCATTGAAAACCTTTGATGCGATGGGGATCCATACCGGTG
ACTCTATCACGGTTGCTCCAGCGCAAACGCTAACAGACAAAGAATATCAAATTATGCGTAATGCCTCGATGGCAG
TATTACGCGAGATTGGGGTTGAAACCGGTGGCCCCAATGTGCAATTTGCCGTTGATCCTAAACAGGGCGTTTAA
TTGTTATTGAAATGAACCTCGTGTTTCTCGCTCATCAGCATTAGCGTCAAAAGCAACAGGTTTCCCAATTGCAA
AAGTCGCGGCAAACTTGCAGTAGGTTATACCCTCGATGAGTTGATGAATGATATCACTGGAGGAAGAACCCAG
CCTCTTTTGAACCTTCTATTGATTATGTAGTGACTAAAATCCCTCGCTTTAACTTTGAAAAATTTGCCGGTACCA
ATGACCGTTTAAACCACGCAAATGAAGTCCGTAGGCGAAGTAAGGGCGAATTCCAGCACACTGGCGGCCGTTACTA
GTGGATCCGAGCTCGGTACCAAGCTTGATGCATAGCTTGAGTATTCTAACGAGTCACCTAAATGCTGGCG

SEQ ID NO. 439 *Proteus vulgaris*

ATTCGCCCTTCGACGATTATGACTGATCCTGAAATGGCGGATGCCACCTACATCGAGCCTATTCATTGGCAAGTC
GTCAGAAAAATTATTGAAAAAGAGCGCCCTGATGCGATTTTGCCAACAATGGGGGGGCAACCGGCATTAAATTGC
GCATTAGAATTAGAACGTCAAGGTGTGTTAGCTGAATTCGGTGTGACCATGATTGGTGCTACGGCCGATGCTATC
GATAAAGCAGAAGATAGACAACGCTTTGATAAAGCAATGAAAAAATCGGCTTAGGCACAGCTCGCTCAGGTATT
GCTCATAATCTAGAAGAAGCTTTTGCCGTCGCTGAAGATGTGCGATTCCCTTGATCATTTCGTCTTCATTTACT
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TCACCGACTAACGAGTTATTGATTGATGAATCACTTATTGGTTGGAAAGAGTATGAAATGGAGGTGGTGCGCGAT
AAAAACGACAACCTGCATTATTGTCTGCTCTATCGAAAACCTTTGATGCGATGGGTATCCATACTGGAGATTTCGATT
ACGTTTGCACCAGCTCAAACGTTAACGGATAAAGAGTACCAAATTATGCGTAATGCCTCGATGGCAGTCTTACGC
GAAATTGGTGTTGAAACAGGTGGCTCTAACGTTTCAGTTTGCTGTTGACCCAAAACAGGACGCTTAATTGNTATTG
AGATGAATCCNCGTGTTTACGTTTCATCAGCGCTAGCGTCAAAGCGACAGGATTTCCCTATCGCTAAAATAGCGG
CAAACTGGCTGTGGGTTATACCCTTGATGAGTTAATGAATGATATCACTGGCGGTAGAACGCCTGCCTCTTTTG
AGCCTTCTATCGATTATGTGGTAACAAAATTCCTCGATTTAATTTTGAAAAATTCGCAGGTACTAATGACAGAT
TAGCCACACAAATGAAATCCGTTGGCGAAGTAAGGGCGAATTCCAGCACACTGGCGGCCGTTACTAGTGGATCCG
AGCTCGGTACCAAGCTTGATGCATAGCTTGAGTATTCTAACGCGTCACCTAAATGGCTGGCG

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SEQ ID NO. 440 *Neisseria meningitidis*

CCAAACGTACCGACCTAAAATCCATCCTTATCATCGGCGCCGGCCCTATCGTTATCGGTCAGGCCTGCGAATTTG
ACTATTCGGGCGCACAGGCCTGCAAGGCTTTGCGTGAAGAAGGCTATAAAGTCATTTTGGTGAATTTCCAACCCCG
CCACGATTATGACCGACCCTGAAATGGCGGATGTTACCTACATCGAGCCGATTATGTGGCAGACGGTGGAGAAGA
TTATCGCCAAGGAGCGGCCTGATGCGATTCTGCCCACGATGGGCGGTCAGACCGCGCTGAACTGTGCGCTGGATT
TGGCACGCAACGGCGTGCTGGCAAATACAATGTGAGCTGATTGGGCGGACGGAAGACGCGATCGACAAGGCGG
AAGACCGCGGCCGCTTTAAAGAAGCGATGGAAAAAATCGGTTTGTCTTGCCCGAAATCTTTTGTCTGCCACACGA
TGAACGAAGCTTTGGCGGCGCAGGAGCAGGTGCGCTTCCCGACGCTGATTTCGTCTTCTTTACGATGGGCGGTT
CGGGCGGCGGCATTGCCTACAATAAAGACGAGTTTTTGGCGATTTGCGAACGCGGTTTCGATGCGTCGCCCACGC
ACGAGCTGCTGATTGAGCAGTCCGTCTCGGCTGGAAAGAGTACGAGATGGAGGTGGTGC GCGATAAGAACGATA
ACTGCATCATCATTTGCTCGATTGAAAACCTTCGACCCGATGGGCGTGATACGGGCGACTCGATTACGGTTGCGC
CGGCGCAAACATTGACAGACAAAGAATACCAAATCATGCGTAATGCTTCGTTGGCAGTATTGCGCGAAATCGGCG
TGGACACGGGTGGCTCAAACGTGCAGTTTGGCGTGAACCCTGAAAACGGCGAGATGATTGTGATTGAGATGAACC
CGCGCGTGAGCCGTTTCATCCGCGCTGGCTTCCAAAGCGACGGGCTTCCCGATTGCGAAGGTGGCGGCGAAACTGG
CGGTTCGGCTTTACGCTGGACGAGTTGCGCAACGACATCACGGGCGGTGCGACGCCCCGCGTCGTTTCGAGCCTTCGA
TTGATTATGTGGTAACCAAAATCCCGCGTTTTGCGTTTTGAAAAATTTCCCGCCGCGACGACCGCCTGACTACGC
AGATGAAATCGGTGGGCGAAGTGATGGCGATGGGACGCACGATTTCAGGAAAGTTTTCCAAAAAGCCCTGCGCGGCT
TGGAAACAGGCTTGTGCGGCTTCAATCCGAGAAGCTCCGACAAAGCGGAAATCCGCCGCG

SEQ ID NO. 441 *Klebsiella oxytoca*

ATTGCCCCCTCGACTATTATGACCGACCCGAAATGGCCGATGCCACCTACATCGAGCCGATTCACTGGGAAGTG
GTGCGCAAGATCATTTAGAAAGAGCGTCCGGATGCGGTTCTGCCGACCATGGGCGGCCAGACGGCGCTGAACTGC
GCGCTGGAGCTGGAGCGTCAGGGCGTGCTGGCCGAGTTGCGCGTGACCATGATTGGGCGGACCGCCGACGCGATT
GATAAAGCCGAAGACCGCCGCCGTTTCGACGTGGCGATGAAGAAAATCGGTCTCGATACCGCGCGTTCCGGTATC
GCGCATACCATGGAAGAAGCGCTGGCGGTTGCCGCTGAAGTTGGCTTCCCGTGATCATCCGTCCGTCTTTACG
ATGGGCGGCACCGGCGGCGGTATCGCCTACAACCGCGAAGAGTTGGAAGAGATCTGCGAACGCGGTCTGGATCTC
TCGCCGACCAACGAGCTGCTGATTGATGAATCGCTGATCGGCTGGAAAGAGTACGAGATGGAAGTGGTGC GTGAT
AAAACGACAACCTGCATCATCGTCTGCTCCATCGAAAACCTTCGACGCGATGGGCGTCCACACCGGCGACTCCATCA
CCGTGGCGCCCGGCGCAGACCCTGACCGACAAAGAGTACCAAATCATGCGTAACGCCTCGATGGCGGTACTGCGTG
AAATCGGCGTAGAGACCGGCGGTTCCAACGTTTCAGTTCTCGGTGAACCCGAAAGATGGTTCGCCTGATCGTTATCG
AAATGAACCCGCGCGTCTCCCGCTCCTCGGCGCTGGCCTCGAAAGCCACCGGCTTCCCGATCGCTAAAGTGGCGG
CGAAGCTGGCGGTTGGTTACACCCTTGATGAGCTGATGAACGATATCACCGGCGGCCGACCCCGGCGTCGTTTG
AGCCGTCCATCGACTACGTCGTGACCAAAATCCCACGCTTCAACTTTGAAAAATTCGTGGGCGCGAACGACCGTC
TGACCACCCAGATGAAATCCGTGCGGGAAGTAAGGGCGAATTCCAGCACACTGGCGGCCGTTACTAGTGGATCCG
AGCTCGGTACCAAGCTTGATGCATAGCTTGAGTATTCTAACGCGTCACCTAAA

SEQ ID NO. 442 *Legionella pneumophila*

TTCGCCCTTCGACTATTATGACTGATCCTGAGCTTGCTGATGCCACCTATATAGAGCCTGTTCAATGGAAAAGAAG
TGGCTCGTATTATCGAAATAGAGAGGCCAGATGCTCTTTTACCGACGATGGGAGGACAAACAGCCTTAAACAGCG
CCTTGGA CT TGGTAAGAGAAGGGGTATTAGCCAAGTACTCTGTTGAAATGATAGGAGCGACGCGTGAAGCCATAG

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ACAGGGCGGAAGATAGAGAAAAATTTGCCAGCTGATGATTAAAATCGGATTGGATATGCCAAGGTCGGCGATTG
CTCATAGCCTGGAAGAAGCAATTCAAGTACAAGCCCGTTTAGGCTTTCCTGCCATCATCAGGCCTTCATTTACCA
TGGGTGGTAGTGGAGGCGGTATTGCCTATAATCGTGAAGAATTTGAAGAAATTTGCATTAGAGGATTGGAGTTGT
CGCCAACTCACGAGCTTTTGATTGATGAATCGGTTCTGGGTTGGAAAGAATATGAAATGGAAGTCGTCAGGGATA
AAAATGATAATTGCATTATTGTTTGTACTATAGAGAATTTTGACCCATATGGGAGTGCATACTGGAGATTCCATTA
CCGTTGCTCCGGCACAAACATTAAGTATAAGAAATACCAACGGATGCGGGATGCGGCGATTAAAGTTCTAAGGG
CAGTTGGTGTGGATACGGGAGGTTCCAACGTTGCGTTTGTCTATTAATCCTGAAGACGGGCGCATGCTGGTTGTGG
AAATGAACCCGCGTGTATCTCGAAGCTCGGCTTTGGCGTCAAAAGCAACCGGTTTTCTATTGCTAAGGTCGCAG
CTAAATTGGCTGTGGGCTATACCTTGGATGAATTGAAAAACGAAATCACCGGAGGTAAAACACCTGCGTCCTTTG
AGCCCAGCATTGATTACGTCGTTACCAAAGTTCCACGGTTTAATTTTGATAAATTTCCACAACTCCAGATACTC
TTACCACACAGATGAAATCAGTCGGCGAAGTAAGGGCGAATTCAGCACACTGGCGGCCGTTACTAGTGGATCCG
AGCTCGGTACCAAGCTTGATGCATAGNCTTGAGTATTNCTAACGCGTCACCTAAATAGCTGGCGAAA

Figure 20 represents sequences amplified with molecular marker VII ((EG10839 & EG11396 or *sfrB* & *yigC*) in Gram-negative bacteria (SEQ ID NOs 443-451).

SEQ ID NO. 443 *Pseudomonas aeruginosa*

tccaccagcagcgccgcgagatatggcagttgccgttgccgcagctctgcggacagtcgtagccaagccgccgg
gcgccatcgaggatgcgttcccccggcagcagctcgaggcaggcgccggacggttgaggacgatacgcatacgt
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cgaagtcgaggtagtcgatggcggtgtgtcgatcatcacctgtgcgcgttggggtccatccgcgtggtgatgg
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gccgcaggaacgaccagaccccgagcatcacgcgcttgccgtgccctgggtactgcttcttcatggtcaccaccg
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cgaacacttcgttcagcgccacccccgaggatcgccggctcgctccggcggaacgcccgtgtagggtgctgtggtaga
tcggtttctgcgggggggtgacgcgctcgacggtgaacaccgggaagcgatcgacctcggttagtagccggtgt
gatcgccataggggccttcgtcgcccatctcgccgggggtggatcaccccttcgaggacgatctcggcgctggccg
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ggttgccgagcaccggcatgtcgaagccgggtcggttttgcgaacagcaatgccgggccccttggcgcgcaacgtgc
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gctggggcgatgaaatcgggagatccttgaacgtcattggcctaaccattcactgcaagacccacatcctacct
gctcccggcccacccggcagcaggcaaacgcggcattcggtcactgctggctggcgatcctcgagtcgctcgaggc
tctgtagcatcggtcgaacaaaggcccgagttcatggggccccctgggtcgaaagggtggttggttatccatgtaca

SEQ ID NO. 444 *Pseudomonas syringae*

ccgagcagacatggcagttaccgttgcgacagctttgcgggcattcatggccagccgctgtgcagcatccagaa
tccgctcgccccggcaggggttcgagtaccgcacccgaggggtgcaagggttacgcgcatcagtcattcccaactg
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cagcgccacacccaggatagccggctcgtccgggtggacgcccgggtgtaggtgctgtggtagatcggttgatgcg
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gcgcagctcggtgacggcttcgcgcccattgcccatggccacgcgctccggcgtgccgaacaggttgccagcac
cggaatatcaaagccaaccgggttttcaaacagcagggccgggctttggcgcgcaaggtagcgtcacagatttc
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atcccttagatctttgaatttcattaaaccggccatttatccaaatagacgcacatcgtaacctgctccgcctc
caaggcagcaaattccagggcgacagggcaaaaaaatggtgccccgaaggacaccattttttgagccagcctgtc
tgttacttgcgtttcatggacaggaagaactcgtcgttgggtcttggtctgcttgagcttgatgaggaactcg

SEQ ID NO. 445 *Bordetella parapertussis*

aratggtgatggggcgggcgcccggtcgggcctgctcaagctggccggcgtggcgctggtgggctggcagg
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tgcgtcagtgggccggcctgttccgacagctggcccaaggagtgaccaccatctcgccgaat

SEQ ID NO. 446 *Neisseria meningitidis*

acagaaaatcctcgaagacaccctgctggaacaatggcagtggtcaaaccctaaagaaccgtaaacaatcctgcgt
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SEQ ID NO. 447 *Shigella flexneri*

ctgaccagcacgaaaagaaaaggccgctctggcacgatgcggacacgatatacgggtatccgtgatagctgctac
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SEQ ID NO. 448 *Escherichia coli* K12

catgactgctttcgcgtaaaggttgatttcagaagcgccaatatgcagctcgataaacctttttcatccggcgt
cgaagccattgagaacggacgtttgtcgcgctcatccatcactaccatcaaatactgaccagcacgaaaagaaaa
ggccgcgtctggcacgatgcggacacgatatacggtatccgtgatagcttctaccgaggtcactttacagcttaa
ggttgtcatgcgcttttctctgtcggatcgataaatagggcaaaacaaacgcgcacatcaggcgcttttacggtgtt
aaaaatagccagttcatccagatggcgtcaatatgcgcgacaacatctggatctttttgatgggacgtcccca
ttcacgctgggtttcccccgccattttattcgtggcatccagccccatttttgaaaccagcccggagacaggcga
ggcaaaatccagataatcaataggcgtattttctaccagaacagtatcccgcgccgggtccatacgggtggtaat
cgcccaaatcacatcgttccagtcgcgtgcgttaacgtcatcatcgaaaacgatcacaaatttagtgtagataaa
ctggcgtaagaacgaccagacgcccattcatgacgcgcttcgcgtgtccggcgtagtgtttttgattgtcactac
cgccaggcgataagagcagccttccggcggcaggtaaaaatcgacaatttccgggaaactgtttttgcagaatcgg
cacaaacacttcgttcagtgcgacaccagcaccggggtcatctggcggaacgcccgtataggtggaatggta
aatcgcatcttcacgctgggtaatatgcgtcacggtaaataccgggaaactatcgacttcattatagtaaccggt
gtggtcgccatacggcccttccggcgaggtttcgcccttggtcgatatacccttccagcacaaatctccgactggc
gggcacttcaagatcattggagatacacttcaccacttcggtcttggtgccacgtagcaatccggcaaaacgcata
ctctgaaagcgtatccggaacgggagtgactgcaccgagaatcgtggcgggatcggcaccacagcgccacagaaac
cgggaaacgttcgcccggatgcgcccacaccactcctgataatccagcgcgcccgccgcgatgcgacagccagcg
cataatcagtttggtttttaccaatcagctgctggcgataaatgccagattctgcgctctttatgtgggccgcg
cgtaactgtcagccccaggtaatcagcggcgcgccatcttccggccagcaggtcataatgggaatgcgattgag
atcgacgtcatcgccagagacgattttttgttggcagggcgccaccacgcagccgctttgtcggcatgttcaatac
ttgcttaaaactgcggcagtttatcaaacaggtcgcggaaccttttggcggtccggctcttttcagaaacgccaa
taattttaccaacttcacgcagcgccgaaacatcttctgccccatgcccacgcgcttttggcgtaccgaa
caggttgacagcaccggcattgagtagccttttagggttttcgaacaacagcgcaggccccaccggcacgcaaagt

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gcgggtcagcaatttcagtgatttccagatgcggtatccaccgggagcgtgatacgttttagctcaccctgctgttc
aagcagcgtcaagaagtcgcgtaaatcggttatatttcattggtccattgtagcctcttaatctgcgcc
cattat

SEQ ID NO. 449 *Escherichia coli* O157:H7

agaagcgccaatatgcagctcgataaaaccctttttcatccggcgctcgaggccattgagaacggacgtttgtcgcg
ctcatccatcactaccatcaaatactgaccagcacgaaaagaaaaggccggtctggcacgatgcggacacgata
tacggtatccgtgatagcttctaccgaggtcactttacagcttaagggtgtcatgcgctttctctgtcggtatcga
taaataggggcaaaacaaacgcgcacatcaggcgctttaccggttggttaaaaatagccagttcatcccagatggcgtc
aatatgtgcgacaacatctggatcttttttgatgggacgtccccattcacgctgggtttcccccgccattttatt
cgtggcatccagccccatttttgaaccagccccggagacaggcgaggcaaaatccagataatcaataggcgattt
ttctaccagaacagtatcccgcgctgggtccatacgggtggtaatcgcccaatcacatcgttccagtcgcgtgc
gttaacgtcatcatcgcaaacgatcacaatttagtgtagataaaactggcgtaagaacgaccagacgcccacatcat
gacgcgcttcgcgtgtccggcgactgttttttgattgtcactaccgccaggcgataagagcagccttcggcgcg
caggtaaaaatcgacaatttccgggaactgcttttgcagaatgggaacaaatacttcggttaacgccactcccag
taccgcgggttcatctggcggaacgccccggtataggtggaatggtaaatcgcatcttcacgctgggttaatatgcgt
cacggtaaataccgggaaactatcgacttcggttatagtaaccagtggtggtcaccatacggctccttctggcgccat
ttcgcccttggtcgatatacccttccagcacaatctccgcactggcgggcacttcgagatcattggaaatacactt
cactacttcggttttgggtgccacgtagcaatccggcaaggcgatttccgacaaagtatctggtactggtgtgac
tgcaccgagaatggttgccggatcagcgccccacgcccacagagatcgggaaacggttcacctggatgcgccgcaca
ccactcctgataatccagcgcgccgcgcgcgatgcgacagccaaacgcataatcagcttggtttttaccaatcagttg
ctggcgataaatgccagattctgtcgctctttatgagggccacgtgtaacgggttagccccatgtaatcagcgg
cgcggtcatcttccggccaacaggtcataatgggaatacgggttgagatcgacgtcatcgccagagacgattttttg
ttggcaggggtgcaccgcgcagtcgctttgtcggcgatgtttaacacctgcttaaactgcggcagcttatcaaacag
atcgcgaaaaccttttggcggtctgtgttctttcagaaatgctaataatttaccgacttcacgcagtgctgaaac
atcttctcgcccataccatcgctacgcgctttggcggtaccgaacaagttgcacagcacccggcattgagtacct
tttagggttttcaaacaacagcgcgagggccaccagcacgcgcgtgcggtcagcaatttcagtgatttccagatg
cgggtccaccgggagcgtgatacgttttagctcaccctgctgttcaagcaacgtcaagaagtcgcgtaaatcggt
atatttcatggcgctccattgtagcctcttaatctgcgccattatacggcggttcattctttgcgatgctgtaaatt

SEQ ID NO. 450 *Bordetella bronchiseptica*

tcccacatggcatccaccggcgcttgaccgcctcgatcatgtgtatggcggtgccccatttcgcggtggtttcg
cccggccacttggttggtggcggtccagccccatcttgccgcccaggccggacaccggcgaggcgaaatcgaggtaa
tcgatcggcggtgttctcgaccagcacctgtgtcgcgacgggggtccatgcgcgtggtcatggcccagaccacttcg
gtccagtcgcgcgggtcgatgtcttcgtcgaccaccacgatgaacttggtgtacatgaactgccgcagcacgctc
cacaggccgaacatcacgcgttggtggtggcggtactgcttgccgatcgacaccaccgccaggcggtagctg
cagccttccgggggaggtagaaatcgacgatttccgggcagctggcggcgcagcagcggcacgaataacctcggtc
agcgccacgcccagcacggccggctcgctggggcggttgccggtataggtggagtggttagatgggggttgcgccgc
atggtgatgcggtccaccgtgaacaccgggaaccagtcctgctcggttgtagtagccggtatggtcgccatagggg
ccttcgagggccatttctgtagccggtggccggggggcggttgggcgccctcgggcacccggcgagcagcgccgcgc

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ggatcgctcgcccggcagcaggtggccctcgagcacgatctcgcccgaggccggcaccgacaggtcgctgcccagc
gccttgacgacctcggtgcgcgagccgcgagcagcccggaactggatttcggacagcgtgtccggcaccggc
gtgaccgcgcccaggatgggtggccgggtcggcacccagcgccacggcgatgggaaacggcttgcccgggtgggc
tgggctggtcgcggaagtccagcgcgcccgcggtgcgacagccagcgcatgatcagcttggtcgccccagc
ggctgctggcggtagatacccaggttctgcccggggcggttcggcccgcgctgatcaccaggccccaggcgagc
agggcgccacatcgcccggccagcaggtctggatgggcaggcgggccaggtcgacgtcgggcgcttcccagacg
atttcttgccagggcgcgctgcgacgggtcttggggctcatgtcccacaggcggtttcagcatggacaccttg
gccagcgctcgcgaggcccttgggcgcttcgggctcgcgaggaggccagcagttcgccggtttcgcgagg
gcgcccagctcgctcgcccccatgcccaggcgacccgcccggcggtgcccgaacaggttgccagcaccggcatg
tcggccggcgcgctcggttggtggcgggcttctgaacagcaggggccgggcccggcgcgagcaccgggtcgga
atctcggtcatttccagccgctcgagaccggcgcggtgatgcgtttgagttcgccctggcggtcaagctgggca

SEQ ID NO. 451 *Bordetella pertussis*

tgtatgggctgccccattcgcggtgggttcgcccggccacttggtgggtggcgctccagccccatcttgccgccc
aggccggacaccggcgaggcgaaatccaggtaatcgataggcggttctcgaccagcaccgtgtcgcgacgggg
tccatgcgctggtcatggcccagaccattcggtccagtcgcgcggtcgatgtcttcgtcgaccaccacgatg
aacttggtgtacatgaactgccgcagcacgctccacaggccgaacatcacgcgcttggcgtggccggcgactgc
ttgcggtatcgacaccaccgcccaggcggtagctgcagccttcggggggcaggtagaaatcgacgatctcgggcagc
tggcgggcgagcagcgggcacgaatacctcggttcagcgccacgcccagcacggccggctcgctcgggcggttgccg
gtatagggtggagtggtagatgggggttcgcccgcagtggtgatgcggtccaccgtgaacaccgggaaccagtcctgc
tcgttgtagtagccggtatggtcgccataggggccttcgagcgccatttcgtagccggtggccggggcggggttg
gcgcccctcgggcaccacggcagcgacggcgcgcggtcgctcgccggcgagcaggtggccctcgagcacgatctcg
gccgaggccggcaccgacaggtcgctgcccagcgcccttgacgacctcggtgcgcgagccgcgagcagccggcg
aactggatttcggacagcgtgtccggcaccggcggtgaccgcgccaggatgggtggccgggtcggcgcccagcgcc
acgggtgatgggaaacggcttgcccgggtgggcctgggcgtgggtcgcggaagtccagcgcgccgcccgggtgcgac
agccagcgcatgatcagcttggtcgccccagcggtgctggcggttagatgccaggttctgcccggggcggttc
ggcccgcgctgatcaccaggccccaggcgagcagggggcgccacgtcgccggccagcaggtctggatgggcagg
cggtcagctcgacgtcggcgccttcccagacgatttctggcaggcgcgctgcgacgggtcttggggctcatg
tcccacaggggcggtttcagcatggacaccttgccagcgcgctcgcgaggcccttgggcgcttcgggctcgcg
agggaggccagcagttcgccggtttcgcgaggggcgccgacgtcgtcggcccccatgccccaggcgacccggcg
ggcggtgccgaacaggttgccagcaccggcatgtcgccggcgcgctcggttggtggcgggcggttctgaacagcagg
gccgggcccggcgcgagcaccgggtcggaatctcggtcatttccagccgctcgagaccggcgcggtgatg
cgtttgagttcgccc

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Figure 21 represents sequences amplified with molecular marker VIII (hypothetic yleA protein) in Gram-negative bacteria (SEQ ID NOs 452-461).

SEQ ID NO. 452 *Haemophilus influenzae*

Tatctgctgctggcgctacctggctcgggctgagtacacaaaactgaagctcatatcaaagtttacttgtgcaatca
aattcatagtttgctcaaaatcttccgcccgtttcaccagggaaccaacaataaagtcagagctgatttgaatat
ctgggcgacagcacgaagtttacgaataatggatttatattctaattgcggtatgagcacgtttcatcattgtta
atacacgggtcagaacctgcttgactggaagatgtaagaaactcactaattcaggcgtatcacgatacacatcaa
taatatcatcggtaaaattctattggatgactgggtgtgaaacgtaaacgggtcaataccatcaattgatgcgacaa
gacgaagcaactcagcaaagctgcaaatttgaccatcatgcgttggcccacgataagcattttacattttgaccaa
gtagattgacctcacgcacacctgttccgcaagttgcgcaatttcaaatagcacatcatctacaggacggctaa
cttcttctccacgagtataaggcacaacacaaaaagtacagtattttattacagccttccataatggaacaaatg
ccgttgggccttctgcgcgaggttctggtaagcgggtcaaatttctcaatttcaggggaaacttacgtctacgacgg
aactttttccaccacgaatttgattaatcatttcaggcaagcgatgcaaagtttgcggggccaaaaataatatcca
cataaggcgacgatggcgaatatgttcccccttcttgagaggctacacagccgcccacaccaatcactaaatttg
gattatttttctttaattctttccaacgcccagttgggtggaacactttttcttgtgctttttcacgaatagaac
aggtatttaataataatacgtctgcttcttcagggtgcttccgtgagttctaataccgtgggtgcttaataaaagat
cagccatttttagatgaatcatattcattcatctggcagccccaagttttaatatgtaatttttgagtcattttct

SEQ ID NO. 453 *Pasteurella multocida*

ctacgcgtgataacgtcccacgcccaggttcatcttctttacaggtacgattaatcaccattttgtggcgattgaac
aacgcgaagtcccatttgttcttcagttctaacgacttcaccacgcagtgagttagtaaacacatccgtgatctt
gatatcaacaaaacttcccaatcatatcaggcgtgcccacaaaattgacgatacgattagtttctgtacgccctgt
gagttccattaaatcttttttcgagggtccttccactaacacgcgctgttctgtgcctaacattgctcgactaaa
ttgcgcggcttgattgttaatgcgttgttgcaacacatataaacggttgtttcttctcttcttctgtcacatcatc
aggcatatctgctgctggcgtgcctggacgtgctgaataaatgaagctgaaactcatatcaaaatttacttgtgc
aattaaattcatggttggctcgaaatcttctgctgtttcgcccgggaaaccgacaataaaatctgagctaatttg
aatctctggacgcaccgctcttaacttccgaataatcgatttatattctaatagccgtatgattgcgtttcatcat
agataacacacgatcagaaccactttgtacaggtaagtgtgaagaaactcaccaactctggcgtatcacggtacac
atcaataatgtcatcagtgaaactcaattgggtgactgggtggtgtaaacgtaaacggtcaataccatcaatagcggc
tactaaacgtaacaattccgcaaaagtacaaataccgtcatcatgagttgcaccacgataagcgttcacgttttg
tcctaataaattcacttcacgcacgccttgcctctgccaaactgtgcaatttcaaataatacatcatccactggacg
actgacttcttccaccgcggtataaggcagcacagaatgagcaatatttattacagccttccataatggatac
gaaagcagttggaccttctgcacgcgggttctggtaaacgggtcgaatttttcaatttctggaaaactgacatcgac
tactgagcttttaccacctctgatctgattgatcatttcaggtaaacgatgtaagggttgggtccaaaaataat
atcgacataaggagcagagtagaatgtgttctccttcttctgtgaggcaacacagcccccaacaccgataacgag
tcccggttatgtttctttaattctttccaacgtcctaattgatggaaaactttttcttgtgctttttcacgaat
tgagcaagtgtttaacaataacacatccgcttcttccggaatttctgttaactctaagccgtgagtagtctgttaa
gagatctgccatttttagatgaatcatattcattcatctgacaacccccacgtttttaatatgtaatttttgcgatcat

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SEQ ID NO. 454 *Haemophilus ducreyi*

ggacgcgcagagtagataaagctaaagctcatatcaaaaattgacttggtcaataattttcattgtttgttcaaag
tcttccgctgtttcgccaggaaagccaacaatgaaatctgagctaatttggatatttggacgaaccgcacgtaat
ttacgaataatggctttgtattctaatacggtgtggttacgtttcatcatggttaaaacacgatcggcgccactt
tgataggtaaatgcaagaagctgaccaattctggagtatcacgatacacttcaataatgtcgtcgggtgaattca
atgggggtggcttggtataacgtaagcggtaataccatcaatggcggcaactaaacgtaataattctgcaaaa
gtgcaaatgccaccatcaaagggtttcaccacggtaagcattaacgttttgaccagcaagttaacttcacgaacg
ccttgctctgctaattgtgcgatttogaataagacatcatcaacagggcgggaaacttcttcaccacgggtataa
ggcactacacagaatgagcagtatattattacagccttccataattgatacgaaagcagttggaccttctgctttg
ggttctggtaagcgggtcgaatttttcaatttctgggaaggagatatcgactactgcacgatcgctgatcggatc
tggttgatcatttctggtaagcgggtgcaatgtttgtggcccaaatactatatcaacaaaaggggcacgttcacgg
atatgttcaccttcttgtgaagcaacacagccaccaacgccaataattaaatcgggtttgtcctttttccagttt
ttccaacgaccaagttgtgaaaagactttttcttgtgctttttcacgaattgagcaagtattcaataataaaaata
tccgcttcttcagggttatcgggttaattctaatacgtgtgttgagtttaagagatctgccatttttgatgagtca
tactcattcatttggcaaccccaagttgtgatatgtaattttgccataattttcaaaaaataataaatatctcaa
taagttaaaataaaaagcgtaaaagagacagttccctttacgcacctttaatcgtgctattctacctgtttgcttat
tttttcgctagagttaatcgcttaataagcaaaaatgccacgatattgctagcgtgacatttttatcatgagaggat
gttattgtttgggttaagggtcaatacaacactttcacccggcaacaacatttccaacttttt

SEQ ID NO. 455 *Vibrio parahaemolyticus*

Aggacgcgctttacgtagtttacggatgatcgacttgactcgatagctgtgtgaggacgcttcatcatcgttag
aatacggtcactaccactttgtactggcagggtgtaggaaactcacaagctccgggggtatcttcgtaaacccgcgat
gatgtcgtctgtaaaactctagcgggtggctagtcgtgaaacgaatacggtcgataccatcgatagatgcaacgag
acgaagcagttcagcaaaaagagcagatctcgccgctcgtgcatagggcccacgggtatgcgtttacgttttgacctag
taggttaacttcacgtacaccttgttccgctagctgtgcaatctcgaataacacgtcatccattggacgactaac
ttcttcaccacgagtgatggtacaacgcagtaagtgcagtattttgaacagccttccatgatagaaacaaacgc
cgtcgcaccttctgcacgtggctcaggtagggcgggtcgaacttttcaatctctgggaacgaaatgtccattaccgg
tgcacgtcagtttgagattgtttgatcatctcaggtagggcgggtgcagagtttgaggggccaaagatcacgtcaac
gtatggtgcacgctcacggatgtggtcaccttcttgtgttgctacacaaccacctacaccgataactacgccagg
ttttttatcttttagtggtttccaacggcctagctgggtggaaaactttctcttgccgtttttcacggatcgaaac
gggtgtaagtagaagtagctctgcttccctcgtgcttccgtcagctcatagccgtttgcagcattaagcaggtc
ggccatttttgatgaatcgatttcgttcatctggcagccccagggttttaattagcagtttcttactcatctcact
ttcgtcgttcagttgtacttaaaattggagagctattgctcaaattatagccgocatcacggcggtaagcggcgt
attgtactgctttaaaaagcacctgactagtgatctgacgaattctctgcaaacctgatgaaatctagtttttt
gccctatatacagcaagggttttttggttaa

SEQ ID NO. 456 *Yersinia pestis*

gaatttaccaatcatgtcgggtgaacctcaaagttcacgcgcgggtgttttccgtacgcccggccagttccat
gacatttttgcgagaggtaccctccacaaaacacgctgtactgtccctaccatcttacggctaatttccatcgc

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ctgttggttaaatgcgttggtgcaggatatgtagccgctgttttttctcctcttcggacacattgttggttaaatac
agccgctggtgtgccgggacgcggggagtaaataaagctgtagctgggtatcaaaatgaatatctgcgaccagttt
catggtctgttcaaaatcctgctgggtttcaccaggaagccgacaataaaatcagaacttatctggatatcagg
gcgtgcttgacgcagtttgcggtgatggctttgtattccaaggcggtatgggcacgcttcatcatggtcaaaat
acggtcagaaccgctttgtaccggcaaatgcaggaagctcaccaattcaggcggtatcgcgataaacatcaatgat
atcgctcagtaaactcaatggggtggctggtggttaaactcgtaacctatcgataccatcaatcgccgcaaccaaacg
caacagctcggcaaaactacagatatcgccatcgtaggttgccccgcggtaggcggttaacattctggccgagtaa
gttgacttcacgtacgccttgagcggctaactgggcgattttcaaaaagaatgtcatcgcttgacggctgacttc
ctcgcctcgggtgtagggtacgcacagaaatgtacaatatattattgcagccttccatgatcgaaacaaacgcagt
tgggccttcagcccggtgttctggcaaacggtcaaatttttcaatttcgggaaaactgatatccacgcacagggt
attcgttccttgacgtgggttaatcatttccggtaaacgatgcagcggtttgtggcccgaagatgacatcgacaca
gggggcgcgctggcgcaattgttcaccttctgtgacgccacgcaaccaccgaccccaataatcaactgcggggtt
tttctctttcaataatttccattgcccagcaggtgaatacttttctgtgcttttcccggtatagaacagggt
atttagcagcagtaaatacgccttcttccgggatgggtgggttaactggtagccatgggtactggccaagagatctgc
catttttagatgaatcgatttattcatctggcaacccaggttttgatatgcagtttttttagtcatcggttatt
catcatcaaaatcacctcgttccgtgcggtactcgggtgtggtagataatctccggtgtagtagagagtcgcaaa
ggcttcgtcggttagggagcattgtagtcatttgcctctgcgatgaccaccgcagaaccggttgagttattctgttg
agtataaaaaatccggttacactgcggttagacaaaaccttgctaattg

SEQ ID NO. 457 *Salmonella typhimurium*

gccgagcatacggcggtccatgccatcgctgctgattgatacgcctcttgcaaatatacagacgctgcttctt
ctcttcttccggcacgtcatcaaccatatcggcagccggcggttcccgacgcgcagagaagataaagctgtagct
catatcaaagttgacgtcagcgataagcttcatggtttttgcgaatcatcggtagtttccgagggaaatccgac
gataaagtcagagcttatctgaatgtccggccgcgcgcgcgcagtttacgggatgattgctttatatccagcgc
agtgtgggtgcgccccatcagattcaacacgcgatcggaaccgctctgtaccggcagatgcaggaaactgaccag
ttccggcggtatcgcggtatacctcgataatatcgtcgggtgaactcaatcggtatggctgggtggttaaagcgaatac
gtcaatgccgtcgatggcggaaccagacgcagcagatcggcaaggtagccggtgggtgccgtcgtagttttctcc
gcgccaggcggttaacgttctggcccagcaggttgacctcacgcacgccttgcgcgcgttaactgggcgatttcgaa
caggatatcgtctgagggacgggtgacttcttcaccgcgggtatacgggtaccacacagtaagtacaatatattatt
gcagccttccatgatagaaaacgaaagcgggtcgggccttctgcgcgcgggttccggcaaacggtcgaaacttctcgat
ttccgggaagctgatatcgaccaccgggtgcgggtcgccacgcacggagttaatcatctccggtaggcggtgtaa
ggtttgcgggcaaaaaataatgtcgacgtaatgggcgcgttgacgaatgtgctcgccttcttgggaagccacgca
gccgcccagcgcgataatcagatcgggatttttctcttttaacagtcctccagcgcacctaatgatggaagacttt
ttcttgagccttctcgcggattgagcaggtattcaacagcagcacatccgccttctccgccacgtcggtcagttg
atagccgtgggtggcgtccagcagatcggccatcttcgatgaatcgtaactcgttcatctgacagccccaggtttt
aatatggagtttttagtcatcgacttgctcttgcgaaatagtggtgaaaagcagggcgcatagtgtaatgctt
tggcgcgggttgtagccagtatgactgacgtcagccctaattgggtaaaaaatcctgtaaacttgctaaaaacgtaa
caggatgaatgaccatgacaaatcaaccaacggaaattgccattgtcggcgggggaatgggtcggcggcgcgctgg
cgctgggtctggcgagcaagggtttacgggtgatggtaataagaacatgccgcgcctgcgcggtttgtggcgga
gccagcctgacgtgc

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SEQ ID NO. 458 *Vibrio cholerae*

tcttcacttcttccgacagatcgcaaggatagtcagcggcggtgtgcctggacgaggtgagaaaaataaagctaa
agctcatgtcgaaatcgacatcgcgatcagcttcatggtgtcttggaatctttgtcggtttccctgggaagc
caacgataaaatcagagctgatttgaatatctggcggtgctttacgtagcttacggatgatggatttgtactcaa
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SEQ ID NO. 459 *Escherichia coli* K12

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SEQ ID NO. 460 *Escherichia coli* O157:H7

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SEQ ID NO. 461 *Pseudomonas aeruginosa*

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